

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 21:55:46 ; Search time 817 Seconds
(without alignments)
10895.563 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383
Sequence: 1 ggcctcaacagcagcacaag.....tcactgtgaccttgagaaga 1383

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb env:*
2: gb pat:*
3: gb ph:*
4: gb pl:*
5: gb pr:*
6: gb ro:*
7: gb sts:*
8: gb sy:*
9: gb un:*
10: gb vi:*
11: gb ov:*
12: gb htg:*
13: gb in:*
14: gb om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1383	100.0	1383	2	AR691934	AR691934 Sequence
2	1333.8	96.4	1708	5	HSU81379	UB1379 Homo sapien
3	1333.8	96.4	2139	5	BC009960	BC009960 Homo sapi
4	1333.8	96.4	3999	5	HS113RA1	Y09328 H.sapiens m
5	1333.8	96.4	4009	2	A63257	A63257 Sequence 3
6	1333.8	96.4	4038	2	AR541611	AR541611 Sequence
7	1333.8	96.4	4039	2	CQ894698	CQ894698 Sequence
8	1333.8	96.4	4039	2	AX335537	AX335537 Sequence
9	1333.8	96.4	4039	2	AX411212	AX411212 Sequence
10	1333.8	96.4	4039	2	HS113RA	Y10659 H.sapiens I
11	1333.8	96.4	11927	2	AR282860	AR282860 Sequence
12	1332.2	96.3	2153	5	BC015768	BC015768 Homo sapi
13	1330.6	94.3	1572	5	HSU62858	U62858 Human inter
14	1304.8	94.3	3960	5	AB209849	AB209849 Homo sapi
15	1262.8	89.4	3906	2	AY892945	AY892945 Synthetic
16	1236.8	85.7	3906	2	AX099392	AX099392 Sequence
17	1185	1260	5	AY312267	AY312267 Macaca fa	
18	1012	73.2	1547	2	AR483302	AR483302 Sequence

C	19	1012	73.2	1547	2	AR483303	AR483303 Sequence
C	20	1012	73.2	1547	2	AX280314	AX280314 Sequence
C	21	1012	73.2	1547	2	AX280316	AX280316 Sequence
C	22	1012	73.2	1547	14	AF314532	AF314532 Canis fam
C	23	1009.8	73.0	2382	2	BD231183	BD231183 Antagonis
C	24	1009.8	73.0	2382	2	CQ796435	CQ796435 Sequence
C	25	1009.8	73.0	2382	2	AR242285	AR242285 Sequence
C	26	1009.8	73.0	2382	2	AR703553	AR703553 Sequence
C	27	1009.8	73.0	2382	2	AX503605	AX503605 Sequence
C	28	995	71.9	1272	14	AY266142	AY266142 Sus scrof
C	29	988.4	71.5	1206	14	AY377582	AY377582 Ovis arie
C	30	983	71.1	1215	2	AR483304	AR483304 Sequence
C	31	983	71.1	1215	2	AR483305	AR483305 Sequence
C	32	983	71.1	1215	2	AX280317	AX280317 Sequence
C	33	983	71.1	1215	2	AX280318	AX280318 Sequence
C	34	959.4	69.4	2355	2	BD231182	BD231182 Antagonis
C	35	959.4	69.4	2355	2	CQ796433	CQ796433 Sequence
C	36	959.4	69.4	2355	2	AR242284	AR242284 Sequence
C	37	959.4	69.4	2355	2	AR703552	AR703552 Sequence
C	38	959.4	69.4	2355	2	AX503603	AX503603 Sequence
C	39	956.4	69.2	966	2	AR577151	AR577151 Sequence
C	40	956.4	69.2	966	2	AX280235	AX280235 Sequence
C	41	946.6	68.4	2331	2	CS162831	CS162831 Sequence
C	42	946.6	68.4	2331	2	CS162833	CS162833 Sequence
C	43	946.6	68.4	2331	2	CS162835	CS162835 Sequence
C	44	946.6	68.4	2331	2	CS162837	CS162837 Sequence
C	45	946.6	68.4	2331	2	CS162839	CS162839 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR691934 1383 bp DNA
DEFINITION Sequence 3 from patent US 6911530.
ACCESSION AR691934
VERSION AR691934.1 GI:74480011
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Willison,T., Nicola,N.A., Hilton,D.J., Metcalf,D. and Zhang,J.G.
TITLE Haemopoietin receptor and genetic sequences encoding same
JOURNAL Patent: US 6911530-A 3 28-JUN-2005;
Amrad Operations, Pty., Ltd., Richmond;
AUX;

FEATURES
source location/Qualifiers
1..1383
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1383; DB 2; Length 1383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTTAACACGACCAAGAGTTTAAACAGTCGCGCGGATTCGAGGCGAGAGGCTGC 60
DB 1 GAGCTTAACACGACCAAGAGTTTAAACAGTCGCGCGGATTCGAGGCGAGAGGCTGC 60
QY 61 ATGAGTGGCGCGCGGCTCTGCGGCGCTGTGGCGCTGCTGCTGCTGCGCGCGCGG 120
DB 61 ATGAGTGGCGCGCGGCTCTGCGGCGCTGTGGCGCTGCTGCTGCTGCGCGCGCGG 120
QY 121 GCGCGGCGCGCGCGCGCTTACGAAACTCAGCACTGTGACCAATTTGAGTGTCT 180
DB 121 GCGCGGCGCGCGCGCGCTTACGAAACTCAGCACTGTGACCAATTTGAGTGTCT 180
QY 181 GTTGAACCTCTGCAACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAAT 240
DB 181 GTTGAACCTCTGCAACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAAT 240

Db	134	CAGCCACCTGTGACAAATTTGAGTGTCTCTGTGTGAAAACCTTGCACAGTAATATGACA	193
OY	211	TGGAATCCACCCGAGGAGGCCAGCTCAATTTGTAGTCTATGTGTAATTTTATGATTTTGGC	270
Db	194	TGGAATCCACCCGAGGAGGCCAGCTCAATTTGTAGTCTATGTGTAATTTTATGATTTTGGC	253
OY	271	GACAAACAAAGATTAAGAAAATAGCTCCGGAACCTCGTCTGTCATATGAAAGTACCCCTGAAT	330
Db	254	GACAAACAAAGATTAAGAAAATAGCTCCGGAACCTCGTCTGTCATATGAAAGTACCCCTGAAT	313
OY	331	GAGAGGATTTTGTCTGCAAGTGGGGTCCAGTGTACCAACATGAGAGGAGAACCTTAGC	390
Db	314	GAGAGGATTTTGTCTGCAAGTGGGGTCCAGTGTACCAACATGAGAGGAGAACCTTAGC	373
OY	391	ATTTTGGTTGAAAAATGCACTCCACCCCGAGAGGTGATTCCTGAGTCTGCTGTGCTAAA	450
Db	374	ATTTTGGTTGAAAAATGCACTCCACCCCGAGAGGTGATTCCTGAGTCTGCTGTGCTAAG	433
OY	451	CTTCATGCAATTTGGCAACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAGGAAT	510
Db	434	CTTCATGCAATTTGGCAACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAGGAAT	493
OY	511	AACGATCCCGACACATACTATCTCTCATATTTGGGACAGAAAGCTTGGAAAAATTTAT	570
Db	494	AACGATCCCGACACATACTATCTCTCATATTTGGGACAGAAAGCTTGGAAAAATTTAT	553
OY	571	CAATGTGAAAAATCTTTTAGAAGAGGCCAATACTTGGTGTCTCTTGATCTGACAA	630
Db	554	CAATGTGAAAAATCTTTTAGAAGAGGCCAATACTTGGTGTCTCTTGATCTGACAA	613
OY	631	GTGAAGATTCACATTTTGAACAACAACAGTGTCCAAATATGTGTCAAGATATATGACAGA	690
Db	614	GTGAAGATTCACATTTTGAACAACAACAGTGTCCAAATATGTGTCAAGATATATGACAGA	673
OY	691	AAAAATTAACCATCTTCAATATATAGTGCCTTTAACTTCCGTTGMAACCTGATCTCCA	750
Db	674	AAAAATTAACCATCTTCAATATATAGTGCCTTTAACTTCCGTTGMAACCTGATCTCCA	733
OY	751	CATATTTAAAAACCTCTCCCTCCACAAATATGACCCATATGTGCAATGGGAATATCCAG	810
Db	734	CATATTTAAAAACCTCTCCCTCCACAAATATGACCCATATGTGCAATGGGAATATCCAG	793
OY	811	AATTTTATTAACAGATGCTATTTTATGAGTAGAAGTCAATTAACAGCCAACTGAGACA	870
Db	794	AATTTTATTAACAGATGCTATTTTATGAGTAGAAGTCAATTAACAGCCAACTGAGACA	853
OY	871	CATAATGTTTTCTACGTCCAAAGGCTAAATGTGGAATCCAGAAATTTGAGAGAAATGTG	930
Db	854	CATAATGTTTTCTACGTCCAAAGGCTAAATGTGGAATCCAGAAATTTGAGAGAAATGTG	913
OY	931	GAGAAATACATCTTGTTCATAGTCCCTGTGTGTCTTCTGATACTTTGAACAACGTGACA	990
Db	914	GAGAAATACATCTTGTTCATAGTCCCTGTGTGTCTTCTGATACTTTGAACAACGTGACA	973
OY	991	ATTAAGAGTCAAAACAAATATAGTTATGCTATGAGATGCAAACTCTGAGATATTTGAGC	1050
Db	974	ATTAAGAGTCAAAACAAATATAGTTATGCTATGAGATGCAAACTCTGAGATATTTGAGC	1033
OY	1051	CAAGAAATGAGTATGATGAGAGGCGCAATTCACACTCTACATTAACCATGTATCTCAT	1110
Db	1034	CAAGAAATGAGTATGATGAGAGGCGCAATTCACACTCTACATTAACCATGTATCTCAT	1093
OY	1111	GTTCCAGTCACTGCTGCGAGGTGCAATCATATGATCTCTGCTTTACCTTAAAAAGGCTCAG	1170
Db	1094	GTTCCAGTCACTGCTGCGAGGTGCAATCATATGATCTCTGCTTTACCTTAAAAAGGCTCAG	1153
OY	1171	ATTATTTATTTCCCTCCAAATTCCTGATCTGCGCAAGATTTTAAAGAAATGTTTGGAGAC	1230
Db	1154	ATTATTTATTTCCCTCCAAATTCCTGATCTGCGCAAGATTTTAAAGAAATGTTTGGAGAC	1213
OY	1231	CAGAATGATGATCTCTGCACTGGAAGAAGTACGACATCTATGAGAACCAACCAAGAG	1290

Db	121	CAGATATGATATGACTCTGCAGCTGGAGAAGAGTACGACATCTATGAGAAAGCAACCAAGAG	1273
Qy	1291	GAATCCGACTCTGTAGTGTGTGATGAAAGAAAGCTCTCACTGATGGAGATPA	1356
Db	1274	GAATCCGACTCTGTAGTGTGTGATGAAAGAAAGCTCTCACTGATGGAGATPA	1333
Qy	1351	TTTATTTTTCCTTCAGCTGTGACCTTGAGAGA	1383
Db	1334	TTTATTTTTCCTTCAGCTGTGACCTTGAGAGA	1366
RESULT 3			
LOCUS	BC009960	2139 bp	mRNA linear PRI 08-MAR-2005
DEFINITION	Homo sapiens interleukin 13 receptor, alpha 1, mRNA (cDNA clone		
ACCESSION	MGC:15228 IMAGE:4300487), complete cds.		
VERSION	BC009960		
KEYWORDS	BC009960.2	GI:39644647	
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
ORGANISM	Homidae; Homo.		
REFERENCE	1 (bases 1 to 2139)		
AUTHORS	Strassburg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shemen CM, Schuller GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bat NK, Hopkins RF, Jordan H, Moore T, Max ST, Wang J, Hsieh F, Diatchenko L, Marnitsina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo WF, Casavant TL, Scheetz TE, Brownstein MJ, Uebli TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loggellano NA, Peters CJ, Abramson RD, Mullaly SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SM, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GD, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butlerfield YS, Krzywinski MI, Skalska U, Smalins DE, Scherch A, Schein JE, Jones SJ and Marra MA.		
CONSTRM	Mammalian Gene Collection Program Team		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2139)		
AUTHORS	Director MGC Project.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Dec 9, 2003 this sequence version replaced gi:14602931.		
COMMENT	Contact: MGC help desk		
COMMENT	Email: gcgabs-remail.nih.gov		
COMMENT	Tissue Procurement: ATCC		
COMMENT	cDNA Library Preparation: Rubin Laboratory		
COMMENT	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)		
COMMENT	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)		
COMMENT	Galtherburg, Maryland;		
COMMENT	Web site: http://www.nisc.nih.gov/		
COMMENT	Contact: nisc_mgc@hgti.nih.gov		
COMMENT	Ahner, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Lega, R., Maduro, Q.L., Masello, C., Maketi, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stattin, P., Thomas, P., Touchman, J.W., Tsougen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		

AUTHORS	Miloux,B., Laurent,P., Bonnin,O., Lupker,J.J., Caput,D., Vltá,N. and Ferrara,P.
TITLE	Cloning of the human IL-13R alpha chain and reconstitution with the ILR alpha of a functional IL-4/IL-13 receptor complex
JOURNAL	FEMS Lett. 401 (2-3), 163-166 (1997)
PUBMED	9013879
REFERENCE	2 (bases 1 to 3999)
AUTHORS	Caput,D.
TITLE	Direct Submission
JOURNAL	Submitted (08-Nov-1996) D. Caput, SANOFI Recherche, BP 137, F-31676 Labège Cedex, FRANCE
FEATURES	
source	location/Qualifiers 1..3999
gene	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1..3999 /gene="IL13RA1"
CDS	34..1317 /gene="IL13RA1" /codon_start=1 /product="IL13 receptor alpha-1 chain" /protein_id="CAA70508.1" /db_xref="GI:1865308" /db_xref="GDB:P78552" /translation="MEMPARLCGLMALLLCGAGGGGGGAAPTEPOPVTNLSVENLCTVATWNPPEGASNSCSLMVFSHFGKODKIAPETRSELEVNLIRICLOVSQOSTNSEKPSILLVEKCISPDGPESAVTELCCIMNLSYMCSSMLPGSTBPDRNTTYMHRSLKEIKHCENIFREGQFSGSPULTKYDSSFEGHSVOIVKNDAKITRSFPIVLPTSRVKPDPPHIKNLSFNNDIIYVMENPNQISECLFEYEAVNNSOETHANVFVQEAKCENPEPERNVENTSCFMVPDLVDITNTYRIARVTKKLCEYDDKLSMSOESIGKKRNSTLYITMLLIIPVIIVAGAIIVALLTVRLKIIIPPIIDPKIKPRMFGDQNDDELHMKVDIIVEKQTRETDTSVVLIENLKKAQG" 3971..3976 polYA_signal /gene="IL13RA1"
ORIGIN	
Query Match	96.4%; Score 1333.8; DB 5; Length 3999;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 1348; Conservative	0; Mismatches 2; Indels 3; Gaps 1;
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Dc	7 CGGCCGGGCTCGAGCGAGAGGCTGCATGAGTGCCGCGCGCTCGCGGCTGTG 66
Dy	94 GCGCTGCTGCTCTGCGCGCGCGGGGCGGGGGCGGGCG--CGCGCTTAGCGAACT 150
Dz	67 GCCTGCTGCTCTGTGCGCGCGCGGGGCGGGGGCGCGCGCTTAAGCAACT 126
Oy	151 CAGCACCTGTGACAATAATTGAGTGTCTCTGTGAAAACCTCTGACAGTAATAAGACA 210
Ob	127 CAGCACCTGTGACAATAATTGAGTGTCTCTGTGAAAACTCTGACAGTAATAAGACA 186
Ov	211 TGGATCCACCAGGAGGAGAGCAGCTCAATTGTAGTCTATGGTATTTAGCATTTGGC 270
Dv	187 TGGATCCACCAGGAGGAGCAGCTCAATTGTAGTCTATGGTATTTAGCATTTGGC 246
Oy	271 GACAAACAGAATTAAGAAAATAGCTCCGAAAACCTGTCGTTCAATGAAGTACCCCCTGAT 330
Dv	247 GACAAACAGAATTAAGAAAATAGCTCCGAAAACCTGTCGTTCAATGAAGTACCCCCTGAT 306
Oy	331 GAGAGGATTTGTCGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAAGAAGCTTAGC 390
Dv	307 GAGAGGATTTGTCGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAAGAAGCTTAGC 366
Oy	391 ATTTGGTTGAAAAATGCATCTCAACCCACAGAAGGTGATCTGAGTCTGCTGTAGTAAA 450
Dv	367 ATTTGGTTGAAAAATGCATCTCAACCCACAGAAGGTGATCTGAGTCTGCTGTAGTAAA 426
Oy	451 CTTCATGCAATTTGGCAACAACCTTAGAGCTAATGAAGTGTCTTGAGCTCCCTGGAAGGAT 510
Dv	427 CTTCATGCAATTTGGCAACAACCTTAGAGCTAATGAAGTGTCTTGAGCTCCCTGGAAGGAT 486

QY	511	ACGAGTCCCGACACATACATACCTCTACACTTGGGACACAGAGCTGGAAAAATTCAT	570
Db	487	ACGAGTCCCGACACATACATACCTCTACACTTGGGACACAGAGCTGGAAAAATTCAT	546
QY	571	CAATGTGAAAACATCTTTAGAGAAAGGCCAATACCTTGGTGTCTCTTGTGATCTGACAA	630
Db	547	CAATGTGAAAACATCTTTAGAGAAAGGCCAATACCTTGGTGTCTCTTGTGATCTGACAA	606
QY	631	GTGAAGAGTTCCAGTTTGGAAACAACAGTGTCCAAATATATGTCACAGATATATGCACGA	690
Db	607	GTGAAGAGTTCCAGTTTGGAAACAACAGTGTCCAAATATATGTCACAGATATATGCACGA	666
QY	691	AAAAATTAACCATCCCTCAATATATAGTGCCTTAACTTCCGGTGTGAAACCTGATCTCCGA	750
Db	667	AAAAATTAACCATCCCTCAATATATAGTGCCTTAACTTCCGGTGTGAAACCTGATCTCCGA	726
QY	751	CATATTTAAAAAAGCTCTCCCTCCACACATGATGACCTATATGTGCAATGGAGAAATCCACAG	810
Db	727	CATATTTAAAAAAGCTCTCCCTCCACACATGATGACCTATATGTGCAATGGAGAAATCCACAG	786
QY	811	AATTTTATTAGCAGATGCTCTATTTTATGTAAGTAAAGTCAATTAACAGCCAAACTGACACA	870
Db	787	AATTTTATTAGCAGATGCTCTATTTTATGTAAGTAAAGTCAATTAACAGCCAAACTGACACA	846
QY	871	CATATGTTTTCTACGTCACAGAGGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG	930
Db	847	CATATGTTTTCTACGTCACAGAGGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG	906
QY	931	GAGAAATACATCTTGTTCATGAGTCCCTGGTGTCTTCTCTGATACCTTGAACACAGTCCAGA	990
Db	907	GAGAAATACATCTTGTTCATGAGTCCCTGGTGTCTTCTCTGATACCTTGAACACAGTCCAGA	966
QY	991	ATTAAGAGTCAAAACAATTAAGTTATGCTATGAGATGACAAACTCTGGAGTAAATTGGAGC	1056
Db	967	ATTAAGAGTCAAAACAATTAAGTTATGCTATGAGATGACAAACTCTGGAGTAAATTGGAGC	1026
QY	1051	CAAGAAATGATATAGGTAAAGGAAGCGCAATTCACACACTATACATTAACCATGTTACTATT	1110
Db	1027	CAAGAAATGATATAGGTAAAGGAAGCGCAATTCACACACTATACATTAACCATGTTACTATT	1086
QY	1111	GTTCCAGTCATCTGTGCGAGGTGCAATAGTACTCTCGTGTACTTAAAGAGCTCAAG	1170
Db	1087	GTTCCAGTCATCTGTGCGAGGTGCAATAGTACTCTCGTGTACTTAAAGAGCTCAAG	1146
QY	1171	ATTATTTATTTCCCTCCCAATTCCTGATCTTGGACAAATTTTAAAGAAATGTTTGGAGAC	1230
Db	1147	ATTATTTATTTCCCTCCCAATTCCTGATCTTGGACAAATTTTAAAGAAATGTTTGGAGAC	1206
QY	1231	CAGAAATATGATCTTCTGCACTGGAAAGATGACACATCTATATGAGAGCAAAACCAAGAG	1290
Db	1207	CAGAAATATGATCTTCTGCACTGGAAAGATGACACATCTATATGAGAGCAAAACCAAGAG	1266
QY	1291	GAAACCGACCTGTAGTGTGATGTAAGAAACCTGAAAGAAAGCCTCTCAGTATGAGATTA	1350
Db	1267	GAAACCGACCTGTAGTGTGATGTAAGAAACCTGAAAGAAAGCCTCTCAGTATGAGATTA	1326
QY	1351	TTTATTTTAACTTCACTGTGACCTTGAAGA	1383
Db	1327	TTTATTTTAACTTCACTGTGACCTTGAAGA	1359
RESULT 5			
LOCUS	A63257	4009 bp	DNA
DEFINITION	Sequence 3 from Patent WO9720926.	linear	PAT 12-MAR-1998
VERSION	A63257		
ACCESSION	A63257.1		
KEYWORDS	GI:3717098		
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	unclassified sequences.		
REFERENCE	1		

D	b		136	CAGCCACCTGTGACAAATTGGATGTCCTCTGTGAAAACCTTGCACGTATATGACA	195
O	y		211	TGGAATCCACCCGAGGAGCACCAGCTCAAAATGTGTATGTATTTTAGTCATTTTGCC	270
D	b		196	TGSAATCACCCGAGGAGCAGCTCAATTGTATGTATTTTAGTCATTTTGCC	255
O	y		271	GACCAACCAAGATTAAGAAAAATAGCTCCGAAAACCTGTCCTCATATGAATGCCCTGAT	330
D	b		256	GACCAACCAAGATTAAGAAAAATAGCTCCGAAAACCTGTCCTCATATGAAGTACCCCTGAT	315
O	y		331	GAGAGATTTGTCTGCAAGTGGGGGTCCAGGTATCACCAATGAGAAGGAGCGCTAGC	390
D	b		316	GAGAGATTTGTCTGCAAGTGGGGGTCCAGGTATCACCAATGAGAAGGAGCGCTAGC	375
O	y		391	ATTTTGGTTGAAAAATGCAATCTCACCCCCAGAGGTGATNCTGATCTGCTGTACTAA	450
D	b		376	ATTTTGGTTGAAAAATGCAATCTCACCCCCAGAGGTGATNCTGATCTGCTGTACTAG	435
O	y		451	CTTCATGCAATTTGGCACAACCTGAGCTAATGAAGTGTCTTGGCTCCCTGGAAAGAT	510
D	b		436	CTTCATGCAATTTGGCACAACCTGAGCTAATGAAGTGTCTTGGCTCCCTGGAAAGAT	495
O	y		511	ACCAATCCCGACACTATATCTCTACTATTTGGCACAGAAAGCTGGAAAAATTCAT	570
D	b		496	ACCAATCCCGACACTATATCTCTACTATTTGGCACAGAAAGCTGGAAAAATTCAT	555
O	y		571	CAATGTGAAAAACATCTTAGAGAAAGGCCAATACTTTGGTTGTCCTTGATCTGACCAA	630
D	b		556	CAATGTGAAAAACATCTTAGAGAAAGGCCAATACTTTGGTTGTCCTTGATCTGACCAA	615
O	y		631	GTGAAGATTCGAGTTTTGAACAACACAGTGTCCAATATATGTTCAGAGATATGACGA	690
D	b		616	GTGAAGATTCGAGTTTTGAACAACACAGTGTCCAATATATGTTCAGAGATATGACGA	675
O	y		691	AAATTTAAACCATCCTTCAATATAGTGGCTTTAACTTCCGTGTGAACCTGATCTTCA	750
D	b		676	AAATTTAAACCATCCTTCAATATAGTGGCTTTAACTTCCGTGTGAACCTGATCTTCA	735
O	y		751	CATATTTAAAACTCTCCTCCACAAATGATGACCAATATGTGCAATGGGAATTCACAG	810
D	b		736	CATATTTAAAACTCTCCTCCACAAATGATGACCAATATGTGCAATGGGAATTCACAG	795
O	y		811	AATTTTATTAGCAGATGCCATTTTATGATAGATGAAATCAATPACGCCAACCTGACACA	870
D	b		796	AATTTTATTAGCAGATGCCATTTTATGATAGATGAAATCAATPACGCCAACCTGACACA	855
O	y		871	CATAATGTTTTCTACGTCCAAAGAGCTTAATGTGGAATCCAGATTTGAGAGAAATGTG	930
D	b		856	CATAATGTTTTCTACGTCCAAAGAGCTTAATGTGGAATCCAGATTTGAGAGAAATGTG	915
O	y		931	GAGAAATCATCTGTTTCATAGTGCCTCCGTGTGTCTTCTGATATCTTTGAACAACAGTCA	990
D	b		916	GAGAAATCATCTGTTTCATAGTGCCTCCGTGTGTCTTCTGATATCTTTGAACAACAGTCA	975
O	y		991	ATAAGAGTCAAAACAATPAGTTTATGATAGAGTGAACAACCTCGAGTAATTTGAGC	1050
D	b		976	ATAAGAGTCAAAACAATPAGTTTATGATAGAGTGAACAACCTCGAGTAATTTGAGC	1035
O	y		1051	CAAGAAATGAGTATAGTTAGAAAGCGCAATTCACAACCTTACATPAACCATGTATCTATT	1110
D	b		1036	CAAGAAATGAGTATAGTTAGAAAGCGCAATTCACAACCTTACATPAACCATGTATCTATT	1095
O	y		1111	GTTCCAGTCACTGTGCGAGGTGCAATCTATATCTCCGTGCTTACCTPAAAAAGCTCAG	1170
D	b		1096	GTTCCAGTCACTGTGCGAGGTGCAATCTATATCTCCGTGCTTACCTPAAAAAGCTCAG	1155
O	y		1171	ATTATATATATTCCTTCAATTCCTGATCTTGCAAGATTTTAAAGAAATGTTTGGAAC	1230
D	b		1156	ATTATATATATTCCTTCAATTCCTGATCTTGCAAGATTTTAAAGAAATGTTTGGAAC	1215
O	y		1231	CAGATGATGATCTCTGCACTGGAGAAGTACGACATCTATGAGAGCAAAACCAAGAG	1290

Df		1216	CAGAAATGATGA	TGTA	CTGTGCACATGGGAAGA	GACATCAT	TATGAGAACCA	ACCAAGAG	1275
OY		1291	GAAA	CCGACTGT	AGTGTGCTGANTGAAAA	ACCCTGAAGAAC	CGTTCA	GTATGAGATAA	1350
Df		1276	GAAAC	CGCAGCTGT	AGTGCTGATGAGAAAA	CCTGAAGAAAG	CGCTTCAG	TATGAGATAA	1335
OY		1351	TTTTATTTT	TACTTCACTGTGAC	CTTTGAGAAGA	1383			
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LOCUS		CQ894698		4039 bp	DNA	linear	PAT 05-NOV-2004		
DEFINITION		Sequence 8 from Patent EP1471075.							
ACCESSION		CQ894698							
VERSION		CQ894698.1		GI:55467447					
KEYWORDS									
SOURCE									
ORGANISM		Homo sapiens (human)							
REFERENCE		Homo sapiens							
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.							
TITLE		Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Brumemendorf,T., Lichtner,R., Staub,E., Roepcke,S. and Li,X.I.							
JOURNAL		Human nucleic acid sequences expressed in pancreatic carcinomas Patient: EP 1471075-A 8 27-OCT-2004; Hitzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian (DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie (DE)							
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Query Match		96.4%; Score 1333.8; DB 2; Length 4039;							
Best Local Similarity		99.6%; Pred. No. 0;							
Matches 1348; Conservative		0; Mismatches 2; Indels 3; Gaps 1;							
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Df		77	GCCTGTGCTCTCTCGCGCGCGCGGGCGGGCGGGCGGGCGCGCGCTTAGGAAACT	136					
OY		151	CAGCCACTGTGACAAATTTGAGTGTCTCTGTGAAACCTCTGCACAGTAATATGACA	210					
Df		137	CAGCCACTGTGACAAATTTGAGTGTCTCTGTGAAACCTCTGCACAGTAATATGACA	196					
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Df		197	TGGAATCCACCCGAGGAGCACGTCAAATTTGATAGTATGATATTTTACTCATTTTGGC	256					
OY		271	GACAAACAAATAGCTCCGAAAACCTGTCTCAATAGAACTACCCCTGAAT	330					
Df		257	GACAAACAAATAGCTCCGAAAACCTGTCTCAATAGAACTACCCCTGAAT	316					
OY		331	GAGAGATTGTCTGCAAGTGGGTCCTCCAGTGAACCAATGAGAGTGAAGCCTAGC	390					
Df		317	GAGAGATTGTCTGCAAGTGGGTCCTCCAGTGAACCAATGAGAGTGAAGCCTAGC	376					
OY		391	ATTTTGTGAAAAATGCATCTCACCCCCAGAAAGTGATCTGAGTCTGTGACTGAA	450					
Df		377	ATTTTGTGAAAAATGCATCTCACCCCCAGAAAGTGATCTGAGTCTGTGACTGAG	436					
OY		451	CTTCAATGCAATTTGGCAACCTGAGATCAATGAAGTTCCTTGGCTCCTCGAAGAAT	510					
Df		437	CTTCAATGCAATTTGGCAACCTGAGATCAATGAAGTTCCTTGGCTCCTCGAAGAAT	496					

OY	51	ACGAGTCCGACACGTAACGTAATCTCTGTACTATATGGCACAGAAAGGCTGGAAAAATTCAT	570
Db	497	ACGAGTCCGACACGTAACGTAATCTCTGTACTATATGGCACAGAAAGGCTGGAAAAATTCAT	556
OY	571	CAATGTGAAAAATCTTTAGAGAAAGGCCAAATACTTTGGTGTGTTCTCTTGATCTGCACAA	630
Db	557	CAATGTGAAAAATCTTTAGAGAAAGGCCAAATACTTTGGTGTGTTCTCTTGATCTGCACAA	616
OY	631	GTGAAGGATTCACAGTTTGGAAACAACAAGTGTCCAAATPAAGGTCAAGATPATGACAGA	690
Db	617	GTGAAGGATTCACAGTTTGGAAACAACAAGTGTCCAAATPAAGGTCAAGATPATGACAGA	676
OY	691	AAAAATTAACCAATCCCTTCGAATATAGTGGCTTTAACTTCCCGGTGMAAAGCTGATCTCCA	750
Db	677	AAAAATTAACCAATCCCTTCGAATATAGTGGCTTTAACTTCCCGGTGMAAAGCTGATCTCCA	736
OY	751	CATATTAATAAACCTCTCTCTCCACATGATGACCTAATATGTGCAATGGAGATCCACAG	810
Db	737	CATATTAATAAACCTCTCTCTCCACATGATGACCTAATATGTGCAATGGAGATCCACAG	796
OY	811	AATTTATATAGCAGATGGCTATTTTATGAAAGAAAGCAATPAACGCCAAACTGACACA	870
Db	797	AATTTATATAGCAGATGGCTATTTTATGAAAGAAAGCAATPAACGCCAAACTGACACA	856
OY	871	CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG	930
Db	857	CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG	916
OY	931	GAGAAATACATCTGTGTTTCATAGTGTCCCTGGTGTCTTCTCGATACTTTGAACACACTGACA	990
Db	917	GAGAAATACATCTGTGTTTCATAGTGTCCCTGGTGTCTTCTCGATACTTTGAACACACTGACA	976
OY	991	ATTAAGAGTCAAAAACAATTAAGTTATAGCATAGAGATGACAACAATCTGAGATTAATGGAGC	1050
Db	977	ATTAAGAGTCAAAAACAATTAAGTTATAGCATAGAGATGACAACAATCTGAGATTAATGGAGC	1036
OY	1051	CAAGAAATGAGTATATGTTAAGAAGGCGAATTCACACTCTACATACCAATGTTACTCATTT	1110
Db	1037	CAAGAAATGAGTATATGTTAAGAAGGCGAATTCACACTCTACATACCAATGTTACTCATTT	1098
OY	1111	GTTCCAGTCACTGTGCGACAGGTGCATCATATGATACCTGCTTACTTAAAGAGCTCAAG	1170
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OY	1171	ATTATTAATATTCCTCCCAATTCCTGATCCTGCGACAAGATTTTTAAAGAAATGTTGAGAC	1230
Db	1157	ATTATTAATATTCCTCCCAATTCCTGATCCTGCGACAAGATTTTTAAAGAAATGTTGAGAC	1216
OY	1231	CAGATATGATGATACCTGTGACCTGGAAGAAAGTACGATCTATGAGAACCAACCAAGAG	1290
Db	1217	CAGATATGATGATACCTGTGACCTGGAAGAAAGTACGATCTATGAGAACCAACCAAGAG	1276
OY	1291	GAAGCCGACTCTGTAGTGTGATAGAAAAACCTGAAGAAAGCTCTCACTGATGAGATTA	1350
Db	1277	GAAGCCGACTCTGTAGTGTGATAGAAAAACCTGAAGAAAGCTCTCACTGATGAGATTA	1336
OY	1351	TTTATTTTACCTTACCTGTGACCTTGGAGAGA	1383
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[illegible]

[illegible][illegible]

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Db	1217	CAGATGATGATGATCTCTGCACTGGAGAAGTACGACATCTATGAGACCAACCAAGAG	1276
Qy	1291	GAACCCGACTCTGTGTGTGTGATTAAGAAACCTGAAGAAAGCCTCTCAGTGTGGAGATTA	1350
Db	1277	GAACCCGACTCTGTGTGTGTGATTAAGAAACCTGAAGAAAGCCTCTCAGTGTGGAGATTA	1336
Qy	1351	TTTATTTTACCTTCACTGTGACCTTGGAGAAGA	1383
Db	1337	TTTATTTTACCTTCACTGTGACCTTGGAGAAGA	1369
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DEFINITION	H.sapiens IL-13RA mRNA.		
ACCESSION	Y10659		
VERSION	Y10659.1 GI:1806035		
KEYWORDS	IL13Ra gene; interleukin-13.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Gauchat, J.F.M., Schlagenhaut, E., Feng, N.P., Moser, R., Yamae, M., Jeanm, P., Alouani, S., Elson, G., Notarangelo, L.D., Wells, T., Eugster, H.P. and Bonney, J.Y.		
TITLE	A novel 4 kb IL-13RA mRNA expressed in human B, T and endothelial cells, encoding for an alternate type two IL-4/IL-13R		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 4039)		
AUTHORS	Gauchat, J.F.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JAN-1997) J.F.M. Gauchat, Geneva Biomedical Research Institute, Immunology, Glaxo Research And Development, 14 Ch Des Aulx, Plan-les-Orates, CH1228, SWITZERLAND		
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	/db_xref="UniProtKB/Swiss-Prot:P78552"		
	/translation="MEMPARCGLMALILCGAGGGGGAAPTEPTPTNLISYVENLCATYIWNPEGASNSCSLPSFSGHKDKTAPETPRISIVPLNIRICLOVSGSCSTNSKRSILVERKISPEEDPSATVETLOCTAHNLSYKSCSLPERNSPDNYTLTYMRSLEKICOCENIFREBOYFGCSFDLTRKXSSFEQHSVQIMVKDNKAKIKPSFNIVPLISRKPDPIHKUSFHNDDLVOEMENPNIFSRCLFEVEVNNOSTETHNVEYVQAKCEKPERPERVENTSCFMVPGVLDLTNTVRAIVKTNKLCYEDDKCMBNNQDM SIGKRRSLKIVYIWMILIVPVIVAAIVLILLYLRKLIIIFPPIDPGKIFKMFQDQNDPLHWKLYDIYERKQTEEDSDVILLENKKASQ"		
gene			
CDS			

ORIGIN	Query Match:	96.4%	Score 1333.8	DB 5	Length 4039
	Best Local Similarity	99.6%	Prod. No. 0's		
	Matches 1348	Conservative	0	Mismatches 2	Indels 3; Gaps 1;
by	34	CGGCCGGTTCCGAGGCGAGGAGGCTGCATGAGTGC	CGCCGCGCGAGCTTCGCGGCTGTGG	93	

Db	17	CGCGCGGGGCTCCGAGGCGCAGAGGCTGCATGAGTGGCCGGCGGCGGCTCTGGCGGGCTGGG	76
Qy	94	GGCGTGTGCTCTGTGGCCGGCGGCGGGGGCGGGGGCGGGG---CGCGCTTACGGAACT	150
Db	77	GGCGTGTGCTCTGTGGCGGCGGCGGGGGCGGGGGCGGGGGCGCGCGCTTACGGAACT	136
Qy	151	CAGCCACTGTGACAAATTTGAGTGTCTGTGAAAACCTGTGCACAGTAATATGACA	210
Db	137	CAGCCACTGTGACAAATTTGAGTGTCTGTGAAAACCTGTGCACAGTAATATGACA	196
Qy	211	TGGAAATCCACCCGAGGAGGCCAGCTCAATTGTAGTCTATGTATTTTATGATTTTGGC	270
Db	197	TGGAAATCCACCCGAGGAGGCCAGCTCAAAATGTATGTATGTATTTTATGATTTTGGC	256
Qy	271	GACAAACAAGATTAAGAAATAGCTCCGAAAACCTGTCGTTCAATAGAGTACCCCTGAAT	330
Db	257	GACAAACAAGATTAAGAAATAGCTCCGAAAACCTGTCGTTCAATAGAGTACCCCTGAAT	316
Qy	331	GAGAGAAATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACATAGAGTGAAGAAGCTTAC	390
Db	317	GAGAGAAATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACATAGAGTGAAGAAGCTTAC	376
Qy	391	ATTTTGGTTGAAAAATGATCTCAACCCCGAAGGTATCTGTAGTCTGTGTGACTGAA	450
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Qy	451	CTTCAATGCAATTTGGCACAACCTGAGCTACATGAAATGTTCTTGGCTCCCTGGAAGAAAT	510
Db	437	CTTCAATGCAATTTGGCACAACCTGAGCTACATGAAATGTTCTTGGCTCCCTGGAAGAAAT	496
Qy	511	ACCAAGTCCCGACACTAACTATCTCTACTATTTGGCA CAGAAGCTTGAAAAAATTCAT	570
Db	497	ACCAAGTCCCGACACTAACTATCTCTACTATTTGGCA CAGAAGCTTGAAAAAATTCAT	556
Qy	571	CAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTTGGTGTCTCTTGATCTGACAAA	630
Db	557	CAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTTGGTGTCTCTTGATCTGACAAA	616
Qy	631	GTGAAGAAATTCAGTTTGAACAACAGAGTCCAAATTAATAGTCAAGGATTAATGACAGA	690
Db	617	GTGAAGAAATTCAGTTTGAACAACAGAGTCCAAATTAATAGTCAAGGATTAATGACAGA	676
Qy	691	AAATTAACACATCCTTCATATATAGTGCCTTAACTTCCGCTGAAACCTGATCTTCCA	750
Db	677	AAATTAACACATCCTTCATATATAGTGCCTTAACTTCCGCTGGAACCTGATCTTCCA	736
Qy	751	CATATTAATAAACTCTCTCTTCCACATGATGACTTATATGTGCATAGGAGAAATCCACAG	810
Db	737	CATATTAATAAACTCTCTCTTCCACATGATGACTTATATGTGCATAGGAGAAATCCACAG	796
Qy	811	AATTTTATTAAGATGCGCTATTTTATAGAAATTAAGACAAATTAACAGCCAACTGACACA	870
Db	797	AATTTTATTAAGATGCGCTATTTTATAGAAATTAAGACAAATTAACAGCCAACTGACACA	856
Qy	871	CATAATGTTTCTACGTCCAGAGGCTTAAATGTGAGAACTCAGAAATTTGAGAGAAATGTG	930
Db	857	CATAATGTTTCTACGTCCAGAGGCTTAAATGTGAGAACTCAGAAATTTGAGAGAAATGTG	916
Qy	931	GAGAAATACATCTTGTTCATGAGTCCCTGAGTTCCTGATTAATTTGAAACACAGTACA	990
Db	917	GAGAAATACATCTTGTTCATGAGTCCCTGAGTTCCTGATTAATTTGAAACACAGTACA	976
Qy	991	ATAAGAGTCAAAACAAATTAAGTATGTCTATAGAGATGACAAACTCTGAGATTAATTTGAGC	1050
Db	977	ATAAGAGTCAAAACAAATTAAGTATGTCTATAGAGATGACAAACTCTGAGATTAATTTGAGC	1036
Qy	1051	CAAGAAATAGATATGTATAGAGGACAAATCCACCTTACATTAACCATTTTACTCATTT	1110
Db	1037	CAAGAAATAGATATGTATAGAGGACAAATCCACCTTACATTAACCATTTTACTCATTT	1096
Qy	1111	GTTCAGTCACTGTGCGAGGTGCATCATATAGTACTCTCTGCTTTA CTTAAAAAGGCTCAG	1170

Db	1097	GTTCCAGTCATCGTGGCAGGTCGCATCATNAGTACTCTTGCTTTACCTTAATAAAGGTCAAG	1158
Oy	1171	ATTATTATATATTCCTCCCAATTCCTGATCCCTGGCAGAATTTTTAAAGAAATGTTGGAGAC	1230
Db	1157	ATTATTATATATTCCTCCCAATTCCTGATCCCTGGCAGAATTTTTAAAGAAATGTTGGAGAC	1216
Oy	1231	CAGATATGATGATCTCTGACCTCAGCTGGAAAAGTACGAATCTATATGAAACCAACCAAGAG	1290
Db	1217	CAGAAATGATGATCTCTGACCTCAGCTGGAAAAGTACGAATCTATGAAACCAACCAAGAG	1276
Oy	1291	GAACCCGACTCTGTAGTGTGCTATAGAAAACTGAAGAAAGCCTTCAGTATGAGATPA	1350
Db	1277	GAACCCGACTCTGTAGTGTGCTATAGAAAACTGAAGAAAGCCTTCAGTATGAGATPA	1336
Oy	1351	TTTATTTTATACCTTCACCTGACCTTGAAGAGA	1383
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LOCUS	Sequence 5 from patent US 6524792.		
DEFINITION	AR282860		
ACCESSION	AR282860.1 GI:29719662		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 11927)		?
AUTHORS	Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.		
TITLE	Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property		
JOURNAL	Patent: US 6524792-A 5 25-FEB-2003; Cyto Bioscience; Zurich-Schlieren;		
FEATURES	CHX:		
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Best Local Similarity	99.6%; Pred. No. 0;		
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Oy	94	GGCGTGTCTGTCTGCGCGCGCGCGGGGGCGGGGGCGGGGG---CGGGCCATAGGAAACT	150
Db	7719	GGCGTGTCTGTCTGCGCGCGCGCGGGGGCGGGGGCGGGGGCGGGCCATAGGAAACT	7778
Oy	151	CAGCACCTGTGACAATAATTGATGTCTCTGTGTGAACCTCTGCACAGTATATGACA	210
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Oy	211	TGGAATCCACCCGAGGGAGCCAGCTCAAAATTGTATGTATGTAATTTTAGTCATTTTGGC	270
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Oy	271	GACAAACAAGATTAAGAAATATAGCTCCGAAACTGGTGGTTCATATAGAAAGTACCCTGANT	330
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Db	7959	GAGAGGATTTGTCTGCAAAGTGCGGTCCAGTGTAGCAACAATGAGAGTGAAGACTTAGC	8018
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Qy	571	CAATGTGAAAACATCTTTAGAGAGGGCCAAATACCTTGGTGTGTCCCTTGATCTGACCAA	630
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Qy	691	AAAATTTAAACCATCTTCAATATATGAGCTTTAACTTCCGTGTGAAAACCTGATCTCCA	750
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Qy	931	GAGATTAATCTTGTTTCATGATGAGTCCCGTGTGTCTTCTGTATCTTTGAAACACAGTCAGA	990
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Qy	1291	GAAACCGACCTCTGATGCTGATATGAAAACTGAAAGAAAGCTCTCAAGTATGAGATTA	1350
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Db	8979	TTTATTTTACCTTCACTGTGACCTTGAAGAGA	9011
RESULT 12			
BC015768			
LOCUS			
DEFINITION Homo sapiens interleukin 13 receptor, alpha 1, mRNA (cDNA clone			
WGC:22204 IMAGE:4868206), complete cds.			
ACCESSION BC015768			

VERSION	KEYWORDS
BC015768.1	GI:16041774
SOURCE	ORGANISM
Homo sapiens (human)	
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	AUTHORS
1 (bases 1 to 2153)	
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Ditchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stiplston, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uceda, T.B., Tomiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Weller, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Scherchen, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
JOURNAL	REFERENCE
12477932	
2 (bases 1 to 2153)	
Strausberg, R.	Direct Submission
Submitted (09-OCT-2001)	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	COMMENT
	NIH-MGC Project URL: http://mgc.nci.nih.gov
	Contact: MGC help desk
	Email: cgapbs-remail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL)
	DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
	info@gscc.bc.ca
	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butlerfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Tekla Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Pirhlu, Parvaneh Saeedi, Jr Santos, Angelique Scherch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
	Series: IRAL Plate: 34 Row: k Column: 19
	This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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LOCUS AB209849
DEFINITION Homo sapiens mRNA for interleukin 13 receptor, alpha 1 precursor
variant protein.
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VERSION AB209849.1 GI:62089283
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
Ohara, O., Nagase, T. and F. Kikuno, R.
TITLE None Title
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 3960)
AUTHORS Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
Ohara, O., Nagase, T. and F. Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,

URL: <http://protein.gsc.riken.go.jp/>, Tel: 81-438-52-3930,
Fax: 81-438-52-3931)
COMMENT This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture
Sports, Science and Technology of Japan. Totoki Y., Toyoda A.,
Takeda T., Sakaki Y., Tanaka A., Yokoyama S., RIKEN Genomic Sciences
Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
e-mail: aktanaka@postman.riken.go.jp
URL: <http://protein.gsc.riken.go.jp/>.
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LOCUS AY892945
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ACCESSION AY892945
VERSION AY892945.1 GI:60654342
KEYWORDS Human ORF project.
SOURCE synthetic construct

ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1284)
AUTHORS Hines, L., Rolfe, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J., and LaBaer, J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1284)
AUTHORS Hines, L., Rolfe, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J., and LaBaer, J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 21:42:46 ; Search time 872 Seconds
(without alignments)
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1333.8	96.4	3999	10	AB297029	AB297029 Human nuc
5	1333.8	96.4	3999	11	ABD20878	ABD20878 Human pul
6	1333.8	96.4	4006	13	ACF87407	ACF87407 Human SIR
7	1333.8	96.4	4006	14	AEC15897	AEC15897 Human int
8	1333.8	96.4	4009	2	AAT85827	AAT85827 Human int
9	1333.8	96.4	4038	4	AAA86907	AAA86907 Human int
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11	1333.8	96.4	4038	12	ADN62574	ADN62574 Human int
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15	1333.8	96.4	4039	6	ABK84753	ABK84753 Human CDN
16	1333.8	96.4	4039	6	ABN97361	ABN97361 Gene #385
17	1333.8	96.4	4039	10	AB297030	AB297030 Human nuc
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19	1333.8	96.4	4039	12	ADL82842	ADL82842 Human PRO
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23	1333.8	96.4	4039	13	ADX97460	ADX97460 Pancreat
24	1333.8	96.4	4466	10	ADB47358	ADB47358 Human CDN
25	1333.8	96.4	11927	2	AAK77356	AAK77356 Polynucle
26	1333.8	96.4	11927	3	AAA90388	AAA90388 Plaemid p
27	1333.8	96.4	14978	3	AAA35216	AAA35216 Human ade
28	1333.8	96.4	14978	3	AAF21338	AAF21338 Human low
29	1333.8	96.4	14978	10	AB297032	AB297032 Human nuc
30	1333.8	96.4	14978	11	ABD20881	ABD20881 Human pul
31	1266.4	91.6	1284	14	ADV42774	ADV42774 Human psy
32	1264.8	91.5	1284	10	ADF17834	ADF17834 Human IL-
33	1238.4	89.5	3880	6	ABK35718	ABK35718 CDNA sequ
34	1236.8	89.4	3906	5	AAF98394	AAF98394 Human CDN
35	1181.4	85.4	1680	6	ABK35719	ABK35719 CDNA enco
36	1039.4	75.2	1389	12	ADO26893	ADO26893 CDNA enco
37	1012	73.2	1547	4	AA559955	AA559955 Canine in
38	1012	73.2	1547	4	AA559954	AA559954 Canine in
39	1009.8	73.0	2382	3	AAA09050	AAA09050 IL-13/IL-
40	1009.8	73.0	2382	10	AA637744	AA637744 Human IL-
41	983	71.1	1215	4	AA559957	AA559957 Canine in
42	983	71.1	1215	4	AA559956	AA559956 Canine in
43	959.4	69.4	2355	3	AAA09049	AAA09049 IL-13/IL-
44	959.4	69.4	2355	10	AA637743	AA637743 Human IL-
45	956.4	69.2	966	6	AA622979	AA622979 Human sol

ALIGNMENTS

RESULT 1

ID	AAT66165	standard; DNA, 1383 BP.
AC	AAT66165;	
DT	15-JUL-1997	(first entry)
XX		
DE	Human interleukin-12 receptor alpha chain NR4 DNA.	
XX		
KW	NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine;	
KW	allergy; aschma; therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	61..1341
FT		/*tag= a
FT	sig_peptide	61..141
FT		/*tag= b
FT	mat_peptide	142..1338
FT		/*tag= c
XX		
PN	W09715663-A1.	
XX		
XX	01-MAY-1997.	
PD		
XX		
PF	23-OCT-1996;	96WO-AU000668.
XX		
PR	23-OCT-1995;	95AU-00006135.
PR	22-DEC-1995;	95AU-00007276.
PR	09-SEP-1996;	96AU-00002208.
XX		
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.	
XX		
PI	Willson T, Nicola NA, Hilton DJ, Metcalfe D, Zhang JG;	
XX		
DR	WPI, 1997-259018/23.	
DR	P-PSDB; AAW09822.	
XX		
PT	DNA encoding animal haemopoietin receptor which interacts with	

PT interleukin-13 - useful to treat asthma, allergy or condition exacerbatd
XX by IgE production.
XX
XX Claim 6; Page 52-54; 93pb; English.
XX
CC DNA sequences (AA66164 and AA66165) respectively code for novel mouse
CC and human haemopoietin receptors (AA09821 and AA09822) designated NR4
CC that comprise the interleukin-13 (IL-13) receptor alpha-chain. A human
CC bone marrow cDNA library was screened with probes comprising nucleotides
CC 82-840 and 840-1270 of murine NR4 cDNA, and a composite sequence for
CC human NR4 was produced from isolated clones. The availability of genetic
CC sequences for NR4 permits the development of a range of agents capable of
CC modulating the activity of IL-13 and related cytokines such as
CC interleukin-4 for the treatment of allergy, asthma and other conditions
CC relating to IgE. The genetic sequences can also be used in prodn. of
CC recombinant NR4 or fusion proteins including NR4
XX
XX Sequence 1383 BP; 421 A; 292 C; 319 G; 351 T; 0 U; 0 Other:
SQ
Query Match 100.0%; Score 1383; DB 2; Length 1383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTTAACACGAGCAAGAGATTAAACAGTCGCGCGCGGTTCCGAGGCGAAGGCTGC 60
DB 1 GAGCTTAACACGAGCAAGAGATTAAACAGTCGCGCGCGGTTCCGAGGCGAAGGCTGC 60
QY 61 ATGAGATGCGCGCGCGCGCTCTCGGGGCTGTGGGCGCTGTGCTCTGCGCGCGCGGCGG 120
DB 61 ATGAGATGCGCGCGCGCGCTCTCGGGGCTGTGGGCGCTGTGCTCTGCGCGCGCGGCGG 120
QY 121 GCGCGGGCGGGGGCGCGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTCTCT 180
DB 121 GCGCGGGCGGGGGCGCGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTCTCT 180
QY 181 GTTGAACACCTCTGCAACAGTAATATGACATGGAATCCACCGAGGAGCCACTCAAT 240
DB 181 GTTGAACACCTCTGCAACAGTAATATGACATGGAATCCACCGAGGAGCCACTCAAT 240
QY 241 TGTAGTCTATGATGATTTTATGATCATTTTGGCGCAACAAAGATTAAGAAAATAGCTCGGAA 300
DB 241 TGTAGTCTATGATGATTTTATGATCATTTTGGCGCAACAAAGATTAAGAAAATAGCTCGGAA 300
QY 301 ACTGTCGTTCAATGAGAATGACCCCTGAATGAGAGATTGTGTGCAAGTGGGCTCCAG 360
DB 301 ACTGTCGTTCAATGAGAATGACCCCTGAATGAGAGATTGTGTGCAAGTGGGCTCCAG 360
QY 361 TGTAGACCAATGAGATGAGAGCCTAGATTTTGGTTGAAAATGCACTCAACCCCA 420
DB 361 TGTAGACCAATGAGATGAGAGCCTAGATTTTGGTTGAAAATGCACTCAACCCCA 420
QY 421 GAAGTGATCTGAGTCTGCTGACTGAACCTCAATGACTTTGGGCAACCTGAGCTAC 480
DB 421 GAAGTGATCTGAGTCTGCTGACTGAACCTCAATGACTTTGGGCAACCTGAGCTAC 480
QY 481 ATGAAAGTGTCTTGGCTCCCTGGAGAGAAATACCAAGTCCGACACTAATTAATCTCTAC 540
DB 481 ATGAAAGTGTCTTGGCTCCCTGGAGAGAAATACCAAGTCCGACACTAATTAATCTCTAC 540
QY 541 TATTTGGCAAGAGCCTGGAAGAAAATTTCAATATGGAAGAACTTTTAGAAGAGCCAA 600
DB 541 TATTTGGCAAGAGCCTGGAAGAAAATTTCAATATGGAAGAACTTTTAGAAGAGCCAA 600
QY 601 TACTTTGGTGTCTCTTTGATCTGACCAAGATGAGGATTCAGTTTGAACAACAGT 660
DB 601 TACTTTGGTGTCTCTTTGATCTGACCAAGATGAGGATTCAGTTTGAACAACAGT 660
QY 661 GTTCAAAATATATGCTCAAGATAATGACAGAAAATTAACCAATCTTCAATATAGTCT 720
DB 661 GTTCAAAATATATGCTCAAGATAATGACAGAAAATTAACCAATCTTCAATATAGTCT 720
QY 721 TTAACCTTCCGCTGAAACCTGATCTCTCAATTTAAAAAAGCTTCTTCCCAATGAT 780
DB 721 TTAACCTTCCGCTGAAACCTGATCTCTCAATTTAAAAAAGCTTCTTCCCAATGAT 780

DB 721 TTAACCTTCCGCTGAAACCTGATCTCTCAATTTAAAAAAGCTTCTTCCCAATGAT 780
QY 781 GACCTATATGTCGATGAGAGATCCACAGAAATTTTATAGAGATGCTTATTTATGA 840
DB 781 GACCTATATGTCGATGAGAGATCCACAGAAATTTTATAGAGATGCTTATTTATGA 840
QY 841 GTTGAAGTCAATTAACGCCAAACTGAGACATATGTTTCTAGCTCCAGAGGCTAA 900
DB 841 GTTGAAGTCAATTAACGCCAAACTGAGACATATGTTTCTAGCTCCAGAGGCTAA 900
QY 901 TGTGAAGATCCGAATTTGAGAAATGTGGAAATACATCTTGTTCATGCGCCCTGGT 960
DB 901 TGTGAAGATCCGAATTTGAGAAATGTGGAAATACATCTTGTTCATGCGCCCTGGT 960
QY 961 GTTCTTCTGATTAATTTGAACACAGTCAGAAATTAAGTCAAAACAAATTAATGCTAT 1020
DB 961 GTTCTTCTGATTAATTTGAACACAGTCAGAAATTAAGTCAAAACAAATTAATGCTAT 1020
QY 1021 GAGGATGACAACTCTGAGTAATTTGAGCCCAAGAAATGATATAGTAAGAGCCCAAT 1080
DB 1021 GAGGATGACAACTCTGAGTAATTTGAGCCCAAGAAATGATATAGTAAGAGCCCAAT 1080
QY 1081 TCCACACTCTACATTAACCAATGTTACTCATTTGTCAGATGTCGAGGTGCAATCAAT 1140
DB 1081 TCCACACTCTACATTAACCAATGTTACTCATTTGTCAGATGTCGAGGTGCAATCAAT 1140
QY 1141 GTACTCTCTTAACTTAAAGAGGCTCAAGATTAATATATTCCTTCAATTCCTGATCT 1200
DB 1141 GTACTCTCTTAACTTAAAGAGGCTCAAGATTAATATATTCCTTCAATTCCTGATCT 1200
QY 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTTGCATGGAAGAG 1260
DB 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTTGCATGGAAGAG 1260
QY 1261 TACGACATCTATGAGAGAGCAACCAAGAGAAACCGACTGTAGTGTGATAGAAAAC 1320
DB 1261 TACGACATCTATGAGAGAGCAACCAAGAGAAACCGACTGTAGTGTGATAGAAAAC 1320
QY 1321 CTGAAGAAAGCCTCTCAATGATGAGATATTTATTTTACCTTCACTGTGACCTTGAG 1380
DB 1321 CTGAAGAAAGCCTCTCAATGATGAGATATTTATTTTACCTTCACTGTGACCTTGAG 1380
QY 1381 AGA 1383
DB 1381 AGA 1383
RESULT 2
AAA35213
ID AAA35213 standard; DNA; 3999 BP.
XX
XX AAA35213;
AC
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO: 87.
XX
XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
PD
XX
PF 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX NYCE JW;
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
XX Disclosure; Page 1252-1253; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosolic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
XX Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
SQ
Query Match 96.4%; Score 1333.8; DB 3; Length 3999;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 34 CGGCCGGGTCGAGGCGAGAGGCTGATGAGTGCGCGGCGGCTCTGCGGGCTGG 93
DB 7 CGGCCGGGTCGAGGCGAGAGGCTGATGAGTGCGCGGCGGCTCTGCGGGCTGG 66
QY 94 GCGCTGCTGCTCTGCGCGCGCGCGGGGCGGGGGCGGGGCGGCGCTTACGGAAC 150
DB 67 GCGCTGCTGCTCTGCGCGCGCGGGGCGGGGGCGGGGCGGCGCTTACGGAAC 126
QY 151 CAGCGACCTGTGCAAAATTTGAGTGCTCTGTGAAACCTCTGCAAGATTAATGACA 210
DB 127 CAGCGACCTGTGCAAAATTTGAGTGCTCTGTGAAACCTCTGCAAGATTAATGACA 186
QY 211 TGGATTCACCCGAGGAGCGAGCTCAATTTGATGATGATTTTATGATTTTGGC 270
DB 187 TGGATTCACCCGAGGAGCGAGCTCAATTTGATGATGATTTTATGATTTTGGC 246
QY 271 GACAAACAAATTAAGAAATTAAGTCCGGAATCTGCTGTTCAATGAAGTCCCTGAT 330
DB 247 GACAAACAAATTAAGAAATTAAGTCCGGAATCTGCTGTTCAATGAAGTCCCTGAT 306
QY 331 GAGAGATTTGTCTGCAAGTGAGGCTCCAGTGATGACCAATGAGTGAAGCTTACG 390
DB 307 GAGAGATTTGTCTGCAAGTGAGGCTCCAGTGATGACCAATGAGTGAAGCTTACG 366
QY 391 ATTTGGTTGAAAAATGATCTCAACCCGAAAGGTGATCTGATGCTGTGACTGAA 450

DB 367 ATTTGGTTGAAAAATGATCTCAACCCGAAAGGTGATCTGATGCTGTGACTGAG 426
QY 451 CTTCAATGCAATTTGGGCAACCTGAGCTACATGAAGTCTTTGGCTCCCTGGAAGAT 510
DB 427 CTTCAATGCAATTTGGGCAACCTGAGCTACATGAAGTCTTTGGCTCCCTGGAAGAT 486
QY 511 ACCAGTCCCGACATTAATCTACTCTGATGATGAGGACAGAGCTGGAAAAATTCAT 570
DB 487 ACCAGTCCCGACATTAATCTACTCTGATGATGAGGACAGAGCTGGAAAAATTCAT 546
QY 571 CAATGTAAAAACATCTTTAGAGAAAGGCAATCTTTGGTGTCTTGTGATCTGACAAA 630
DB 547 CAATGTAAAAACATCTTTAGAGAAAGGCAATCTTTGGTGTCTTGTGATCTGACAAA 606
QY 631 GTGAAGATTCAGATTTGGAACCAACAGTGTCCAAATTAATGTCAGAGATTAATGACGA 690
DB 607 GTGAAGATTCAGATTTGGAACCAACAGTGTCCAAATTAATGTCAGAGATTAATGACGA 666
QY 691 AAATTTAAACCATCTTCAATATATGATGCTTTTACCTCCGTTGAAACCTGATCTTCA 750
DB 667 AAATTTAAACCATCTTCAATATATGATGCTTTTACCTCCGTTGAAACCTGATCTTCA 726
QY 751 CATATTAACCACTCTCTCTTCCACATGATGACCTATATGTCATGAGGAGATCCACAG 810
DB 727 CATATTAACCACTCTCTCTTCCACATGATGACCTATATGTCATGAGGAGATCCACAG 786
QY 811 AATTTTATGAGAGATGCTTATTTTATGAAATGATGAATGATTAACAGCAATGACGA 870
DB 787 AATTTTATGAGAGATGCTTATTTTATGAAATGATGAATGATTAACAGCAATGACGA 846
QY 871 CATATGTTTTCATACGTCGAAGAGGCTAAATGATGAGATCCAGATTTGAGAAATGTG 930
DB 847 CATATGTTTTCATACGTCGAAGAGGCTAAATGATGAGATCCAGATTTGAGAAATGTG 906
QY 931 GAGATATCATCTTGTTCATGATGCTCCGATGCTTCTCTGATTAACCAACAGTGA 990
DB 907 GAGATATCATCTTGTTCATGATGCTCCGATGCTTCTCTGATTAACCAACAGTGA 966
QY 991 ATTAAGATCAAAACAAATTAATGATGCTATGAGATGACAACTGTGAGTAATGAGC 1050
DB 967 ATTAAGATCAAAACAAATTAATGATGCTATGAGATGACAACTGTGAGTAATGAGC 1026
QY 1051 CAAAGAAATGATATGATGATGAAGCGCAATTCACATCTACATTAACCATTTCTCAT 1110
DB 1027 CAAAGAAATGATATGATGATGAAGCGCAATTCACATCTACATTAACCATTTCTCAT 1086
QY 1111 GTTCAAGTCACTGCTGAGGAGTGAATCATATGATCTCTGCTTTAAGCAAAAGCTCAAG 1170
DB 1087 GTTCAAGTCACTGCTGAGGAGTGAATCATATGATCTCTGCTTTAAGCAAAAGCTCAAG 1146
QY 1171 ATTATTAATTCCTCCCAATTCCTGATCTGAGCAAGATTTTAAAGAAATGTTTGAAC 1230
DB 1147 ATTATTAATTCCTCCCAATTCCTGATCTGAGCAAGATTTTAAAGAAATGTTTGAAC 1206
QY 1231 CAGAATGATATCTGCTGCACTGGAAGATTAAGCACTATGAGAGCAAAACCAAGAG 1290
DB 1207 CAGAATGATATCTGCTGCACTGGAAGATTAAGCACTATGAGAGCAAAACCAAGAG 1266
QY 1291 GAAACGACCTGATGATGCTGATGAAGAAACCTGAAGAAACCTCTCAGTATGAGATTA 1350
DB 1267 GAAACGACCTGATGATGCTGATGAAGAAACCTGAAGAAACCTCTCAGTATGAGATTA 1326
QY 1351 TTTATTTTACCTTCACTGATGACCTTGAAGA 1383
DB 1327 TTTATTTTACCTTCACTGATGACCTTGAAGA 1359
RESULT 3
AAFP21335
ID AAFP21335 standard; DNA; 3999 BP.
XX AAFP21335;
AC

XX		
DT	14-MAR-2001	(first entry)
XX		
DE	Human low adenosine antisense oligonucleotide related sequence #2902.	
XX		
KW	low adenosine antisense oligonucleotide; phosphorothioate; allergy;	
KM	human, airway disorder; bronchoconstriction; lung inflammation;	
KM	surfactant depletion; respiratory; bronchodilator; antiinflammation;	
KM	immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;	
KM	respiratory obstruction; pulmonary obstruction; impeded respiration;	
KM	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	
KM	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	
KM	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	
KM	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	
KM	cancer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20062736-A2.	
XX		
PD	26-OCT-2000.	
XX		
PF	24-MAR-2000; 2006MO-US008020.	
XX		
PR	06-APR-1999; 99US-0127958P.	
XX		
PA	(UYEC-) UNIV EAST CAROLINA.	
PA	(NYCE/) NYCE J W.	
XX		
P1	Nyce JW;	
DR	WPI; 2000-679539/66.	
XX		
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger	
PT	adenosine receptors during metabolism, useful e.g. for treating cancers	
PT	and respiratory obstructions.	
XX		
PS	Disclosure; Page 1336-1337; 1592pp; English.	
XX		
CC	The present invention describes low adenosine (A) content antisense	
CC	oligonucleotides and compositions (I) comprising them. In the antisense	
CC	oligonucleotides the A is replaced by a "Universal" or alternative base.	
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,	
CC	immunosuppressive, antisthmatic, hypotensive and cytostatic activities.	
CC	The antisense oligonucleotides and (I) can be used to down-regulate the	
CC	expression and/or activity of target polypeptides associated with	
CC	lung/respiratory disorders and malignancies, such as stimulating and	
CC	activating peptide factors and transmitters, transcription factors,	
CC	immunoglobulins and antibodies, antibody receptors, cytokines and	
CC	chemokines, endogenously produced specific and non-specific enzymes,	
CC	binding proteins, adhesion molecules and their receptors, cytokine and	
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central	
CC	nervous system (CNS) and peripheral nervous and non-nervous system	
CC	receptors, CNS and peripheral nervous and non-nervous system peptide	
CC	transmitters, defensins, growth factors, vasocactive peptides and	
CC	receptors, binding proteins and malignancy associated proteins. The	
CC	antisense oligonucleotides may be used in this way to treat disorders	
CC	including respiratory obstruction (especially pulmonary obstruction	
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or	
CC	surfactant hypoproduction which are associated with a disease or	
CC	condition selected from pulmonary vasocostriction, inflammation,	
CC	allergies, asthma, impeded respiration, respiratory distress syndrome	
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary	
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),	
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,	
CC	and/or cancer. AA18434 to AA21543 represent human polynucleotide	
CC	fragments and antisense oligonucleotides used in the exemplification of	
CC	the present invention	
XX		
Sequence	3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;	
Query Match	96.4%; Score 1333.8; DB 3; Length 3999;	
Best Local Similarity	99.6%; Pred No. 0;	

	Matches	1346:	Conservative	0:	Mismatches	2:	Indels	3:	Gaps	1:
OY	34	CGGCCGGGATTC	CCGAGCGAGAGGCTGCATGAGTGGCCGGCGCGGCTTCGCGGGCTGTGG	93						
Db	7	CGGCGGGGCTTC	CGAGGGGAGGCTGCATGAGTGGCCGGCGCGGCTTCGCGGGCTGTGG	66						
OY	94	GGCGTGTCTCT	CGCCGCGCGCGGGGGCGGGGGCGGGGG--CGCGCTTACGGAAACT	150						
Db	67	GGCGTGTCTCT	CGCGCGCGGGGGCGGGGGCGGGGGCGCGGGCGCGCTTACGGAAACT	126						
OY	151	CAGCCACCTTGACA	CAAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGTGACA	210						
Db	127	CAGCCACCTGTGACA	AAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGTGACA	186						
OY	211	TGGAATCCACC	CCGAGGAGCGAGCTCAAAATTTGATAGTATGTAATTTTATGCAATTTTGGC	270						
Db	187	TGGAATCCACC	CGAGGAGCGAGCTCAAAATTTGATAGTATGTAATTTTATGCAATTTTGGC	246						
OY	271	GACAAACAG	TTAAGAAATATAGCTCCGGAAACTGTGTTCATATGAAATATCCCTTAAT	330						
Db	247	GACAAACAG	TTAAGAAATATAGCTCCGGAAAACCTGTGTTCATATGAAATATCCCTTAAT	306						
OY	331	GAGAGGATTTGT	CTCGCAAGTGGGGTCCCACTGTATGACAACAATGAGATGTGAAGCCTAGC	390						
Db	307	GAGAGGATTTGT	CTCGCAAGTGGGGTCCCACTGTATGACAACAATGAGATGTGAAGCCTAGC	366						
OY	391	ATTTTGGTGG	AAAAATGCAATCTCACCCCCAGAAAGGTATCCTGAGTGTGCTGTGTAAGTAA	450						
Db	367	ATTTTGGTGG	AAAAATGCAATCTCACCCCCAGAAAGGTATCCTGAGTGTGCTGTGTAAGTAA	426						
OY	451	CTTCAATGCAT	TTTGGCAACAACCTGAGGTACATGAAGTGTTCCTTGGCTCCCTGGAAGGAAT	510						
Db	427	CTTCAATGCAT	TTTGGCAACAACCTGAGGTACATGAAGTGTTCCTTGGCTCCCTGGAAGGAAT	486						
OY	511	ACCGATCCCGCA	CACTAATCTATCTCTCTTACATATTTGGACAAGAAAGCCCTGGAATAATTCAT	570						
Db	487	ACCGATCCCGCA	CACTAATCTATCTCTCTTACATATTTGGACAAGAAAGCCCTGGAATAATTCAT	546						
OY	571	CAATGTAAAA	CAATCTTTAGAGAAAGCCCAATATCTTGGTGTCTCTTGTGATCTGCACAA	630						
Db	547	CAATGTAAAA	CAATCTTTAGAGAAAGCCCAATATCTTGGTGTCTCTTGTGATCTGCACAA	606						
OY	631	GTCGAGGATTC	CAATTTTGAACAACAACAGTGTCCAAATTAATGTCANAGATATATGCAGA	690						
Db	607	GTCGAGGATTC	CAATTTTGAACAACAACAAGTGTCCAAATTAATGTCANAGATATATGCAGA	666						
OY	691	AAAAATTA	ACATCTCTTCAATATATGTGTCCTTTAACTCCCGTGTGAAAACCTGATCTCTCA	750						
Db	667	AAAAATTA	ACATCTCTTCAATATATGTGTCCTTTAACTCCCGTGTGAAAACCTGATCTCTCA	726						
OY	751	CATATTTAAAA	CCCTCTCTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG	810						
Db	727	CATATTTAAAA	CCCTCTCTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG	786						
OY	811	AATTTTAT	TATGACAGATGCTATTTTATGAAGTGAAGATCAATTAACAGCCAAACTGAGACA	870						
Db	787	AATTTTAT	TATGACAGATGCTATTTTATGAAGTGAAGATCAATTAACAGCCAAACTGAGACA	846						
OY	871	CATAATGTTT	CTAAGCTCCAAAGGCTTAAATGTGAGATCCAGATATTTGAGACAAATGTG	930						
Db	847	CATAATGTTT	CTAAGCTCCAAAGGCTTAAATGTGAGATCCAGATATTTGAGACAAATGTG	906						
OY	931	GAGAAATCA	TCCTGTTCAATGTGCCCGGTGTTCTTCTGATACCTTTGAAACAACGTGAGA	990						
Db	907	GAGAAATCA	TCCTGTTCAATGTGCCCGGTGTTCTTCTGATACCTTTGAAACAACGTGAGA	966						
OY	991	ATAAGAGTCA	AAAAAATAATGTTATGCTATGAGGATGACAAACTCTGAGATATTTGAGC	1050						
Db	967	ATAAGAGTCA	AAAAAATAATGTTATGCTATGAGGATGACAAACTCTGAGATATTTGAGC	1026						
OY	1051	CAAGAAATGA	TATAGGTAAAGAACGCAATTTCCACACTTACATTAACCATGTATCTCATTT	1110						
Db	1027	CAAGAAATGA	TATAGGTAAAGAACGCAATTTCCACTTACATTAACCATGTATCTCATTT	1086						

QY 871 CATATGTTTCTAGCTCCAGAGGCTAAATGTGAGATCCGAATTTGAGAAATGTG 930
| | | | |
DB 847 CATATGTTTCTAGCTCCAGAGGCTAAATGTGAGATCCGAATTTGAGAAATGTG 906
| | | | |
QY 931 GGAATACACTCTGTTCAATGGTCCCTGGTCTTCCGATGATCTTGAACACAGTCAGA 990
| | | | |
DB 907 GGAATACACTCTGTTCAATGGTCCCTGGTCTTCCGATGATCTTGAACACAGTCAGA 966
| | | | |
QY 991 ATTAGAGTCAAAACAAATAGTTATGCTATGAGATGACAAACTGAGTAATTTGGAGC 1050
| | | | |
DB 967 ATTAGAGTCAAAACAAATAGTTATGCTATGAGATGACAAACTGAGTAATTTGGAGC 1026
| | | | |
QY 1051 CAGAAGATGATAGTAAAGAGCCGAATTCACACTATCAATTAACCATGTTACTCAT 1110
| | | | |
DB 1027 CAGAAGATGATAGTAAAGAGCCGAATTCACACTATCAATTAACCATGTTACTCAT 1086
| | | | |
QY 1111 GTTCCGATCGTCCGAGGTGCAATCATGATCTCTGCTTTAACTTAAAGGCTCAAG 1170
| | | | |
DB 1087 GTTCCGATCGTCCGAGGTGCAATCATGATCTCTGCTTTAACTTAAAGGCTCAAG 1146
| | | | |
QY 1171 ATTATATATTCCTCCCAATTCCTGATTCCTGCAAGATTTTAAAGAAATGTTGGAGAC 1230
| | | | |
DB 1147 ATTATATATTCCTCCCAATTCCTGATTCCTGCAAGATTTTAAAGAAATGTTGGAGAC 1206
| | | | |
QY 1231 CAGATGATGATACCTGTGCACTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAG 1290
| | | | |
DB 1207 CAGATGATGATACCTGTGCACTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAG 1266
| | | | |
QY 1291 GAAACCGACTCTGTACTGCTGATGATGAAACCTGGAAGAAAGCTCTGATGATGAGATGA 1350
| | | | |
DB 1267 GAAACCGACTCTGTACTGCTGATGATGAAACCTGGAAGAAAGCTCTGATGATGAGATGA 1326
| | | | |
QY 1351 TTTATTTTACCTTCACTGATGAGAGAGA 1383
| | | | |
DB 1327 TTTATTTTACCTTCACTGATGAGAGAGA 1359
| | | | |
RESULT 5
ABD20878
ID ABD20878 standard; DNA; 3999 BP.
XX
AC ABD20878;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #489.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX

PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12271; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antisthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
Query Match 96.4%; Score 1333.8; DB 11; Length 3999;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 34 CGGCGGGTTCCGAGGCGAGAGGCTGATGAGATGCGCGGCGGCTGCGGGGCTGTGG 93
| | | | |
DB 7 CGGCGGGCTCCGAGGCGAGAGGCTGATGAGATGCGCGGCGGCTGCGGGGCTGTGG 66
| | | | |
QY 94 GCGCTGCTGCTGCGCGCGCGCGGGGCGGGGCGGGGG--CGCGCTACGGAAC 150
| | | | |
DB 67 GCGCTGCTGCTGCGCGCGCGGGGCGGGGCGGGGGCGCGCGCTACGGAAC 126
| | | | |
QY 151 CAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAACCTCTGCACAGTAATATGACA 210
| | | | |
DB 127 CAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAACCTCTGCACAGTAATATGACA 186
| | | | |
QY 211 TGGATTCACCCGAGGAGCGAGCTCAATATGATCTATGATTTTATGCTTTTGGC 270
| | | | |
DB 187 TGGATTCACCCGAGGAGCGAGCTCAATATGATCTATGATTTTATGCTTTTGGC 246
| | | | |
QY 271 GACAAACAGATTAAGAAAATAGCTCCGAAACCTGCTGTTCAATAGAACTACCTGTAAT 330
| | | | |
DB 247 GACAAACAGATTAAGAAAATAGCTCCGAAACCTGCTGTTCAATAGAACTACCTGTAAT 306
| | | | |
QY 331 GAGAGATTTGTTGCAAGTGGGCTCCAGTGTAGACCAATAGAGTGAAGAGCTAGC 390
| | | | |
DB 307 GAGAGATTTGTTGCAAGTGGGCTCCAGTGTAGACCAATAGAGTGAAGAGCTAGC 366
| | | | |
QY 391 ATTTGGTTGAAAAAATGCAATTCACCCGAGAAAGATTCCTGAGCTGTGTCAGTAA 450
| | | | |
DB 367 ATTTGGTTGAAAAAATGCAATTCACCCGAGAAAGATTCCTGAGCTGTGTCAGTAA 426
| | | | |
QY 451 CTTCAATGATTTTGCAACAACCTGAGCTACATGAAGTGTCTTGCTCCCTGGAAGAAAT 510
| | | | |

Db 257 GACAAACAAAGATAGAAAAATAGCTCCGAAACCTGCTTCAATAGAAAGTACCCTGAAT 316
331 GAGAGATTGTTGTCGAAAGGGGTCCTCAGTAGAGCCAAATGAGAGTGAAGCCTAGC 390
Db 317 GAGAGATTGTTGTCGAAAGGGGTCCTCAGTAGAGCCAAATGAGAGTGAAGCCTAGC 376
391 ATTTGGTTGAAAAATGCAATCTCACCCCGAAGGGTATCTGAGTCTGCTGACTGAA 450
377 ATTTGGTTGAAAAATGCAATCTCACCCCGAAGGGTATCTGAGTCTGCTGACTGAG 436
451 CTTCATGAGATTGGACAACTGAGCTACATGAGGTTCTTGGCTCCCTGGAAGGAAT 510
437 CTTCATGAGATTGGACAACTGAGCTACATGAGGTTCTTGGCTCCCTGGAAGGAAT 496
511 ACCAGTCCGACACTATCTCTCTACTATTTGGACAGAGACCTGAAAAAATTCAT 570
497 ACCAGTCCGACACTATCTCTCTACTATTTGGACAGAGACCTGAAAAAATTCAT 556
571 CAATGAAAAACATCTTTAGAGAGGCCAATACCTTGGTTGTTCTTTGATCTGACCAA 630
557 CAATGAAAAACATCTTTAGAGAGGCCAATACCTTGGTTGTTCTTTGATCTGACCAA 616
631 GTGAGAGATTCCAGTTTGAACAACACAGTGTCCAAATATGTCGAAGATTAATGACGA 650
617 GTGAGAGATTCCAGTTTGAACAACACAGTGTCCAAATATGTCGAAGATTAATGACGA 676
691 AAAATTAACCATCTTCAATATAGTAGCTTAATCTCCCGTGGAAACCTGATCCCTCA 750
677 AAAATTAACCATCTTCAATATAGTAGCTTAATCTCCCGTGGAAACCTGATCCCTCA 736
751 CATATTAAAAACCTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810
737 CATATTAAAAACCTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 796
811 AATTTATATGAGAGATGCCATTTTATGAGTAGAAGTCAATAACGCCAAACTGAGACA 870
797 AATTTATATGAGAGATGCCATTTTATGAGTAGAAGTCAATAACGCCAAACTGAGACA 856
871 CATATGTTTTTACAGTCCCAAGAGGCTAATGTGAGAAATCAGAAATTTGAGAGAAATGTG 930
857 CATATGTTTTTACAGTCCCAAGAGGCTAATGTGAGAAATCAGAAATTTGAGAGAAATGTG 916
931 GAGAAATACATCTTGTTCATGTGCTCCGTGATCTTCTTCTGATATCTTTGAACACAGTCAGA 990
917 GAGAAATACATCTTGTTCATGTGCTCCGTGATCTTCTTCTGATATCTTTGAACACAGTCAGA 976
991 ATTAAGGTCAAAACAATAAGTTATGTATGAGATGACAAACTCTGAGATTAATGGAGC 1050
977 ATTAAGGTCAAAACAATAAGTTATGTATGAGATGACAAACTCTGAGATTAATGGAGC 1036
1051 CAAGAATGAGTATGAGTGAAGAGCGCAATTCACACTTACATTAACCATGTTACTATT 1110
1037 CAAGAATGAGTATGAGTGAAGAGCGCAATTCACACTTACATTAACCATGTTACTATT 1096
1111 GTTCCAGTATCGTCGAGGTGCAATCATAGTATCTCCGTTTAACTTAAAGGCTCAAG 1170
1097 GTTCCAGTATCGTCGAGGTGCAATCATAGTATCTCCGTTTAACTTAAAGGCTCAAG 1156
1171 ATTTATATATTCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAGAC 1230
1157 ATTTATATATTCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAGAC 1216
1231 CAGAATGAGTATCTCTGCACTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAG 1290
1217 CAGAATGAGTATCTCTGCACTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAG 1276
1291 GAAACCGACTCTGTAGTGTGATAGAAAACCTGAAAGAAACCTCTCATGTAGGAGATAA 1350
1277 GAAACCGACTCTGTAGTGTGATAGAAAACCTGAAAGAAACCTCTCATGTAGGAGATAA 1336
1351 TTTATTTTAACTTCACTGTGACCTTGAAGA 1383
|||||

Db 1337 TTTATTTTAACTTCACTGTGACCTTGAGAAGA 1369
RESULT 7
AECL5897
ID AECL5897 standard; RNA; 4006 BP.
XX
AC AECL5897;
XX
DT 20-OCT-2005 (first entry)
XX
DE Human interleukin-13 receptor alpha 1 (IL-13RA1) cDNA.
KW RNA interference; gene silencing; cancer; hyperproliferation; neoplasm;
KW cytostatic; viral infection; infection; virolysis; inflammation;
KW antiinflammatory; autoimmune disease; immune disorder; immunosuppressive;
KW pulmonary disease; respiratory disease; respiratory-gen.;
KW cardiovascular disease; cardiovascular-gen.; neurological disease;
KW neuroprotective; renal disease; endocrine disease; genitourinary disease;
KW nephrotropic; endocrine-gen.; liver disease; gastrointestinal disease;
KW hepatotropic; ocular disease; ophthalmological; reproductive disorder;
KW infertility; antiinfertility; gynecology and obstetrics; andrology;
KW mitochondrial disease; prion disease; degeneration;
KW interleukin-13 receptor alpha 1; IL-13 receptor alpha 1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 44..1327
FT /tag a
FT /product= "interleukin-13 receptor alpha 1 (IL-13RA1)"
XX
PD US2005182007-A1.
XX
18-AUG-2005.
XX
PF 20-AUG-2004; 2004US-00922675.
XX
18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 17-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 14-FEB-2003; 2003WO-US004566.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
PR 09-JUN-2004; 2004US-00863973.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L;
XX
DR WPI: 2005-581759/59.
XX
DR REFSQ; NM_001560.
XX

PT New chemically synthesized double stranded siRNA molecule that directs
PT cleavage of an interleukin-13 receptor (IL-13R) RNA via RNA interference,
PT useful in preparing a composition for treating e.g., inflammatory
PT disorders.

PS Claim 32; Page; 127pp; English.

XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of receptors for interleukin-
CC 13 (e.g., IL-13 receptor (IL-13R), IL-4 receptor (IL-4R) and IL-2
CC receptor gamma (IL-2RG)) by RNA interference. The invention also relates
CC to similar siRNAs which interfere with the expression of the ligands for
CC these receptors, namely IL-13 and IL-4. The siRNAs of the invention may or
CC may not comprise ribonucleotides, can contain deoxyribonucleotides, can
CC be chemically modified and may be double or single stranded. They further
CC comprise sense and antisense regions, or alternatively are assembled from
CC a sense oligonucleotide and an antisense oligonucleotide. Specifically,
CC the siRNAs include short interfering RNA (siRNA), double-stranded RNA,
CC micro-RNA (miRNA) and short hairpin RNA (shRNA). The invention also
CC relates to pharmaceutical compositions comprising an siRNA targeted to
CC human IL-13R (e.g., IL-13R alpha 1 (IL13RA1), see RefSeq accession number
CC NM 001560), IL-4R, IL-2RG, IL-4 or IL-13, especially the siRNAs shown in
CC AEC14082-AEC15892. The invention further discloses expression vectors and
CC host cells comprising an siRNA of the invention. The siRNAs exhibit
CC increased resistance to nuclease degradation compared to the prior art.
CC The siRNAs of the invention can be used to modulate expression of their
CC target genes in cells, tissue explants or organisms (e.g., by ex vivo
CC gene therapy), or in grafts and transplants for the treatment of a
CC variety of interleukin-related conditions. They may be used in the
CC treatment of cancers and other proliferative conditions, viral infection,
CC inflammatory conditions, autoimmune diseases, respiratory and pulmonary
CC diseases (e.g., asthma, chronic obstructive pulmonary disease (COPD),
CC allergies), cardiovascular diseases, neurological diseases, renal
CC diseases, ocular diseases, liver diseases, mitochondrial diseases,
CC endocrine diseases, prion diseases and reproduction-related conditions.
CC The siRNAs may also be used in drug screening, diagnosis, therapeutic
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents a cDNA
CC corresponding to human IL-13RA1 mRNA, which is specifically claimed as a
CC target for siRNAs of the invention. Note: The present sequence is not
CC shown in the specification, but was obtained from RefSeq accession number
CC NM 001560. Other sequence data for this patent is also available in
CC electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docid=20050182007.

XX Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Query Match 96.4%; Score 1333.8; DB 14; Length 4006;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 34 CGGCGGGGTTCCGAGGCGAGAGCTGATGAGTGCGCGGCGGCTCTGCGGGCTGTGG 93
DB 17 CGGCGGGGCTCCGAGGCGAGAGCTGATGAGTGCGCGGCGGCTCTGCGGGCTGTGG 76
QY 94 GCGCTGCTGCTCGCGCGCGCGCGGGGGCGGGGGCGGGGG--CGGCGCTACGGAAACT 150
DB 77 GCGCTGCTGCTCGCGCGCGCGCGGGGGCGGGGGCGGGGGCGCGCGCTACGGAAACT 136
QY 151 CAGCCACTGTGACCAATTGAGTGTCTGTTGAAAACTCTGCACAGTAATATGAGCA 210
DB 137 CAGCCACTGTGACCAATTGAGTGTCTGTTGAAAACTCTGCACAGTAATATGAGCA 196
QY 211 TGAATTCACCCGAGGAGCCAGCTCAAAATTTGATGTATGTTATTTAGCATTTTGGC 270
DB 197 TGAATTCACCCGAGGAGCCAGCTCAAAATTTGATGTATGTTATTTAGCATTTTGGC 256
QY 271 GACAAACAAGATAGAATAATAGCTCCGAAACTGTGTTCAATAGAAAGTACCCCTAAT 330
DB 257 GACAAACAAGATAGAATAATAGCTCCGAAACTGTGTTCAATAGAAAGTACCCCTAAT 316
QY 331 GAGAGATTTTGTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCCTTAGC 390

DB 317 GAGAGATTTTGTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCCTTAGC 376
QY 391 ATTTTGGTTGAAAAATGATCTCACCCCGAAGAGTATCTGTGATCTGTGATCTGAA 450
DB 377 ATTTTGGTTGAAAAATGATCTCACCCCGAAGAGTATCTGTGATCTGTGATCTGAA 436
QY 451 CTTCAATGATTTGGGCAACCTAGCTAGTACAGTGAAGTGTCTGTGGCTCCCTGGAAGAT 510
DB 437 CTTCAATGATTTGGGCAACCTAGCTAGTACAGTGAAGTGTCTGTGGCTCCCTGGAAGAT 496
QY 511 ACCAGTCCGACACTAATCTATCTCTACTATTGGCAAGAGCTGTGAAAAATTCAT 570
DB 497 ACCAGTCCGACACTAATCTATCTCTACTATTGGCAAGAGCTGTGAAAAATTCAT 556
QY 571 CAATGTAAAAATCTTTAGAGAAAGCCAAATCTTTGTGTTCTTCTTGTATCTGACAA 630
DB 557 CAATGTAAAAATCTTTAGAGAAAGCCAAATCTTTGTGTTCTTCTTGTATCTGACAA 616
QY 631 GTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 690
DB 617 GTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 676
QY 691 AAAATTAACCATCTTCAATATATAGTGTCTTAACTTCCGTTGAAACCTGATCTCCA 750
DB 677 AAAATTAACCATCTTCAATATATAGTGTCTTAACTTCCGTTGAAACCTGATCTCCA 736
QY 751 CATATTAAAACTCTCTCCACATGATGATCACTATATGTGCAATGGAGAAATCCACAG 810
DB 737 CATATTAAAACTCTCTCCACATGATGATCACTATATGTGCAATGGAGAAATCCACAG 796
QY 811 AATTTTATGAGATGCGCTATTTTATGAGTATGATGATCACTATGAGTATGAGTATG 870
DB 797 AATTTTATGAGATGCGCTATTTTATGAGTATGATGATCACTATGAGTATGAGTATG 856
QY 871 CATATGTTTCTACGTCCAAAGAGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG 930
DB 857 CATATGTTTCTACGTCCAAAGAGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG 916
QY 931 GAGATATCATCTGTTTCAATGATGTCCTGTTGTTCTTCTGATCTTTGAACACAGTCA 990
DB 917 GAGATATCATCTGTTTCAATGATGTCCTGTTGTTCTTCTGATCTTTGAACACAGTCA 976
QY 991 ATTAAGATCAAAACAATAATGATATGATGATGATGATGATGATGATGATGATGATG 1050
DB 977 ATTAAGATCAAAACAATAATGATATGATGATGATGATGATGATGATGATGATGATG 1036
QY 1051 CAAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1110
DB 1037 CAAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
QY 1097 GTTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1156
DB 1171 GTTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1230
QY 1157 GTTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1216
DB 1231 CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1290
QY 1217 CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1276
DB 1291 GAAACGATCTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1350
QY 1277 GAAACGATCTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
DB 1351 TTTATTTTACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
QY 1337 TTTATTTTACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369

RESULT 8

AA85827
ID AA85827 standard; DNA; 4009 BP.
XX
AC AA85827;
XX
DT 22-JUN-1998 (first entry)
XX
DE Human interleukin-13 alpha receptor DNA.
XX
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..1317
FT /*tag= a
FT /product= "IL-13_alpha_receptor"
XX
PN MO9720926-A1.
XX
PD 12-JUN-1997.
XX
PF 07-NOV-1996; 96MO-FR001756.
XX
PR 06-DEC-1995; 95FR-00014424.
XX
PA (SNF1) SANOFI SA.
XX
PI Caput D, Petrara P, Laurent P, Vltta N;
XX
DR WPI; 1997-319773/29.
XX
DR P-BSDB; AAMW4973.
XX
PT New purified human interleukin-13 receptors - and related nucleic acids,
PT useful for diagnosis and treatment of inflammation, allergy, etc.
XX
PS Claim 12; Page 44-45; 83pp; French.
XX
CC This sequence encodes human interleukin-13 (IL-13) alpha receptor. The
CC invention relates to new purified peptides comprising 380 or 427 amino
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC affinity, but acquires high affinity when associated with the IL-4
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC diagnostic probes to identify aberrant synthesis or genetic anomalies
CC such as loss of heterozygosity and rearrangements, or chromosomal
CC anomalies. They are also used for production of recombinant IL-13R beta
CC and alpha which can be used as IL-13 antagonists, specifically to
CC regulate IL-13-induced responses for treatment of inflammation and
CC allergy. IL-13 receptors are also useful as antisense molecules for gene
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC immunosassays) to diagnose diseases associated with abnormal expression of
CC IL-13 receptors; when coupled to a toxin also for treatment of
CC overproduction of IL-13R. Cells that express IL-13R at the surface are
CC used to identify ligands and modulators of IL-13R
XX
SQ Sequence 4009 BP; 1137 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
Query Match 96.4%; Score 1333.8; DB 2; Length 4009;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 34 CGGCGGGGTTCCAGGCGAGGCTGATGAGTGGCGGGCGGCTCTGCGGGCTGTGG 93
DB 7 CGGCGGGGCTCCAGAGCGAGAGGCTGATGAGTGGCGGGCGGCTCTGCGGGCTGTGG 66
QY 94 GCGCTCTGCTGTGCGCGCGGCGGGGCGGGGCGGGGCGGCGGCTTACCGAAACT 150
DB 67 GCGCTCTGCTGTGCGCGCGGCGGGGCGGGGCGGGGCGGCGGCTTACCGAAACT 126
QY 151 CAGCCACTGTGACAAATTTGAGTGTCTCTTTGAAAACCTTGCACAGTAATTTGACA 210
|||||

DB 127 CAGCCACTGTGACAAATTTGAGTGTCTCTTTGAAAACCTTGCACAGTAATTTGACA 186
QY 211 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGAGTCTATGATTTTATGCTATTTGGC 270
DB 187 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGAGTCTATGATTTTATGCTATTTGGC 246
QY 271 GACAAACAAAGATTAAGAAATAGCTCCGAAACTCGTCTTCAATAGAAAGTACCCCTGAAT 330
DB 247 GACAAACAAAGATTAAGAAATAGCTCCGAAACTCGTCTTCAATAGAAAGTACCCCTGAAT 306
QY 331 GAGAGATTGTTGTGCAAGTGGGGTCCAGTGTAGGACCAATAGAGTGAAGGCTTACG 390
DB 307 GAGAGATTGTTGTGCAAGTGGGGTCCAGTGTAGGACCAATAGAGTGAAGGCTTACG 366
QY 391 ATTTGGTTGAAAATGCAATCTCACCCGAGAGGATGATCTGTGCTGTGACTGAA 450
DB 367 ATTTGGTTGAAAATGCAATCTCACCCGAGAGGATGATCTGTGCTGTGACTGAG 426
QY 451 CTTCATGCAATTTGGGACAACTGAGCTTACATGAAGTGTCTTGCTCCCTGGAGGAAT 510
DB 427 CTTCATGCAATTTGGGACAACTGAGCTTACATGAAGTGTCTTGCTCCCTGGAGGAAT 486
QY 511 ACCAGTCCCGACACTAATCTCTCTATTTGGACAGAAAGCCGGAATAATTCAT 570
DB 487 ACCAGTCCCGACACTAATCTCTCTATTTGGACAGAAAGCCGGAATAATTCAT 546
QY 571 CAATGTGAAAACATCTTTAGAGAGGCCAATATCTGTTGTTCTTGTATCTGACCAA 630
DB 547 CAATGTGAAAACATCTTTAGAGAGGCCAATATCTGTTGTTCTTGTATCTGACCAA 606
QY 631 GTGAAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATAGTCAAGATTAATGACAGA 690
DB 607 GTGAAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATAGTCAAGATTAATGACAGA 666
QY 691 AAAATTAACCAATCTTCAATATAGTGTCTTAACTCCGATGAAACCTGTATCTCCA 750
DB 667 AAAATTAACCAATCTTCAATATAGTGTCTTAACTCCGATGAAACCTGTATCTCCA 726
QY 751 CATATTAACCAATCTTCTCTTCCACAAATGATGACCTATATATGTAATGAGAAATCCACAG 810
DB 727 CATATTAACCAATCTTCTCTTCCACAAATGATGACCTATATATGTAATGAGAAATCCACAG 786
QY 811 AATTTTATTAAGCAGATGCTTATTTTGAAGTGAAGTCAATTAACGCCAACTGAGACA 870
DB 787 AATTTTATTAAGCAGATGCTTATTTTGAAGTGAAGTCAATTAACGCCAACTGAGACA 846
QY 871 CATATGTTTTTACGTCACAGAGGCTAAATGGAATCCAGAAATTTGAGAAATGTG 930
DB 847 CATATGTTTTTACGTCACAGAGGCTAAATGGAATCCAGAAATTTGAGAAATGTG 906
QY 931 GAGAAATACATCTTGTTCATGTGTCCTGTGTCTTCTGTATACCTTGAACACAGTCAGA 990
DB 907 GAGAAATACATCTTGTTCATGTGTCCTGTGTCTTCTGTATACCTTGAACACAGTCAGA 966
QY 991 ATTAAGTCAAAAACAAATTAATGTTATGCTATGAGATGACAAATCTGTGAGTAATTGGAGC 1050
DB 967 ATTAAGTCAAAAACAAATTAATGTTATGAGATGACAAATCTGTGAGTAATTGGAGC 1026
QY 1051 CAAAGAAATGATTAAGTAAAGAGGCAATTCACACTGTACATTAACATGTTACTCATTT 1110
DB 1027 CAAAGAAATGATTAAGTAAAGAGGCAATTCACACTGTACATTAACATGTTACTCATTT 1086
QY 1111 GTTCCAGTCATCGTCCAGGTGCAATCATAGTCTCTGTCTTACCTTAAAGGCTCAAG 1170
DB 1087 GTTCCAGTCATCGTCCAGGTGCAATCATAGTCTCTGTCTTACCTTAAAGGCTCAAG 1146
QY 1171 ATTATTAATTCCTTCCAAATTCCTGATTCCTGGCAAGATTTTAAAGAAATGTTTGGAGAC 1230
DB 1147 ATTATTAATTCCTTCCAAATTCCTGATTCCTGGCAAGATTTTAAAGAAATGTTTGGAGAC 1206
QY 1231 CAGAAATGATATCTGTGACCTGGAAGAGTGAAGATGATATGATGAAGCAACCAAGAG 1290
DB 1207 CAGAAATGATATCTGTGACCTGGAAGAGTGAAGATGATATGATGAAGCAACCAAGAG 1266
|||||

QY 1291 GAAACGACTCTGTAGTGTGATGAGAAACCTCTCAGTATGAGATAA 1350
DB 1267 GAAACGACTCTGTAGTGTGATGAGAAACCTCTCAGTATGAGATAA 1326
QY 1351 TTTATTTTTCCTTCACTGTGACCTTGAGAGA 1383
DB 1327 TTTATTTTTCCTTCACTGTGACCTTGAGAGA 1359

RESULT 9
AA88907
ID AAA88907 standard; cDNA; 4038 BP.
AC AAA88907;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human interleukin-13 receptor alpha-1 cDNA.
XX
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KM atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX dermatological; antiasthmatic; antiallergic; therapy; diagnosis; ss.
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 43..1326
FT sig_peptide 43..120
FT mat_peptide 121..1323
FT /*tag= b
FT /*tag= c
XX
PN US6143871-A.
XX
PD 07-NOV-2000.
XX
XX 12-NOV-1997; 97US-00969125.
PF
XX 13-DEC-1996; 96GB-00025899.
PR
XX
XX (GAUC/) GAUCHAT J.
PA (BONN/) BONNEFOY J.
XX
PI Gauchat J, Bonnefoy J;
XX
XX WPI; 2001-006445/01.
DR P-PSDB; AAB19807.
XX
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.
XX
XX Example 1; Fig 1A-B; 26pb; English.
PS
XX The present sequence is that of cDNA encoding a protein (see AAB19807)
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
CC 4 (IL-4) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR
CC primers (see AAA88908-10) were designed from expressed sequence tags
CC isolated from a database using mouse IL-13 receptor alpha. The primers
CC were used to amplify human IL-13 receptor cDNA from activated tonsillar B
CC cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10
CC library of activated tonsillar B cell cDNA and sequencing of the largest
CC cDNA insert provided the present sequence. This IL-13 receptor alpha-1
CC can be used to inhibit IL-13 or IL-4 induced IGE synthesis in B cells,
CC useful in the treatment of diseases where IGE or Th2 differentiation
CC plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma or AIDS. Antibodies raised against the polypeptide are useful for
CC detecting IL-13 and IL-4 receptor or parts of them which have been shed
CC from cells as a result of disease, e.g. cancer, leukaemia, atopy, atopic
CC dermatitis, allergies, rhinitis, eczema, asthma, AIDS, lupus
CC erythematosus, thyroiditis, diabetes, uveitis, dermatitis, psoriasis,

CC urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel
CC disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome and
CC toxoplasmosis
XX
SQ Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
Query Match 96.4%; Score 133.8; DB 4; Length 4038;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 34 CGGCCGGGTTCCGAGGCGAAGAGGTGATGAGTGGCCGCGGCTCTGCGGGCTGTG 93
DB 16 CGGCCGGGTTCCGAGGCGAAGAGGTGATGAGTGGCCGCGGCTCTGCGGGCTGTG 75
QY 94 GCGCTGTGCTCTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150
DB 76 GCGCTGTGCTCTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 135
QY 151 CAGCCACCTGTGACCAATTTGAGTGTCTGTGAAACCTCTGACACGTAATATGAGACA 210
DB 136 CAGCCACCTGTGACCAATTTGAGTGTCTGTGAAACCTCTGACACGTAATATGAGACA 195
QY 211 TGGATATCCACCGAGGAGCGACGCTCAATTTGATGTATGTATTTTACTATTTGGC 270
DB 196 TGGATATCCACCGAGGAGCGACGCTCAATTTGATGTATGTATTTTACTATTTGGC 255
QY 271 GACAAACAGATTAAGAAATAGCTCCGGAACCTGCTCATATGAAAGTACCCCTGAAT 330
DB 256 GACAAACAGATTAAGAAATAGCTCCGGAACCTGCTCATATGAAAGTACCCCTGAAT 315
QY 331 GAGAGATTTTGTCTGCAAGTGGGGTCCCACTGTAGACCAATGAGTGAAGACCTAGC 390
DB 316 GAGAGATTTTGTCTGCAAGTGGGGTCCCACTGTAGACCAATGAGTGAAGACCTAGC 375
QY 391 ATTTTGGTTGAAAAATGATCTCAACCCCGAAGAGTATCTGATCTGTGACTGAA 450
DB 376 ATTTTGGTTGAAAAATGATCTCAACCCCGAAGAGTATCTGATCTGTGACTGAG 435
QY 451 CTTCAATGCAATTTGGGACCAACCTGAGCTATAGTAAGTCTTGCGTCCCTGGAAGGAAT 510
DB 436 CTTCAATGCAATTTGGGACCAACCTGAGCTATAGTAAGTCTTGCGTCCCTGGAAGGAAT 495
QY 511 ACCAGTCCGACACTACTACTACTCTACTATTTGGACAGAAAGCTCGAAAAATTCAT 570
DB 496 ACCAGTCCGACACTACTACTACTCTACTATTTGGACAGAAAGCTCGAAAAATTCAT 555
QY 571 CAATGTGAAAAACATCTTTAGAGAAAGCAATACCTTTGTGTTCTTTGATCTGACCAA 630
DB 556 CAATGTGAAAAACATCTTTAGAGAAAGCAATACCTTTGTGTTCTTTGATCTGACCAA 615
QY 631 GTGAAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATGTGTCAAGATATGCGAGA 690
DB 616 GTGAAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATGTGTCAAGATATGCGAGA 675
QY 691 AAATTTAAACCAATCTTCAATATATAGTGCCTTTAACTCCCGTGTGAAACCTGATCTCCCA 750
DB 676 AAATTTAAACCAATCTTCAATATATAGTGCCTTTAACTCCCGTGTGAAACCTGATCTCCCA 735
QY 751 CATATTTAAACCTCTCTCTCCCAATATGATGACCTATATGTGAGAGAAATCCACAG 810
DB 736 CATATTTAAACCTCTCTCTCCCAATATGATGACCTATATGTGAGAGAAATCCACAG 795
QY 811 AATTTTATTTAGCAGATGCTTATTTTATGAAATGAAATCAATTAACGCCAACTGTAGACA 870
DB 796 AATTTTATTTAGCAGATGCTTATTTTATGAAATGAAATCAATTAACGCCAACTGTAGACA 855
QY 871 CATATGTTTTTCTACGTTCCAGAGGCTTAATGTGAGATTCAGAAATTTTGAGAAATGTG 930
DB 856 CATATGTTTTTCTACGTTCCAGAGGCTTAATGTGAGATTCAGAAATTTTGAGAAATGTG 915
QY 931 GAGAAATACATCTTTTTCATGTGCTCGTGTCTTCTCTGATATCTTTGAACACAGTCAGA 990
DB 916 GAGAAATACATCTTTTTCATGTGCTCGTGTCTTCTCTGATATCTTTGAACACAGTCAGA 975

QY 751 CATATTAACAACTCTCTCTCCACATGATGACCTATATGTGCAATGGAGAAATCCAG 810
 DB 736 CATATTAACAACTCTCTCTCCACATGATGACCTATATGTGCAATGGAGAAATCCAG 795
 QY 811 AATTTTATACAGATGCTTTTATGAGTAAAGTCAATTAACGCCAATCAGACA 870
 DB 796 AATTTTATGCAATGCTTTTATGAGTAAAGTCAATTAACGCCAATCAGACA 855
 QY 871 CATATGCTTTTCTAGTCCAGAGGCTTAATGTGGAATCCAGAAATTTGAGAAATG 930
 DB 856 CATATGCTTTTCTAGTCCAGAGGCTTAATGTGGAATCCAGAAATTTGAGAAATG 915
 QY 931 GAGAAATCATCTTTCTAGTCCAGAGGCTTTCTCTGATGATCTTTGAAACAGTCA 990
 DB 916 GAGAAATCATCTTTCTAGTCCAGAGGCTTTCTCTGATGATCTTTGAAACAGTCA 975
 QY 991 ATTAAGATCAAAACAAATTAAGTTATGCTATGAGATGACAAATCTTGAGTAATTGAGC 1050
 DB 976 ATTAAGATCAAAACAAATTAAGTTATGCTATGAGATGACAAATCTTGAGTAATTGAGC 1035
 QY 1051 CAAGAATGAGTATAGGTAAGAGGCAATCCACATCTATACCATGTTACTCAT 1110
 DB 1036 CAAGAATGAGTATAGGTAAGAGGCAATCCACATCTATACCATGTTACTCAT 1095
 QY 1111 GTTCCAGTCAATCTGCGAGGTGCAATGATGATCTCTGCTTTTAAAGGCTCAG 1170
 DB 1096 GTTCCAGTCAATCTGCGAGGTGCAATGATGATCTCTGCTTTTAAAGGCTCAG 1155
 QY 1171 ATTTTATTTCTCTCCATTTCTGATCTGCGCAAGTTTAAAGAAATGTTGAGAC 1230
 DB 1156 ATTTTATTTCTCTCCATTTCTGATCTGCGCAAGTTTAAAGAAATGTTGAGAC 1215
 QY 1231 CAGAAATGATGATCTCTGCACTGGAAGATGACATGATCTCTGCTTTTAAAGGCTCAG 1290
 DB 1216 CAGAAATGATGATCTCTGCACTGGAAGATGACATGATGATGAAAGCAACCAAGAG 1275
 QY 1291 GAAACCGACTCTGATGCTGATGAAAGCTGGAAGAGGCTCTGATGATGAGATTA 1350
 DB 1276 GAAACCGACTCTGATGCTGATGAAAGCTGGAAGAGGCTCTGATGATGAGATTA 1335
 QY 1351 TTTATTTTACCTTCACTGATGACCTTGAAGA 1383
 DB 1336 TTTATTTTACCTTCACTGATGACCTTGAAGA 1368

RESULT 11
 ID ADN62574 standard; cDNA; 4038 BP.
 XX ADN62574;
 AC XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human cDNA encoding interleukin 13 (IL-13) receptor alpha 1 chain.
 XX
 KW Human; ss; gene; interleukin 13 receptor alpha 1 chain; IL-13; IL-4;
 KW atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
 KW cancer; inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
 KW lupus erythematosus; chyloditis; diabetes; uveitis; psoriasis;
 KW uticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
 KW Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
 KW Lyme disease; tuberculosis; malaria; leishmaniasis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1326
 FT /*tag= b
 FT /product= "IL-13 receptor alpha 1 chain"
 FT sig_peptide 43..120
 FT /*tag= a
 FT mat_peptide 121..1323

FT /*tag= c
 FT /note= "Mature IL-13 receptor alpha 1 chain"
 XX
 XX US6743604-B1.
 XX
 XX 01-JUN-2004.
 XX
 XX 06-APR-2000; 2000US-00545002.
 XX
 XX 13-DEC-1996; 96GB-00025899.
 XX 12-NOV-1997; 97US-00969125.
 XX
 XX (SMIK) SWITKLINE BEECHAM CORP.
 XX
 XX Bonney J, Gauchat J;
 XX
 XX WPI; 2004-409324/38.
 XX P-PSDB; ADN62575.
 XX
 XX New isolated nucleic acid molecule encoding a polypeptide capable of
 PT binding human IL-13 and/or binding human IL-4, useful in medicine, in
 PT diagnostics or for producing antibodies.
 XX
 XX Claim 1; SEQ ID NO 8; 24bp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule (ADN62574),
 CC which encodes the mature form of a polypeptide capable of binding human
 CC IL-13 (interleukin 13) and/or binding human IL-4 (designated IL-13
 CC receptor alpha 1 subunit) appearing as ADN62575. Also included are a
 CC vector comprising the nucleic acid molecule and a host cell comprising
 CC the vector. The nucleic acids are useful as probes or primers or in the
 CC analysis of allelic variation. The polypeptides are useful for binding
 CC human IL-13 and/or binding human IL-4 and act as inhibitors by
 CC interfering with the interaction between human IL-13 or IL-4 and their
 CC natural receptors. They can also be used in medicine, e.g. for treatment
 CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
 CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
 CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
 CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
 CC uticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
 CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
 CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
 CC used for producing antibodies, which can be used for diagnosing diseases.
 CC The present sequence encodes IL-13 receptor alpha 1 subunit.
 XX
 XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 96.4%; Score 1333.8; DB 12; Length 4038;
 XX Best Local Similarity 99.6%; Pred. No: 0;
 XX Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
 QY 34 CGGCGGGGTTCCGAGGCGGAGGCTGATGAGTGGCGGCGGCTCTGCGGGCTGTGG 93
 DB 16 CGGCGGGGTTCCGAGGCGGAGGCTGATGAGTGGCGGCGGCTCTGCGGGCTGTGG 75
 QY 94 GCGGTGCTGTCTGCGCGCGCGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGG 150
 DB 76 GCGGTGCTGTCTGCGCGCGCGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGG 135
 QY 151 CAGGACCTGTGACCAATTTGAGTGTCTGTTGAAACCTCTGACAGTAATATGACA 210
 DB 136 CAGGACCTGTGACCAATTTGAGTGTCTGTTGAAACCTCTGACAGTAATATGACA 195
 QY 211 TGAATCCACCCGAGGAGGCGAGCTCAATTTGATGATGATTTTATGATTTTGGC 270
 DB 196 TGAATCCACCCGAGGAGGCGAGCTCAATTTGATGATGATTTTATGATTTTGGC 255
 QY 271 GACCAACCAAGTAAGAAATTAAGCTCCGGAACCTGCTCATAGAAATTAATCCCTTAAT 330
 DB 256 GACCAACCAAGTAAGAAATTAAGCTCCGGAACCTGCTCATAGAAATTAATCCCTTAAT 315
 QY 331 GAGAGATTGTCTGCAAGTGGGCTCCAGCTGATGACCAATGAGAGTGAAGCTTAGC 390

Db 316 GAGAGATTGTTCTGCAAGTGGGGTCCAGTGTAGCAACAATGAGAGTGAAGACCTTACG 375
QY 391 ATTTGGTTGAAAAATGATCTCACCCCGAAGAGTATCTGATCTGCTGTGACTGAA 450
XX |||||
Db 376 ATTTGGTTGAAAAATGATCTCACCCCGAAGAGTATCTGATCTGCTGTGACTGAG 435
QY 451 CTTCATGCAATTTGGGCAACACTGAGCTACATGATGTTCTTGGCTCCCTGGAAGGAAT 510
XX |||||
Db 436 CTTCATGCAATTTGGGCAACACTGAGCTACATGATGTTCTTGGCTCCCTGGAAGGAAT 495
QY 511 ACCAGTCCGAGCACTACTACTCTACTATTTGGGACGAAGCCCTGGAAAAATTCAT 570
XX |||||
Db 496 ACCAGTCCGAGCACTACTACTCTACTATTTGGGACGAAGCCCTGGAAAAATTCAT 555
QY 571 CAATGGAACCACTCTTTAGAGAGGCAATACCTTGGTGTCTTGGATCTGACCAAA 630
XX |||||
Db 556 CAATGGAACCACTCTTTAGAGAGGCAATACCTTGGTGTCTTGGATCTGACCAAA 615
QY 631 GTGAGGATTCAGTTTGAACAACAAGTGTCCAAATAATGTCGAAGATTAATGACAGA 690
XX |||||
Db 616 GTGAGGATTCAGTTTGAACAACAAGTGTCCAAATAATGTCGAAGATTAATGACAGA 675
QY 691 AAAATTAACCACTCTTCAATATAGGCTTAACTCCGCTGGAACCTGATCTCTCCA 750
XX |||||
Db 676 AAAATTAACCACTCTTCAATATAGGCTTAACTCCGCTGGAACCTGATCTCTCCA 735
QY 751 CATATTAACCACTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810
XX |||||
Db 736 CATATTAACCACTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 795
QY 811 AATTTTATTAGACATGCTTATTTTATGAAGTGAAGTCAATAACAGCCAAACTGACAGA 870
XX |||||
Db 796 AATTTTATTAGACATGCTTATTTTATGAAGTGAAGTCAATAACAGCCAAACTGACAGA 855
QY 871 CATTAAGTTTTCACGTCCAGAGGCTAAATGTGGAATCCCAATTTGGAGAAATGTG 930
XX |||||
Db 856 CATTAAGTTTTCACGTCCAGAGGCTAAATGTGGAATCCCAATTTGGAGAAATGTG 915
QY 931 GAGAAATACATCTTGTTCATGTGCTCCGTGATCTTCTCTGATCTTTGAACACAGTACAGA 990
XX |||||
Db 916 GAGAAATACATCTTGTTCATGTGCTCCGTGATCTTCTCTGATCTTTGAACACAGTACAGA 975
QY 991 ATTAAGTCAAAAACAATAAGTTATGTCTATGAGATGACAAACTCTGAGTAAATTTGAGAGC 1050
XX |||||
Db 976 ATTAAGTCAAAAACAATAAGTTATGTCTATGAGATGACAAACTCTGAGTAAATTTGAGAGC 1035
QY 1051 CAGAATAAGTATAGGTAGAGAGCGCAATTCACACTCACTAACCACTGATCTACTCAT 1110
XX |||||
Db 1036 CAGAATAAGTATAGGTAGAGAGCGCAATTCACACTCACTAACCACTGATCTACTCAT 1095
QY 1111 GTTCCAGTATCGTCCAGGTGCAATCATATGTACTCCTGCTTTTAACTTAAAGAGCTCAAG 1170
XX |||||
Db 1096 GTTCCAGTATCGTCCAGGTGCAATCATATGTACTCCTGCTTTTAACTTAAAGAGCTCAAG 1155
QY 1171 ATTATTAATTCCTCCCAATTCCTGATCTGTGCAAGATTTTAAAGAAATGTTTGGAGAC 1230
XX |||||
Db 1156 ATTATTAATTCCTCCCAATTCCTGATCTGTGCAAGATTTTAAAGAAATGTTTGGAGAC 1215
QY 1231 CAGAAATGATATCTCTGCACTGGAAGAGTATGACATCTATAGAGAAACCAACAGAG 1290
XX |||||
Db 1216 CAGAAATGATATCTCTGCACTGGAAGAGTATGACATCTATAGAGAAACCAACAGAG 1275
QY 1291 GAAACCGACTCTGTAGTGTGATAGAAAACTGGAAGAAAGCTCTGATGATGAGATTA 1350
XX |||||
Db 1276 GAAACCGACTCTGTAGTGTGATAGAAAACTGGAAGAAAGCTCTGATGATGAGATTA 1335
QY 1351 TTTATTTTAACTTCACTGTGACCTTGAGAAGA 1383
XX |||||
Db 1336 TTTATTTTAACTTCACTGTGACCTTGAGAAGA 1368
XX |||||

RESULT 12
AAA35214

ID AAA35214 standard; DNA; 4039 BP.
XX
AC AAA35214;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:88.
XX
KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiasthmatic; cyrostatic; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-ANG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 1253-1254; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antisthmatic, cyrostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
SQ Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;
XX
Query Match 96.4%; Score 1333.8; DB 3; Length 4039;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 34 CGGCCGGGTTCCGAGCGAGAGGCTGCATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 93

Db	17	CGCGCGGGGCTCCGAGGCGAGAGGCTGCAAGTGAGTGCGCGCGCGCGGCTGCGGGCGTGTGG	76
OY	94	GGCGTGCCTGCTCGCGCCGGCCGGCGGGGGCGGGGGCGGGGG---GCCGCTTCGGAACT	150
Db	77	GGCGTGCCTGCTCGCGCCGGCCGGCGGGGGCGGGGGCGGGGGCGCGCGCTTCGGAACT	136
OY	151	CAGCCACCTGTGACAAAAATTTGAGTGTCTGTGTGAAAACCTCTGCAAGATATATGAGCA	210
Db	137	CAGCCACCTGTGACAAATTTGAGTGTCTGTGTGAAAACCTCTGCAAGATATATGAGCA	196
OY	211	TGGAATCCAACCCGAGGGAGCCAGCTCAAAATTGAGTCTATGAGTATTTTATGATTTTGGC	270
Db	197	TGGAATCCAACCCGAGGGAGCCAGCTCAAAATTGAGTCTATGAGTATTTTATGATTTTGGC	256
OY	271	GACAAACAAGATPAAGAAAAATAGCTCCGGAAATCGTCGTCAAATAGAAATACCCCTGAT	330
Db	257	GACAAACAAGATPAAGAAAAATAGCTCCGGAAATCGTCGTCAAATAGAAATACCCCTGAT	316
OY	331	GAGAGATTTTGTCTGCAAGTGGGGTCCGAGTGTACACCAATGAGAGTGAAGGCTTACG	390
Db	317	GAGAGATTTTGTCTGCAAGTGGGGTCCGAGTGTACACCAATGAGAGTGAAGGCTTACG	376
OY	391	ATTTTGGTTGAAAAATGCATCTCACCCCAAGAGGTATCCTGAGCTGTGCTGTGA	450
Db	377	ATTTTGGTTGAAAAATGCATCTCACCCCAAGAGGTATCCTGAGCTGTGCTGTGA	436
OY	451	CTTCATGTCATTTGGGACACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAAGAT	510
Db	437	CTTCATGTCATTTGGGACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAAGAT	496
OY	511	ACCACTCCCGACACTTAACCTTACTCTCTACTATTTGGCAACAGAGCCTGGAAAAATTTAT	570
Db	497	ACCACTCCCGACACTTAACCTTACTCTCTACTATTTGGCAACAGAGCCTGGAAAAATTTAT	556
OY	571	CAATGTGAAAAACATCTTTTAGAGAAAGCCCAATCTTTGGTGTCTCTTGATCTGACCAA	630
Db	557	CAATGTGAAAAACATCTTTTAGAGAAAGCCCAATCTTTGGTGTCTCTTGATCTGACCAA	616
OY	631	GTGAAGAGTTCAGATTTTGAAACAACAAGTGTCCAAATATATGGTCAAGATATATCAAGA	690
Db	617	GTGAAGAGTTCAGATTTTGAAACAACAAGTGTCCAAATATATGGTCAAGATATATCAAGA	676
OY	691	AAAATTTAAACCATCTTCAATATAGTGCCTTTTAACTTCCCGTGAACCTGATCTTCA	750
Db	677	AAAATTTAAACCATCTTCAATATAGTGCCTTTTAACTTCCCGTGAACCTGATCTTCA	736
OY	751	CATATTTAAAAACCTCTCCTTCCACAAATGATACCTATATATGTCATGGGAATATCCAG	810
Db	737	CATATTTAAAAACCTCTCCTTCCACATATATGACCTATATATGTCATGGGAATATCCAG	796
OY	811	AATTTTATTTAGCAGATGCTTATTTTATGATAGTAGAAGTCAATTAACGCCAACTGAGACA	870
Db	797	AATTTTATTTAGCAGATGCTTATTTTATGATAGTAGAAGTCAATTAACGCCAACTGAGACA	856
OY	871	CATATATGTTTCTTACGTCCAAAGAGGCTTAATATGTGAAATCCAGAAATTTGAGAAATATG	930
Db	857	CATATATGTTTCTTACGTCCAAAGAGGCTTAATATGTGAAATCCAGAAATTTGAGAAATATG	916
OY	931	GAGAAATACATCTTGTTCATGCTCCCTGATGTCTTCTGTATACCTTTGAAACAGCTGAGA	990
Db	917	GAGAAATACATCTTGTTCATGCTCCCTGATGTCTTCTGTATACCTTTGAAACAGCTGAGA	976
OY	991	ATTAAGTTCAAAACAATTAAGTATGTATAGATGAGTGAACAATCTGAGATTAATTTGAGC	1050
Db	977	ATTAAGTTCAAAACAATTAAGTATGTATAGATGAGTGAACAATCTGAGATTAATTTGAGC	1036
OY	1051	CAAGAAATGAGATATGTATGAAGGAGCAATTCACACTTACATPAACCATGTTACTATT	1110
Db	1037	CAAGAAATGAGATATGTATGAAGGAGCAATTCACACTTACATPAACCATGTTACTATT	1096
OY	1111	GTTCCAGTCAATGCTGCGCAGGTGCAATCAATGACTCTGCTTTTAACTTAAAAAGCTCAAG	1170

Accession	Sequence	Length
Db	GTCCAGTCATCGTGGAGGGTCAATCATAGTACTCCTGGCTTTACAAAAAGGCTCAG	1156
Qy	ATTATATATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTAAAGAAATGTTGGAGAC	1230
Db	ATTATATATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTAAAGAAATGTTGGAGAC	1216
Qy	CAGATGATGATCTCTGCACTGGAGAAGTACACATCTATGGAAGCAAAACCAAGAG	1290
Db	CAGATGATGATCTCTGCACTGGAGAAGTACACATCTATGGAAGCAAAACCAAGAG	1276
Qy	GAAAACCGACTCTGTAGTGTGTATGAAAACCTGAAAGAACCTCTCAGTATGAGATAA	1350
Db	GAAAACCGACTCTGTAGTGTGTATGAAAACCTGAAAGAACCTCTCAGTATGAGATAA	1336
Qy	TTTATTTTACCTCAGCTGAGACCTTAGAAGA	1383
Db	TTTATTTTACCTCAGCTGAGACCTTAGAAGA	1369

CC	RESULT 13
XX	AAF21336
XX	ID AAF21336 standard; DNA; 4039 BP.
AC	
XX	AAF21336;
DT	14-MAR-2001 (first entry)
DE	
XX	Human low adenosine antisense oligonucleotide related sequence #2903.
KM	
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary ablation; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.
KM	
KW	Homo sapiens.
OS	
XX	
XX	Wo200062736-A2.
PB	
PD	26-OCT-2000.
XX	
XX	24-MAR-2000; 2000MO-USO08020.
PE	
PR	06-APR-1999; 99US-0127958P.
XX	
PA	(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
XX	
F1	Nyce JW;
DR	
XX	WPI; 2000-679539/66.
PT	
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
PS	
XX	Disclosure; Page 1337-1338; 1592gp; English.
XX	
CC	The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and
CC	

	CC	chemokines, endogenously produced specific and non-specific enzymes,
	CC	binding proteins/adhesion molecules and their receptors, cytokine and
	CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
	CC	nervous system (CNS) and peripheral nervous and non-nervous system
	CC	receptors, CNS and peripheral nervous and non-nervous system peptide
	CC	transmitters, defensins, growth factors, vasoactive peptides and
	CC	receptors, binding proteins and malignant associated proteins. The
	CC	antisense oligonucleotides may be used in this way to treat disorders
	CC	including respiratory obstruction (especially pulmonary obstruction
	CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
	CC	surfactant hypoproduction which are associated with a disease or
	CC	condition selected from pulmonary vasooconstriction, inflammation,
	CC	allergies, asthma, impeded respiration, respiratory distress syndrome
	CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
	CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
	CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
	CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
	CC	fragments and antisense oligonucleotides used in the exemplification of
	CC	the present invention
XX		
SQ	Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;	
	Query Match	96.4%; Score 1333.8; DB 3; Length 4039;
	Best Local Similarity	99.6%; Pred. No. 0;
	Matches 1348; Conservative	0; Mismatches 2; Indels 3; Gaps 1;
OY	34 CGGCGGGGTTCGAGCGAGAGGCTGCATGAGTGCGCGCGGCTTCCGGGCTGTGG	93
DB	17 CGGCGGGGCTCGAGGCGAGAGGCTGCATGAGTGCGCGCGGCTTCCGGGCTGTGG	76
OY	94 GCGCTGCTGCTTGTGGCGGGCGGGGGCGGGGGCGGGGG--CGCGCTTAGGAACCT	150
DB	77 GCGCTGCTGCTTGTGGCGGGCGGGGGCGGGGGCGGGGGCGCGCGCTTAGGAACCT	136
OY	151 CAGCACCACTGTGACAATAATTGAGTGTCTGTGTAAACCCTGTGACAGTAATATAGACA	210
DB	137 CAGCCACTGTGACAAATTGAGTGTCTGTGTAAACCCTGTGACAGTAATATAGACA	196
OY	211 TGGAATCCACCCGAGGAGGCCAGCTCAATTGTACTGTATGGTATTTAGCATTTTGGC	270
DB	197 TGGAATCCACCCGAGGAGGCCAGCTCAATTGTACTGTATGGTATTTAGCATTTTGGC	256
OY	271 GACAAAACAAGATTAAGAAATAGCTCCGAAACTGTCGTTCAATAGAATACCCCTGAT	330
DB	257 GACAAAACAAGATTAAGAAATAGCTCCGAAACTGTCGTTCAATAGAATACCCCTGAT	316
OY	331 GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTACCAACATAGAAGAGAACGCTACG	390
DB	317 GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTACCAACATAGAAGAGAACGCTACG	376
OY	391 ATTTTGTGTAAAAATGCACTCACCCCCAGAGGTGATCCTGAGTCTGCTGACTGAA	450
DB	377 ATTTTGTGTAAAAATGCACTCACCCCCAGAGGTGATCCTGAGTCTGCTGACTGAG	436
OY	451 CTTCATGCAATTTGGCAACACTGAGCTACATGAAGTCTTGGCTCCCTGGAAAGAT	510
DB	437 CTTCATGCAATTTGGCAACACTGAGCTACATGAAGTCTTGGCTCCCTGGAAAGAT	496
OY	511 ACCAGTCCCGACATTAACATATCTCTCACTTAATGGCAACAGAGCTGGAAAAATTCAT	570
DB	497 ACCAGTCCCGACATTAACATATCTCTCACTTAATGGCAACAGAGCTGGAAAAATTCAT	556
OY	571 CAATGTGAAAAATCATTTTGAAGAAAGCCAATCTTTGGTGTCTTTGATCTGACAA	630
DB	557 CAATGTGAAAAATCATTTTGAAGAAAGCCAATCTTTGGTGTCTTTGATCTGACAA	616
OY	631 GTGAAGATTCAGTTTTGAACAACAACAGTGTCAAATATAGTCAAGATTAATGACAGA	690
DB	617 GTGAAGATTCAGTTTTGAACAACAACAGTGTCAAATATAGTCAAGATTAATGACAGA	676
OY	691 AAAATTAACCATCTTCAATATAGTGCCTTTAACTCCCGTGTAAACCTGATCTTCCA	750
DB	677 AAAATTAACCATCTTCAATATAGTGCCTTTAACTCCCGTGTAAACCTGATCTTCCA	736

QY	751	CATTTTAAAAACCCCTCCTTCCCAAAATGAGACCTTATATGCGAAATGGGAATCCACAG	810
Db	737	CATTTTAAAAACCTCTCTCTCCACAAATGATGACCTTATATGCGAAATGGGAATCCACAG	796
QY	811	AATTTTATTTAGCAGATCCCTATTTTATGAAATGAACTCAATTAACGCCAAACTGAGACA	870
Db	797	AATTTTATTTAGCAGATCCCTATTTTATGAAATGAACTCAATTAACGCCAAACTGAGACA	856
QY	871	CATTAATGTTTTCTACGTCGCCAAGAGCTTAATATGAGAAATCCAAATTTGAGAGAAATGTG	930
Db	857	CATATATGTTTTCTACGTCGCCAAGAGCTTAATATGAGAAATCCAAATTTGAGAGAAATGTG	916
QY	931	GAGAAATCAATCTTGTTCATATGATGCTCCGTGATCTTCTCTGATATCTTGAACACAGTCAGA	990
Db	917	GAGAAATCAATCTTGTTCATATGATGCTCCGTGATCTTCTCTGATATCTTGAACACAGTCAGA	976
QY	991	ATAAAGCTCAAAACAAATTAAGTTATGCTATGAGAGTACAAACTCTGAGTAATTGGAGC	1050
Db	977	ATAAAGCTCAAAACAAATTAAGTTATGCTATGAGAGTACAAACTCTGAGTAATTGGAGC	1036
QY	1051	CAAAATAATGAGTATAGGTAAGAAGCGCAATTTCCAACCTCACTAATCAACATGTTACTCATTT	1110
Db	1037	CAAGAAAATGAGTATAGGTAAGAAGCGCAATTTCCAACCTCACTAATCAACATGTTACTCATTT	1096
QY	1111	GTTCCAGTCATCGTCGCGAGGTGCATCATATGTACTCTCGCTTTTAACTPAAAAAGGCTCAAG	1170
Db	1097	GTTCCAGTCATCGTCGCGAGGTGCATCATATGTACTCTCGCTTTTAACTPAAAAAGGCTCAAG	1156
QY	1171	ATTATATTATTTCCCTCCCAATTTCTCGATCTCGGCAAGATTTTAAAGAAATGTTTGGAGAC	1230
Db	1157	ATTATATTATTTCCCTCCCAATTTCTCGATCTCGGCAAGATTTTAAAGAAATGTTTGGAGAC	1216
QY	1231	CAGAAATGATGATCTGCTGCACTGGAAAGATAGACATCTATGAGAAAGCAACCAAGAGAG	1290
Db	1217	CAGAAATGATGATCTGCTGCACTGGAAAGATAGACATCTATGAGAAAGCAACCAAGAGAG	1276
QY	1291	GAACCCGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCCCTCTCAGTGTGAGATAA	1350
Db	1277	GAACCCGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCCCTCTCAGTGTGAGATAA	1336
QY	1351	TTTATTTTTTACCTTCACCTGTGAGACTTGAGAGA	1383
Db	1337	TTTATTTTTTACCTTCACCTGTGAGACTTGAGAGA	1369
RESULT 14			
ABLe67709 standard; DNA; 4039 BP.			
AC	ABLe67709;		
XX	15-MAY-2002 (first entry)		
DE	Oesophagus cancer related gene sequence SEQ ID NO:6046.		
KM	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
KM	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KM	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;		
XX	gene; ds.		
OS	Homo sapiens.		
PN	MO200194629-A2.		
PD	13-DEC-2001.		
PF	30-MAY-2001; 2001WO-US010838.		
PR	05-JUN-2000; 2000US-0209473P.		
PR	05-JUN-2000; 2000US-0209531P.		
PR	18-SEP-2000; 2000US-0233133P.		
PR	18-SEP-2000; 2000US-0233617P.		

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:02:42 ; Search time 6243 Seconds
(without alignments)
12387.704 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383

Sequence: 1 gagctcaacgacgcagcaagg.....tcactgtcacttgagaaga 1383

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_est7: *
7: gb_est8: *
8: gb_est9: *
9: gb_est10: *
10: gb_est11: *
11: gb_gss1: *
12: gb_gss2: *
13: gb_gss3: *
14: gb_gss4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	84.9	1756	6	CR603161 full-length
2	978.2	70.7	1016	1	AL543336 AL543336
3	911.6	65.9	1865	6	AK0898984 Mus muscu
4	908.4	65.7	1817	6	AK082889 Mus muscu
5	902.2	65.2	1677	6	AK080147 Mus muscu
6	899	64.5	3718	6	AK154675 Mus muscu
7	891.6	64.5	3662	6	AK143292 Mus muscu
8	863.8	62.5	951	3	BM905033 AGNCOURT
9	785	56.8	978	3	BO678245 AGNCOURT
10	766.2	55.4	799	4	CB956372 AGNCOURT
11	739.4	53.5	866	14	DQ034842 Homo sapi
12	720.8	52.1	729	14	DQ034843 Homo sapi
13	710	51.3	764	2	BG699187 602678850
14	655	47.4	842	5	CK000442 AGNCOURT
15	631.4	45.6	633	4	CA391344 csl4a05.y
16	631	45.7	724	2	BP969803 602272251
17	601.8	43.5	621	8	CN265110 170005321
18	601	43.5	902	4	CA488843 AGNCOURT
19	593.8	42.9	1009	2	BI464939 603207417

20	577	41.7	580	9	DA102323
21	573	41.4	573	9	DB150552
22	567	41.0	567	9	DA757245
23	565.8	40.9	673	1	AL036221
24	560.4	40.5	632	1	AI768613
25	560.2	40.5	624	2	BG565689
26	555	40.1	570	9	DA707381
27	554.4	40.1	556	9	DB148485
28	553.8	40.0	578	3	BP267255
29	552	39.9	552	9	DA992396
30	549.2	39.7	634	7	BE971462
31	548.8	39.7	581	9	DA549879
32	545.4	39.4	547	9	DA340823
33	544.8	39.4	580	3	BP268026
34	543.6	39.3	589	3	DN105857
35	543.6	39.3	719	9	DN114427
36	543	39.3	543	9	DA990183
37	542.8	39.2	887	3	BQ938919
38	541	39.1	541	4	CB161269
39	538.8	39.0	599	3	BM788541
40	538.4	38.9	552	9	DA294933
41	538.4	38.9	619	7	BE971324
42	537.2	38.8	595	3	BM763177
43	533.4	38.6	551	9	DB061920
44	532.2	38.5	560	9	DA325930
45	530.6	38.4	706	9	DN114783

ALIGNMENTS

RESULT 1
CR603161
LOCUS
DEFINITION
full-length cDNA clone CSOD1001YN10 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR603161
VERSION
CR603161.1 GI:50483968
KEYWORDS
HNC; CNSIT_CDNA.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 1756)
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
Redwood City, CA 94061
REFERENCE
2 (bases 1 to 1756)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1756
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSOD1001YN10"
/tissue="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 84.9%; Score 1174; DB 6; Length 1756;

Best Local Similarity 98.5%; Pred. No. 2.8e-309; Matches 1196; Conservative 0; Mismatches 15; Indels 3; Gaps 1;									
QY	61	ATGAGTGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGCGGCGGG	120						
Db	1	ATGGAATGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGCGGCGGG	60						
QY	121	GGCGGGGGCGGGG---CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGC	177						
Db	61	GGCGGGGGCGGGGCGCGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGC	120						
QY	178	TCTGTTGAAAACTCTGCGACAGTAATATGACATGGAATCCACCCGAGGGAGCCAGTCA	237						
Db	121	TCTGTTGAAAACTCTGCGACAGTAATATGACATGGAATCCACCCGAGGGAGCCAGTCA	180						
QY	238	AATTGATCTATGATATTTAGTCAATTTTGGCGACAAACAGATAAGAAATAGCTCG	297						
Db	181	AATTGATCTATGATATTTAGTCAATTTTGGCGACAAACAGATAAGAAATAGCTCG	240						
QY	298	GAAACTGCTGTTCAATAGAAATACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCC	357						
Db	241	GAAACTGCTGTTCAATAGAAATACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCC	300						
QY	358	CAGTGTAGACCAATAGAGTGAAGCCCTAGCATTTTGGTGAATAATGCACTCACCC	417						
Db	301	CAGTGTAGACCAATAGAGTGAAGCCCTAGCATTTTGGTGAATAATGCACTCACCC	360						
QY	418	CCAGAAGTGAATCTGAGTCTGCTGACGAACTTCAATGCAATTTGGCGACCACTGAGC	477						
Db	361	CCAGAAGTGAATCTGAGTCTGCTGACGAACTTCAATGCAATTTGGCGACCACTGAGC	420						
QY	478	TACATGAAGTCTTCTGGCTCCCTGGAAGAAATACAGTCCGACACTAACTATCTCTC	537						
Db	421	TACATGAAGTCTTCTGGCTCCCTGGAAGAAATACAGTCCGACACTAACTATCTCTC	480						
QY	538	TACTATTTGGACAGAAAGCCCTGGAATAATTCATCATATGTGAATAACTCTTTAGAGAGC	597						
Db	481	TACTATTTGGACAGAAAGCCCTGGAATAATTCATCATATGTGAATAACTCTTTAGAGAGC	540						
QY	598	CAATACCTTTGGTGTCTCTTGTATCTGACCAAAAGTGAAGATTCAGTTTGAACAAAC	657						
Db	541	CAATACCTTTGGTGTCTCTTGTATCTGACCAAAAGTGAAGATTCAGTTTGAACAAAC	600						
QY	658	AGTGTCCAATAATGTGTCAAGATTAATGACAGAAAAATTAACCATCTTCAATATATGT	717						
Db	601	AGTGTCCAATAATGTGTCAAGATTAATGACAGAAAAATTAACCATCTTCAATATATGT	660						
QY	718	CCTTTAATCTCCGCTGTGAAACCTGATCTCTCCACATTTAAAAACCTCTCTCCCAAT	777						
Db	661	CCTTTAATCTCCGCTGTGAAACCTGATCTCTCCACATTTAAAAACCTCTCTCCCAAT	720						
QY	778	GATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTATTTAT	837						
Db	721	GATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTATTTAT	780						
QY	838	GAAATGAAGTCAATAACAGCCAACTGAGACACATTAATGTTTCTTACGTCGAAGAGCT	897						
Db	781	GAAATGAAGTCAATAACAGCCAACTGAGACACATTAATGTTTCTTACGTCGAAGAGCT	840						
QY	898	AAATGTGAATTCAGAAATTTGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCT	957						
Db	841	AAATGTGAATTCAGAAATTTGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCT	900						
QY	958	GGTGTCTTCTGATATCTTTGAACACAGTCAATTAAGATCAAAACAAATTAAGTATGC	1017						
Db	901	GGTGTCTTCTGATATCTTTGAACACAGTCAATTAAGATCAAAACAAATTAAGTATGC	960						
QY	1018	TATGAGATGACAAACTCTGAGTAATTTGAGCCCAAGAAATGAGTATAGGTAAAGAGCG	1077						
Db	961	TATGAGATGACAAACTCTGAGTAATTTGAGCCCAAGAAATGAGTATAGGTAAAGAGCG	1020						
QY	1078	AATTCAACTCTACATTAACATGTTACTATTTGCACTCATCTGCGAGGTGCATC	1137						

Db	1021	AATTCCAACTCTACATTAACCATGTTACTCATTTGCTCAGTCACTGCGAGGTGCATC	1080
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Db	1081	ATAGTACTCCTGCTTACCTTAATAAAGCTCAAGATTTATTAATTCCTCCAAATTCGTAT	1140
QY	1198	CCTGGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTGTGCACTGGAG	1257
Db	1141	CCTGGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTGTGAAACAAAC	1200
QY	1258	AAGTAGCAGCATCTTA	1271
Db	1201	CATCAGGCTTCCCA	1214
RESULT 2			
LOCUS	AL543336	1016 bp	mRNA linear EST 24-MAR-2004
DEFINITION	AL543336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA	clone CSOD1001YN10 5-PRIME, mRNA sequence.	
ACCESSION	AL543336		
VERSION	AL543336.3	GI:45718896	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1016)	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31265183.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequenage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen. This sequence belongs to sequence cluster		
	11048.f		
	For more information about this cluster, see		
	http://www.genoscope.cns.fr/cdna?s=CSOD1001D6050P1&c=11048.f.		
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/clone="CSOD1001YN10"			
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"			
/note="1st strand cDNA was primed with a NotI-oligo(dT)			
primer. Five prime end enriched, double-strand cDNA was			
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
ORIGIN			
Query Match 70.7%; Score 978.2; DB 1; Length 1016;			
Best Local Similarity 98.1%; Pred. No. 8.5e-256;			
Matches 997; Conservative 3; Mismatches 12; Indels 4; Gaps 1;			
QY	61	ATGAGTGGCGCGGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGGCGGG	120
Db	1	ATGGAATGGCGCGGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGGCGGG	60
QY	121	GGCGGGGGCGGGG-----CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGT	176
Db	61	GGCGGGGGGGGGGGCGGCGGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGT	120
QY	177	CTCTGTTGAAAACTCTGCAAGTAAATATGACATGGAATCCACCCGAGGAGCCAGCTC	236

Db	121	CTCTGTGAAAA	CTCTGCACAGTATATG	CACTGGATCCACC	CGAGGAGCC	AGC	180
OY	237	AAATTGTAGT	CTATGTATATTTT	TAGTCATTTTGG	CCGACAAACAA	GATTAAGAAATAGCTCC	296
Db	181	AAATTGTAGT	CTATGTATATTTT	TAGTCATTTTGG	CCGACAAACAA	GATTAAGAAATAGCTCC	240
OY	297	GGAAACTCGT	CGTTCAAT	TGAAGTACCCT	TGATGAGAGATTTTG	CTGCAAGTGGGGTC	356
Db	241	GGAAACTCGT	CGTTCAAT	TGAAGTACCCT	TGATGAGAGATTTTG	CTGCAAGTGGGGTC	300
OY	357	CCAGTGTAGC	ACCAATGAGAGT	GAGAGGCT	TAGCATTTTGGT	GGAAAAATGCACTCAC	416
Db	301	CCAGTGTAGC	ACCAATGAGAGT	GAGAGGCT	TAGCATTTTGGT	GGAAAAATGCACTCAC	360
OY	417	CCCAAGGTGAT	CCCTGAGTCTG	CTGTGCTGA	CTTAACCTTCA	ATGCACTTTGGCACAACCTGAG	476
Db	361	CCCAAGGTGAT	CCCTGAGTCTG	CTGTGCTGA	CTTAACCTTCA	ATGCACTTTGGCACAACCTGAG	420
OY	477	CTACATGAGT	GTGTTCTTG	GCTCCCTG	GAAGAAATAC	CAAGTCCGACACATTAATCTCT	536
Db	421	CTACATGAGT	GTGTTCTTG	GCTCCCTG	GAAGAAATAC	CAAGTCCGACACATTAATCTCT	480
OY	537	CTACTATTGG	CACAGAA	GCTG	GGAAAAATTCAT	CAATGTGAAAAATCTTTT	596
Db	481	CTACTATTGG	CACAGAA	GCTG	GGAAAAATTCAT	CAATGTGAAAAATCTTTT	540
OY	597	CCAATACTTTG	GGTTGTTCTT	GTGATCTGTG	CAAAAGGAAAGAT	CCAGTTTGGAAACA	656
Db	541	CCAATACTTTG	GGTTGTTCTT	GTGATCTGTG	CAAAAGGAAAGAT	CCAGTTTGGAAACA	600
OY	657	CAGTGTCCAA	TATATGTC	CAAGGATATG	CAGAAAAATTTAA	ACCATCTTCAATATAGT	716
Db	601	CAGTGTCCAA	TATATGTC	CAAGGATATG	CAGAAAAATTTAA	ACCATCTTCAATATAGT	660
OY	717	GCCTTTA	CTTCCG	GTGAAACCT	GTATCC	CAATTAACCTCTCTTCCACGA	776
Db	661	GCCTTTA	CTTCCG	GTGAAACCT	GTATCC	CAATTAACCTCTCTTCCACGA	720
OY	777	TGATGACCT	TATATG	CAATGG	GAATCCAC	AGATTTTATAGCAGATGCTTATTA	836
Db	721	TGATGACCT	TATATG	CAATGG	GAATCCAC	AGATTTTATAGCAGATGCTTATTA	780
OY	837	TGAAGTAA	AGTCAATTA	CAGCCAA	ACTGAG	CACATTAATGTTTCTACGTCCAAAGAGC	896
Db	781	TGAAGTAA	AGTCAATTA	CAGCCAA	ACTGAG	CACATTAATGTTTCTACGTCCAAAGAGC	840
OY	897	TAAATGTAGA	TCCAGAA	TTTGA	BAGAAATGTG	AGAAATATCTTGTTCAATGCTCC	956
Db	841	TAAATGTAGA	TCCAGAA	TTTGA	BAGAAATGTG	AGAAATATCTTGTTCAATGCTCC	900
OY	957	TGTGTGTT	CTTCTGT	ACTTTG	AMACAG	CTCAGATTAAGTCAAAACAAATTAATGTTAG	1016
Db	901	TGTGTGTT	CTTCTGT	ACTTTG	AMACAG	CTCAGATTAAGTCAAAACAAATTAATGTTAG	960
OY	1017	CTATGAGAT	GATCAAACT	CTG	AGTAAATTTG	GAGCCAAAGAAATGATATAGGTAA	1072
Db	961	CTATGAGAT	GATCAAACT	CTG	AGTAAATTTG	GAGCCAAAGAAATGATATAGGTAA	1016

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AK089984		1865 bp mRNA linear HTC 02-SEP-2006	AK089984	AK089984.1	Mus musculus colon RCB-0549 C1e-H3 cDNA, RIKEN full-length enriched library, clone:G310044106 product:interleukin 13 receptor, alpha 1, full insert sequence.	HTC; CAP trapper.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurgonahii; Muridae; Murinae; Mus.
						Mus musculus (house mouse)	

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komoto, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichipillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

4 Genome Res. 10 (11), 1757-1771 (2000)

5 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

6 The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

7 RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)

8 The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)

9 Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imomani, K., Iehi, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Socabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
Kanagawa, 220-0045, Japan (E-mail: genome-res@gsc.riken.jp,
Url: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

10 cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
Url: http://genome.gsc.riken.jp/

FEATURES
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

source

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/c1sue_type="colon"

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ORIGIN

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Matches 1099; Conservative 0; Mismatches 244; Indels 11; Gaps 3;

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RESULT 4
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DEFINITION
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:G430004G12 product:interleukin 13 receptor,
alpha 1, full insert sequence.
AK082889
ACCESSION
AK082889.1 GI:26350060
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
HTC; CAP trapper.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
AUTHORS
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
AUTHORS
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubaki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE
AUTHORS
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED
REFERENCE
AUTHORS
5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED
REFERENCE
AUTHORS
6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense transcription in the mammalian transcriptome
JOURNAL Science 309, 1564-1566 (2005)
PUBMED
REFERENCE
AUTHORS
7 The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The transcriptional landscape of the mammalian genome
JOURNAL Science 309, 1559-1563 (2005)
PUBMED
REFERENCE
AUTHORS
8 (bases 1 to 1817)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission
TITLE Submitted (16-APR-2002) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
Location/Qualifiers

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Db 1316 TTTCTTTCTTGCTTCAATGTGACCTGTGAGAA 1349

RESULT 5
AK080147 1677 bp mRNA linear HTC 02-SEP-2005
LOCUS
DEFINITION AK080147 1677 bp mRNA linear HTC 02-SEP-2005
Musc musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:530070009 product:Interleukin 13 receptor,
alpha 1, full insert sequence.
ACCESSION AK080147
VERSION AK080147.1 GI:26099027
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
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AUTHORS 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
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Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE
AUTHORS 4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE
AUTHORS 5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
AUTHORS 6 RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
REFERENCE
AUTHORS 7 The FANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
TITLE The Transcriptional Landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE
AUTHORS 8 (bases 1 to 1677)
ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P.,
FUKUDA, S., FURUKO, M., HANAGAKI, T., HARA, A., HASHIZUME, W.,
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KATOH, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONO, H., KONDA, M.,
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NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAO, N.,
OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N.,
SANO, H., SASAKI, D., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T.,
SOGABE, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKAKU-AKAIHARA, S.,
TAKEDA, Y., TANAKA, T., TOMARI, A., TOYA, T., YASUNISHI, A.,
MURAMATSU, M. and HAYASHIZAKI, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-resgsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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CONSRM
RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium

TITLE
JOURNAL
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AUTHORS

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 Nature 409 (6821), 685-690 (2001)
 11217851

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 Shinkawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R.,
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 Gustincich, S., Habbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,
 Hill, D., Hummel, K., Iacono, M., Ikeo, K., Iwana, A., Ishikawa, T.,
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 Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J.,
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CONSRM
RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

8
 The transcriptional landscape of the mammalian genome
 Science 309 (5740), 1559-1563 (2005)
 16141072

CONSRM
RIKEN Genome Exploration Research Group Phase II Team and the
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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

9
 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M.,
 Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H.,
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RIKEN Genome Exploration Research Group Phase II Team and the
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JOURNAL
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REFERENCE
AUTHORS

10
 RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

11
 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
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 Kanagawa, 230-0045, Japan (E-mail: genome-resgsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers
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Matches 1098; Conservative 0; Mismatches 245; Indels 12; Gaps 4;

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DB 1076 GCACAGATATAGTGAAGAGCAAACTCCACTTCTACACACCACTATGATCTCACTCA 1135
QY 1114 CCACTCATCTGCGAGGTGCAATCATATGATCTCTGCTTAACTTAAAGAGCTCAAGATT 1173
DB 1136 CCACTCTTGTGCGAGTGGCAGTCAATATCTCTCTTTTAACTGAAAGAGCTTAAAGATC 1195
QY 1174 ATTATATTTCCCTCAATTTCTGATCTGCGCAAGATTTTAAAGAAATGTTTGAAGACAG 1233
DB 1196 ATTATATTTCTCCAAATCTCTGATCTGCGCAAGATTTTAAAGAAATGTTTGAAGACAG 1255
QY 1234 AATGATATATCTGCACTGGAAGAGTACATGATGATGAGAGCAACCAAGAGAGAA 1293
DB 1256 AATGATATATCTCTGCACTGGAAGAGTACATGATGAGAGCAACCAAGAGAGAA 1315
QY 1294 ACCGACTCTGATGCTGATGAGAAACCTGAGAAAGCTCTCATGATGAGATTAATT 1353
DB 1316 ACGGATTTCTGATGCTGATGAGAAACCTGAGAAAGCTCTCATGATGAGAGAGT 1375
QY 1354 ATTT-----TTACTTCACTGTGACCTTGAAGAA 1383
DB 1376 ATTTCTTTCTGCTTCAATGTGACCTCTGAGAA 1410

RESULT 7
AKI43292
LOCUS
DEFINITION
Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
full-length enriched library, clone:E2300508 product:interleukin
13 receptor, alpha 1, full insert sequence.
ACCESSION
AKI43292
VERSION
AKI43292.1 GI:74226353
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
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prepare full-length cDNA libraries for rapid discovery of new genes
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TITLE

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Yan, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
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CONSRM

TITLE

JOURNAL

PUBMED

REFERENCE

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Nature 420 (6915), 563-573 (2002)

12466851

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Croke, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,
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16141073

(bases 1 to 3662)

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Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wataniki, A.,
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Direct Submissions

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URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. 3662

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/strain="C57BL/6J"

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/clone="E230035008"

REFERENCE

AUTHORS

CONSRM

TITLE

JOURNAL

PUBMED

REFERENCE

7

COMMENT

FEATURES

source

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LTSYKRPDPPHIITGLIKNALLVOKNSQNPFRCLTTEVENNTQDTHNLEVEE
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TLOLEEV"
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polyA_signal 3634..3639

Query Match 64.5%; Score 891.6; DB 6; Length 3662;
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Matches 1094; Conservative 0; Mismatches 249; Indels 13; Gaps 4;

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RESULT 8
BM905033
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
BM905033
VERSION
BM905033.1
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EST.
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ORGANISM
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Hominoidea; Homo.
REFERENCE
1 (bases 1 to 951)
NIH-MGC <http://mgi.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DPF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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FEATURES High quality sequence stop: 719.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5557892"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 Kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 62.5%; Score 863.8; DB 3; Length 951;
Best Local Similarity 97.8%; Pred. No. 1.7e-224;
Matches 918; Conservative 0; Mismatches 17; Indels 4; Gaps 4;

166 AATTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACATGATCCACCCGAG 225
13 AATTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACATGATCCACCCGAG 72
226 GGAAGCAGCTCAATTTGTATGTCTATGTCTATTTTATTTGCGCAAAACAATTAAG 285
73 GGAAGCAGCTCAATTTGTATGTCTATGTCTATTTTATTTGCGCAAAACAATTAAG 132
286 AAAATAGCTCCGGAACCTGCTGCTCAATAGAGTACCCCTGATGAGAGATTTCTCG 345
133 AAAATAGCTCCGGAACCTGCTGCTCAATAGAGTACCCCTGATGAGAGATTTCTCG 192
346 CAAGTGGGCTCCAGTGTAGCAACAATGAGTGAAGAGCTATTTGTTGTTGAAAA 405
193 CAAGTGGGCTCCAGTGTAGCAACAATGAGTGAAGAGCTATTTGTTGTTGAAAA 252
406 TGCATCTCAACCCAGAGGTGATCTGAGTCTGCTGTGACATGAATCTTCAATCATTTG 465
253 TGCATCTCAACCCAGAGGTGATCTGAGTCTGCTGTGACATGAATCTTCAATCATTTG 312
466 CAACCTGAGTCAATGAGTGTCTGCTGCTCCGGAAGAAATACCCGAGCACT 525
313 CAACCTGAGTCAATGAGTGTCTGCTGCTCCGGAAGAAATACCCGAGCACT 372
526 AACTATCTCTCTACTATTGGCAGAGAGCTGGAAAAATTCATCAATGTGAAAAATC 585
373 AACTATCTCTCTACTATTGGCAGAGAGCTGGAAAAATTCATCAATGTGAAAAATC 432
586 TTTAGAGAAAGCCAAATCTTGTGTTCTTTGATCTGACCAAGTGAAGATTCAGT 645
433 TTTAGAGAAAGCCAAATCTTGTGTTCTTTGATCTGACCAAGTGAAGATTCAGT 492
646 TTTAGAGAAAGCCAAATCTTGTGTTCTTTGATCTGACCAAGTGAAGATTCAGT 705
493 TTTAGAGAAAGCCAAATCTTGTGTTCTTTGATCTGACCAAGTGAAGATTCAGT 552
706 TTTCAATATAGTGCCTTTAACTTCCGTTGGAACCTGATCTCCATATTTAAAACTC 765
553 TTTCAATATAGTGCCTTTAACTTCCGTTGGAACCTGATCTCCATATTTAAAACTC 612
766 TCTCTTCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATTAGAGA 825
613 TCTCTTCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATTAGAGA 672
826 TGCATATTTTATGAAAGTGAAGTCAATTAAGCAAGCAATGAGACATTAATGTTTCTAC 885
673 TGCATATTTTATGAAAGTGAAGTCAATTAAGCAAGCAATGAGACATTAATGTTTCTAC 732
886 GTTCAAGAGGCTAAATGTGAGATCCAGATTTGAGAGAAATGTGAGAAATACATCTGT 945
733 GTTCAAGAGGCTAAATGTGAGATCCAGATTTGAGAGAAATGTGAGAAATACATCTGT 792
946 TTCAATGTGCTCT-GGTGTTCTTCTGATTAATCTTTGAAACACAGTCAAGATTAAGTCAAAC 1004

Db 793 TTCAATGTGCTCTGGGTTCTTCTGATTAATCTTTGAAACACAGTCAAGTCAAGTCAAAC 852
Qy 1005 AATAAGTTAT-GCTATGAGATGACAAACTCT-GAGTAATTTGAGCCAGAAATGAGT 1062
Db 853 CATTAAGTTATGCTATGAGATGACAAACTCTGGAGATTTGAGAGCCAGAAATGAGT 912
Qy 1063 AT-AGGTAAAGAGCCAAATTCACACTCTTACATTAACCAT 1100
Db 913 ATTAAGGTAAAGAGCCCAATTCACACTCTTACATTAACCAT 951

RESULT 9
B0678245 978 bp mRNA linear EST 15-JUL-2002
LOCUS
DEFINITION
AGENCOURT 8419682 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6274012
5', mRNA sequence.
ACCESSION
B0678245
VERSION
B0678245.1 GI:21790924
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 978)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LNCM2454 row: 0 column: 05
High quality sequence stop: 627.
Location/Qualifiers
1..978

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6274012"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 112"
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
ggcagcagc(g). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 56.8%; Score 785; DB 3; Length 978;
Best Local Similarity 94.8%; Pred. No. 6e-203;
Matches 888; Conservative 0; Mismatches 40; Indels 9; Gaps 7;

33 GGGCGGGGTTCCGAGCGAGGCTGCATGAGTGGCGGGGCTGCGGGGCTG 92
16 GAGCGGGGCTCCGAGCGAGAGCTGCATGAGTGGCGGGGCTGCGGGGCTG 75
Qy 93 GGGCGCTGCTCTGTGGCGCGCGCGGGCGCGGGCGCGGGCGG--CGCGCTACGGAAC 149
Db 76 GGGCGCTGCTCTGTGGCGCGCGCGGGCGCGGGCGCGGGCGCGCGCTACGGAAC 135
Qy 150 TCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTGCAAGTAAATATGAC 209

Db 136 TCACCCACCTGTGCAAAATTTGAGTGTCTGTTGAAAACTCTGCACAGTAATATGAC 195
 Qy 210 ATGGAATCCACCCGAGGAGGAGCAGCTCAATTTGATGATATGATTTTAACTTTGG 269
 Db 196 ATGGAATCCACCCGAGGAGGAGCAGCTCAATTTGATGATATGATTTTAACTTTGG 255
 Qy 270 CGACAAACAAAGATAAGAAATAGCTCCGAAAATCTGTGTTCAATAGAAAGTACCCTGAA 329
 Db 256 CGACAAACAAAGATAAGAAATAGCTCCGAAAATCTGTGTTCAATAGAAAGTACCCTGAA 315
 Qy 330 TGAAGAGATTTGTCTGCAAGTGGGTCCCAATGACCAATGAGATGAGAGCTTAG 389
 Db 316 TGAGAGATTTGTCTGCAAGTGGGTCCCAATGACCAATGAGATGAGAGCTTAG 375
 Qy 390 CATTTGGTTGAAAAATGCACTCAACCCCGAAGGTGATCTCTGATGCTGTGACGTA 449
 Db 376 CATTTGGTTGAAAAATGCACTCAACCCCGAAGGTGATCTCTGATGCTGTGACGTA 435
 Qy 450 ACTTCAATGCAATTTGGCAACAACCTGAGCTACATGAGTGTCTTGCTCCCTGGAAGAA 509
 Db 436 GCTTCAATGCAATTTGGCAACAACCTGAGCTACATGAGTGTCTTGCTCCCTGGAAGAA 495
 Qy 510 TACAGATCCGACACTAATATCTCTCTACTATTGGCAACAAGAGCTGAAAAAATTC 569
 Db 496 TACAGATCCGACACTAATATCTCTCTACTATTGGCAACAAGAGCTGAAAAAATTC 555
 Qy 570 TCAATGTAAAAACATCTTTAGAGAGGCAATCTTGTTGTTCTTGTGATCTGA -CCA 628
 Db 556 TCAATGTAAAAACATCTTTAGAGAGGCAATCTTGTTGTTCTTGTGATCTGA -CCA 615
 Qy 629 AAGTGAAGATTCAGATTTGGAACAACAAGTGTCAAAATATAGTCAAGATATGAG 688
 Db 616 AAGTGAAGATTCAGATTTGGAACAACAAGTGTCAAAATATAGTCAAGATATGAG 675
 Qy 689 GAAAAATTTAAACCATCTCTCAATATAGTGTCTTAACTT -CCGCTGGAACCTGATCTT 747
 Db 676 GAAAAATTTAAACCATCTCTCAATATAGTGTCTTAACTT -CCGCTGGAACCTGATCTT 735
 Qy 748 CCAATATTTAAAACTCTCTCTCCACCAAT -GATGACCTATATGCAATGGG -AGATC 805
 Db 736 CCAATATTTAAAACTCTCTCTCCACCAATGATGACCTATATGCAATGGGCAATC 795
 Qy 806 CACAGATTTTATAGCAGATGCTATTTTATGAGTGAAGTCAATTAACGCCAACTG 865
 Db 796 CACAGATTTTATAGCAGATGCTATTTTATGAGTGAAGTCAATTAACGCCAACTG 854
 Qy 866 AGACACATTAATGTTTCTACGTCGAAGAGGCTAAATGTG -AGAAATCCAGAAATTTGAGGA 924
 Db 855 AAACCATTAATGTTTCTACGTCGAAGAGGCTAAATGGAAGATTTCCCAATTTGAGACA 914
 Qy 925 AATGTGAGAAATCATCTTGTTCATAGTGTCCCTGCTG 961
 Db 915 AATGTGAGAAATCATCTTGTTCATAGTGTCCCTGCTG 951
 RESULT 10
 CB956372
 LOCUS CB956372 799 bp mRNA linear EST 29-Apr-2003
 DEFINITION ABEHCOURT_1366655 NIH MGC 184 Homo sapiens cDNA clone
 IMAGE:3053391 5', mRNA sequence.
 VERSION CB956372
 KEYWORDS CB956372.1 GI:30212489
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 799)
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: NDCM154 row: a column: 16
 High quality sequence stop: 651.
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 source
 1..799
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3053391"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Pooled-glandular; Vector: pDR-LIB; Site_1:
 SfiI (ggccatagggc); Site_2: SfiI (ggcgccgcgcg);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTAAGGC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 55.4%; Score 766.2; DB 4; Length 799;
 Best Local Similarity 99.2%; Pred. No. 7.8e-198;
 Matches 790; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 Qy 258 TAGCATTTTGGGCACAAACAAGATAGAAATAGTCCGGAATCTGCTCAATAGA 317
 Db 3 TAGCATTTTGGGCACAAACAAGATAGAAATAGTCCGGAATCTGCTCAATAGA 62
 Qy 318 AGTACCCCTGATAGAGATTTGTCTGCAAGTGGGTCCTGAGTACCAATGAGAG 377
 Db 63 AGTACCCCTGATAGAGATTTGTCTGCAAGTGGGTCCTGAGTACCAATGAGAG 122
 Qy 378 TGAGAACCTTAGCATTTTGGTTGAAAAATGATCTCACCCGAGAAGGTATCTGAGTC 437
 Db 123 TGAGAACCTTAGCATTTTGGTTGAAAAATGATCTCACCCGAGAAGGTATCTGAGTC 182
 Qy 438 TGCTGTACCTGAATTCATATGCAATTTGGGCACACCTGAGTACATGAAAGTCTTGACT 497
 Db 183 TGCTGTACCTGAATTCATATGCAATTTGGGCACACCTGAGTACATGAAAGTCTTGACT 242
 Qy 498 CCTGGAAGAAATTCAGTCCCGACACTAATATCTCTACATTTGGGACAGAGAGCT 557
 Db 243 CCTGGAAGAAATTCAGTCCCGACACTAATATCTCTACATTTGGGACAGAGAGCT 302
 Qy 558 GAAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAGGCCAATATCTTGGTTCCTT 617
 Db 303 GAAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAGGCCAATATCTTGGTTCCTT 362
 Qy 618 TGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAAGTGTCCAAATATAGTGTCAA 677
 Db 363 TGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAAGTGTCCAAATATAGTGTCAA 422
 Qy 678 GGATTAATGAGAAAAATTAACCATCTTCAATATAGTCTTTAACTTCCCGTGA 737
 Db 423 GGATTAATGAGAAAAATTAACCATCTTCAATATAGTCTTTAACTTCCCGTGA 482
 Qy 738 ACCTGATCTCCACATTTAAAAACCTGCTCTCCACATGATGAGCTATATGTGCATG 797
 Db 483 ACCTGATCTCCACATTTAAAAACCTGCTCTCCACATGATGAGCTATATGTGCATG 542

QY 798 GGAGAAATCCACAGAAATTTATTTAGCAGATGCTATTTTATGAAGTAGAAGCTCAATACAG 857
| | | | |
Db 543 GGAGATCCACAGAAATTTATTTAGCAGATGCTATTTTATGAAGTAGAAGCTCAATACAG 602
| | | | |
QY 858 CCAAACTGAGACCATTAATTTTCTTACGCTCAAGAGGCTAAATGTGAGATCCAGAAAT 917
| | | | |
Db 603 CCAAACTGAGACCATTAATTTTCTTACGCTCAAGAGGCTAAATGTGAGATCCAGAAAT 662
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QY 918 TGAGAAATGTGAGAAATCATCTTGTTCATGATGCTGAGT-TCTTCTGATCTT 976
| | | | |
Db 663 TGAGAAATGTGAGAAATCATCTTGTTCATGATGCTGAGTCTTCTGATCTT 722
| | | | |
QY 977 TGAACAGCTCAGAAATPAGAGTCAAAACAAATTAATTATGAGATGACAAATC- 1035
| | | | |
Db 723 TGAACAGCTCAGAAATPAGAGTCAAAACAAATTAATTATGAGATGACAAATCT 782
| | | | |
QY 1036 TGGAGTAATTGGAGCC 1051
| | | | |
Db 783 TGGAGTAATTGGAGCC 798
| | | | |

RESULT 11
DQ034842 866 bp DNA linear GSS 02-JUN-2005
LOCUS Homo sapiens IL13RA1 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ034842
VERSION DQ034842.1 GI:66886051
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homin.
REFERENCE 1 (bases 1 to 866)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) Plos Biol. 3 (6), E170 (2005)
15869325

JOURNAL
PUBMED 15869325
REFERENCE 2 (bases 1 to 866)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-May-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
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/gene="IL13RA1"
/locus_tag="HC4262"

ORIGIN
Query Match 53.5%; Score 739.4; DB 14; Length 866;
Best Local Similarity 88.6%; Pred. No. 1.7e-190;
Matches 740; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 146 AAACCTCAGCCACCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 205
| | | | |
Db 1 AAACCTCAGCCACCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 60
| | | | |
QY 206 GGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTTAGTGTATGGTATTTTATGTCATT 265
| | | | |

Db 61 GGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTTAGTGTATGGTATTTTATGTCATT 120
| | | | |
QY 266 TTGGCCGCAAAACAAGATTAAGAAATAGCTCCGAAACTGCTGTTCAATGAATGATACCC 325
| | | | |
Db 121 TTGGCCGCAAAACAAGATTAAGAAATAGCTCCGAAAACCTGCTTCAATGAATGATACCC 180
| | | | |
QY 326 TGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGGTAGCACCAATGAGAGTGAAGC 385
| | | | |
Db 181 TGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGGTAGCACCAATGAGAGTGAAGC 240
| | | | |
QY 386 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGGTATCTTGAATCTGCTGTGA 445
| | | | |
Db 241 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGGTATCTTGAATCTGCTGTGA 300
| | | | |
QY 446 CTGAACCTCAATCATTTTGGCAACAACCTGAGTACATGAAAGTTCCTTGGCTCCCTGAA 505
| | | | |
Db 301 CTGAGCTTCAATCATTTTGGCAACAACCTGAGTACATGAAAGTTCCTTGGCTCCCTGAA 360
| | | | |
QY 506 GGAATACAGTCCCGACACTAACTATCTCTACTATTGGCACAGAAAGCTGGAAAAA 565
| | | | |
Db 361 GGAATACAGTCCCGACACTAACTATCTCTACTATTGGCACAGAAAGCTGGAAAAA 420
| | | | |
QY 566 TTGATCAATGTGAAAAATCTTTTGAAGAGGCCAATACCTTGGTTCTTCTTGAATCTGA 625
| | | | |
Db 421 TTGATCAATGTGAAAAATCTTTTGAAGAGGCCAATACCTTGGTTCTTCTTGAATCTGA 480
| | | | |
QY 626 CCAAGTGAAGAGATTCAGTTTGAACAACAACAGTGCCTCAATATGATGATGATATG 685
| | | | |
Db 481 CCAAGTGAAGAGATTCAGTTTGAACAACAACAGTGCCTCAATATGATGATGATATG 540
| | | | |
QY 686 CAGAAAAATTAAACCATCTCTCAATATAGTGCCTTAACTTCCGTTGAAAACCTGATC 745
| | | | |
Db 541 CAGAAAAATTAAACCATCTCTCAATATAGTGCCTTAACTTCCGTTGAAAACCTGATC 600
| | | | |
QY 746 CTCACATATTAATAAACCCTCTCTTCCACATATATACCTATTTGGCAATGGAGAAATC 805
| | | | |
Db 601 CTCACATATTAATAAACCCTCTCTTCCACATATATACCTATTTGGCAATGGAGAAATC 660
| | | | |
QY 806 CACAGATTTTATTTAGCAGATGCTTATTTATAGTAGAAGCAATTAACAGCAAACTG 865
| | | | |
Db 661 CACAGATTTTATTTAGCAGATGCTTATTTATAGTAGAAGCAATTAACAGCAAACTG 720
| | | | |
QY 866 AGACACATATATGTTTCTAGCTCAAGAGGCTAAATGTGAGATCCAGAAATTTGAGAA 925
| | | | |
Db 721 AGACACATATATGTTTCTAGCTCAAGAGGCTAAATGTGAGATCCAGAAATTTGAGAA 780
| | | | |
QY 926 ATGTGAGAAATPACATCTTGTTCATGATGCTCCCTGCTTCTTCTGATCTTTGAA 980
| | | | |
Db 781 NNA 835
| | | | |

RESULT 12
DQ034843 729 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes IL13RA1 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ034843
VERSION DQ034843.1 GI:66886052
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
REFERENCE 1 (bases 1 to 729)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) Plos Biol. 3 (6), E170 (2005)
15869325

JOURNAL
PUBMED 15869325

REFERENCE	2 (bases 1 to 729)						
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.D., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.						
TITLE	Direct Submission						
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA						
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.						
FEATURES							
source	Location/Qualifiers 1..729 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <1..>729 /gene="IL13RA1" /locus_tag="HC4262"						
ORIGIN							
Query Match	52.1%; Score 720.8; DB 14; Length 729;						
Best Local Similarity	99.0%; Pred.No. 2e-185;						
Matches	722; Conservative 0; Mismatches 7; Indels 0; Gaps 0;						
Dy	157	CCTGGAACAAATTAGTGTCTCTGTTGAAAACCTTGCAACGTAATATGACATGAAT	216				
Dy	1	CCTGGACAATAATTGAGTGTCTGTGTAAAAAACCCTCACAGTAATATGACATGAAT	60				
Dy	217	CCACCCCGGAGGAGCAGCTCAAATTGTAGTCATAGSTATTATAGCATTTTGGCGACAA	276				
Dy	61	CCACCCGAGGAGGCCAGCTCAAAATTGTAGTCATAGSTATTATAGCATTTTGGCGACAA	120				
Dy	277	CAAGTAAGAATAATAGCTCCGGAACCTGCTGTTCAATAGAAAGTACCCCTGAATAGAGG	336				
Dy	121	CAAGTAAGAATAATAGCTCCGGAACCTGCTGTTCAATAGAAAGTACCCCTGAATAGAGG	180				
Dy	337	ATTGTCTCGCAAGTGGGGTCCCAGTGTAGCAACCAATGAGTAGAGAACCTTAGCATTTTG	396				
Dy	181	ATTGTCTCGCAAGTGGGGTCCCAGTGTAGCAACCAATGAGTAGAGAACCTTAGCATTTTG	240				
Dy	397	GTTGAAAAATGCATCTCACCCCCAGAGAGTATCCTGAGTCTGCTGTACTGAACTTAA	456				
Dy	241	GTTGAAAAATGCATCTCACCCCCAGAGAGTATCCTGAGTCTGCTGTACTGAACTTAA	300				
Dy	457	TGCATTTGGCAACACCTGAGCTACAATGAAGTGTCTTGCGTCCCTGSAAGGATACCACT	516				
Dy	301	TGCATTTGGCAACACCTGAGCTACAATGAAGTGTCTTGCGTCCCTGSAAGGATACCACT	360				
Dy	517	CCGCAACATACTACTCTCTACTATTGGGACAGAACCTTGAAAATAATTCATCAATGT	576				
Dy	361	CCGCAACATACTACTCTCTACTATTGGGACAGAACCTTGAAAATAATTCATCAATGT	420				
Dy	577	GAAAAACATCTTTAGGAAGCCCAATACCTTGTTGTTCTTTGATCTGACCAAGTAGAG	636				
Dy	421	GAAAAACATCTTTAGGAAGCCCAATACCTTGTTGTTCTTTGATCTGACCAAGTAGAG	480				
Dy	637	GATTCACGTTTGAACAACAAGTGTCCAATAATATGTCACAGGATTAATGACGAGAAAAAT	696				
Dy	481	GATTCACGTTTGAACAACAAGTGTCCAATAATATGTCACAGGATTAATGACGAGAAAAAT	540				
Dy	697	AAACATCTCTCAATATAGTCCCTTAATCTCCCGTGTGAACCTGATCCTCCACATTT	756				
Dy	541	AAACATCTCTCAATATAGTCCCTTAATCTCCCGTGTGAACCTGATCCTCCACATTT	600				
Dy	757	AAAAAACCTCTCTCCACATGATGACCTTATATGTGCATGGGAGAAATCCACAGATTTT	816				
Dy	601	AAAAAACCTCTCTCCACATGATGACCTTATATGTGCATGGGAGAAATCCACAGATTTT	660				
Dy	817	ATTAGCAGATGCTATTTTATGAGTGAAGTAATCAATTAACCCAAACCTGACACATAT	876				
Dy	661	ATTAGCAGATGCTATTTTATGAGTGAAGTAATCAATTAACCCAAACCTGACACATAT	720				
Dy	877	GTTTTCTAC 885					

DB		721 GTTTCTAC 729	
RESULT 13	BG699187	764 bp	mRNA linear EST 07-MAY-2001
LOCUS	BG699187		
DEFINITION	602678850r1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811485 5', mRNA sequence.		
ACCESSION	BG699187		
VERSION	BG699187.1	GI:13967231	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
JOURNAL	Contact: Robert Strusberg, Ph.D.		
COMMENT	Email: csqabp@email.nih.gov Tissue procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10702 row: d column: 14 High quality sequence stop: 755. Location/Qualifiers		
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ORIGIN			
Query Match	51.3%; Score 710; DB 2; Length 764;		
Best Local Similarity	98.2%; Pred. No. 1.8e-182;		
Matches 729; Conservative	0; Mismatches 10; Indels 3; Gaps 1;		
OY	34 CGGCCGGGTTCGAGCGGAGAAGGCTCATGATGAGTGCCCGCGCGGCTTCGGGGCTGTGG 93		
Db	8 CGGCCGGGCTTCGAGCGGAGAAGGCTCATGATGAGTGCCCGCGCGGCTTCGGGGCTGTGG 67		
OY	94 GCCTGTGCTCTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150		
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OY	151 CAGCCACTGTGACAATTGAGTGTCTCTGTGAATAAACCCTTGCACAGTAATATGACA 210		
Db	128 CAGCCACTGTGACAATTGAGTGTCTCTGTGAATAAACCCTTGCACAGTAATATGACA 187		
OY	211 TGGAATCACCCGAGGAGGAGCAGCTCAAAATTGATGATATGATATTTTAGTCATTTTGGC 270		
Db	188 TGGAATCACCCGAGGAGGAGCAGCTCAAAATTGATGATATGATATTTTAGTCATTTTGGC 247		

QY 271 GACAAACAGATAGAAAAATAGCTCGGAAACCTGTCCTTCAATAGAGTACCCCTGAT 330
 DB 248 GACAAACAGATAGAAAAATAGCTCGGAAACCTGTCCTTCAATAGAGTACCCCTGAT 307
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 DB 308 GAGAGATTTGTTGCAAGTGGGGTCCCACTGTAAGCAACCAATGAGTGAAGCCCTAGC 367
 QY 391 ATTGTTGTTGAAAAATGATCTGACCCCGAAGAGTATCTGAGTCTGCTGACTGAA 450
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 QY 451 CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAAGTGTCTTGGCTCCCTGGAAGGAT 510
 DB 428 CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAAGTGTCTTGGCTCCCTGGAAGGAT 487
 QY 511 ACCAGTCCGACCACTAATCTTACTCTTACTATTGGACAGAAAGCCCTGGAAGGAT 570
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 QY 571 CAATGTGAAAAACATCTTTAGAGAGGCCAATTAATCTTGGTGTCTTGTGATGACCAAA 630
 DB 548 CAATGTGAAAAACATCTTTAGAGAGGCCAATTAATCTTGGTGTCTTGTGATGACCAAA 607
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 QY 691 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTTCCCGTGTGAAAACCTGATCTCCA 750
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 QY 751 CATATTAAAAACCTCTCTCTCC 772
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RESULT 14
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 CRO00442
 CRO00442.1 GI:38526476
 EST.
 Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 842)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@ds-femail.nih.gov
 Tissue Procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
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 http://image.lnl.gov
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ORIGIN
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 Site 2: NotI; Library is oligo-dT primed and directionally
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 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to RNA size fraction, ligated with
 EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-Ase vector. Average insert size
 4-5kb. Adaptors 5' (AATTCGACAGAG) 3' and 5' d
 (CCTGATGCG) 3'. 3' linker sequence - GGCGCGCTGAAGGCC T18.
 Sequencing primers 3' end: T3 promoter primer 5' d
 (ATTAACTCTCACTAAGGAG) 3'. 5' End: T7 promoter primer 5' d
 (TAATCGACTCACTATAGAG) 3'. Library was constructed in the
 laboratory of M. Bento Soares. Note: this is a NIH_MGC
 Library"

QY 729 CCGTGTGAAACCTGATCTTCCACATATTAACACCTCTCTTCCACATGATGACCTATA 788
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 QY 789 TGTGCAATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTATGAACTAGAACT 848
 DB 86 TGTGCAATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTATGAACTAGAACT 145
 QY 849 CAATAACAGCCAACTGAGACACATATATGTTTCTACGTCCTCAAGAGGCTTAATGTGAA 908
 DB 146 CAATAACAGCCAACTGAGACACATATATGTTTCTACGTCCTCAAGAGGCTTAATGTGAA 205
 QY 909 TCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTC 968
 DB 206 TCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTC 265
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 QY 1089 CTACATTAACCATGTTTACATGTTTCCAGTCATGTCGACAGTGAATCATAGTACTCTT 1148
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 DB 506 TTTTAAGAAATGTTTGGAGACAGATGATGATCTGCACTGGAAGAGTACAGCAT 565
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RESULT 15
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 LOCUS CA391344


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DEFINITION     cs14a05.y1 Human Retinal pigment epithelium/choroid cDNA
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                5', mRNA sequence.
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VERSION        CA391344.1 GI:24723148
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      1 (bases 1 to 633)
AUTHORS        Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
                Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
                Expressed sequence tag analysis of human RPE/choroid for the
                NIHBank Project: Over 6000 non-redundant transcripts, novel genes
                and splice variants
                Mol. Vis. 8 (4), 205-220 (2002)
JOURNAL        12107410
COMMENT        Contact: Wistow G
                Section on Molecular Structure and Function
                National Eye Institute
                6/331, NIH, Bethesda, MD 20892-2740, USA
                Tel: 301 402 3452
                Fax: 301 496 0078
                Email: grame@helix.nih.gov
                Plate: 14 row: a column: 05
                Seq primer: M13RPL reverse primer (ABI).
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                /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
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                dissected RPE/choroid tissue. This in turn yielded 340 ug
                of total RNA and 7 ug of mRNA. A directionally cloned cDNA
                library in the pCMVSPORT6 vector was constructed at Life
                Technologies (Rockville, MD; now part of Invitrogen Corp),
                essentially following the protocols of the SuperScript
                Plasmid System (Invitrogen Corp.
                <http://www.invitrogen.com/>). The library code
                designation was cs. For this library, cDNA inserts were
                cloned into the NotI/MluI sites of the vector. EST
                analysis was performed on the unamplified library at the
                NIH Intramural Sequencing Center (NISC)."
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ORIGIN

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Query Match      45.7%; Score 631.4; DB 4; Length 633;
Best Local Similarity 99.8%; Pred. No. 5,5e-161;
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 198 AGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATGTAGTCTATGCTATTT 257
    |||
DB 61 AGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATGTAGTCTATGCTATTT 120

QY 258 TAGTCATTTTGGGACAAAGATTAAGAAATAGCTCCGAAACCTGCTTCAATAGA 317
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QY 318 AGTACCCTTAATGAGAGATTGTCTGCAAGTGGGCTCCAGTGTAGCAACCAATGAGAG 377
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QY 378 TGAGAGCCTAGCATTTTGGTTGTAAGAAATGATCTCACCCGAGAGGTGATCCTGAGTC 437
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DB 301 TGCTGTGACCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

QY 498 CCTGTGAAGATTCAGTCCGACACTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 557
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DB 361 CCTGTGAAGATTCAGTCCGACACTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420

QY 558 GGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 617
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QY 618 TGATCTGACCAAGATGAGATTCAGTTTGAACAACAGTGTCCAAATATGATCA 677
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QY 678 GGATTAATGAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
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DB 601 ACCGATCCTCCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 633
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:06:21 ; Search time 297 Seconds
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Title: US-09-051-843D-3

Perfect score: 1383
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1383	100.0	1383	US-09-688-286D-3	Sequence 3, Appli
2	1333.8	96.4	3999	US-08-543-679A-2902	Sequence 2902, Ap
3	1333.8	96.4	4038	US-08-969-125-8	Sequence 8, Appli
4	1333.8	96.4	4038	US-09-545-002-8	Sequence 8, Appli
5	1333.8	96.4	4039	US-09-949-016-223	Sequence 223, App
6	1333.8	96.4	4039	US-09-880-107-3856	Sequence 3856, Ap
7	1333.8	96.4	4039	US-09-543-679A-2903	Sequence 2903, Ap
8	1333.8	96.4	11927	US-09-193-707-5	Sequence 5, Appli
9	1333.8	96.4	14978	US-09-543-679A-2905	Sequence 2905, Ap
10	1012	73.2	1547	US-09-828-995B-51	Sequence 49, Appli
11	1012	73.2	1547	US-09-828-995B-51	Sequence 51, Appli
12	1009.8	73.0	2382	US-09-313-942-31	Sequence 31, Appli
13	1009.8	73.0	2382	US-10-282-162-31	Sequence 31, Appli
14	983	71.1	1215	US-09-828-995B-52	Sequence 32, Appli
15	983	71.1	1215	US-09-828-995B-53	Sequence 32, Appli
16	959.4	69.4	2355	US-09-313-942-29	Sequence 53, Appli
17	959.4	69.4	2355	US-10-282-162-29	Sequence 29, Appli
18	956.4	69.2	966	US-09-825-561A-81	Sequence 81, Appli
19	907.4	65.6	1680	US-09-688-286D-1	Sequence 1, Appli
20	692.8	50.1	701	US-09-949-016-2679	Sequence 2679, Ap
21	388.2	28.1	483	US-09-828-995B-48	Sequence 48, Appli
22	191.6	13.9	24000	US-09-949-016-14421	Sequence 14421, A
23	136	9.8	42975	US-09-949-016-11965	Sequence 11965, A

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	33	45.6	3.3	1355	2	US-07-757-390-4	Sequence 4, Appli
	34	45.6	3.3	1355	2	US-07-757-390-16	Sequence 16, Appli
	35	45.6	3.3	1355	2	US-08-442-282-4	Sequence 4, Appli
	36	45.6	3.3	1355	2	US-08-442-282-16	Sequence 16, Appli
	37	45.6	3.3	1355	2	US-08-442-281-4	Sequence 4, Appli
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	39	45.6	3.3	1355	2	US-08-939-727-4	Sequence 4, Appli
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	41	45.6	3.3	1808	2	US-07-757-390-2	Sequence 2, Appli
	42	45.6	3.3	1808	2	US-07-757-390-15	Sequence 15, Appli
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ALIGNMENTS

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RESULT 1
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Sequence 3, Application US/09688286D
Patent No. 6911530
GENERAL INFORMATION:
APPLICANT: Willson, Tracey
APPLICANT: Nicola, Nicos
APPLICANT: Hilton, Douglas
APPLICANT: Metcalf, Donald
APPLICANT: Zhang, Jian
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding sar
FILE REFERENCE: 23199-215
CURRENT APPLICATION NUMBER: US/09/688, 286D
CURRENT FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: AU PN6135
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: AU PN7276
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: AU PP2208
PRIOR FILING DATE: 1996-09-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1383
TYPE: DNA
ORGANISM: human
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(1338)
OTHER INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61 ATGAGAGTGGCGGCGGCGGCTCTGCGGCGCTGCGGCGCTGCTGCTGCGCGCGGCGG 120
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QY      121 GCGCGGGGCGGCGGCGGCGGCTTACGGAACCTAGCCACCTGTGACAAATTGAGTGTCT 180
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Db		1216	CAGATGATGTACTCTTCGACATCGAAGAAGTACGCATCTATGAGAAACAAGCAGAG	1275
OY		1291	GAAACCACTCTGTAGTGCTGATAGAAAACTGAAGAAAGCCTTCAGTAGAGATTA	1350
Db		1276	GAAACCACTCTGTAGTGCTGATAGAAAACTGAAGAAAGCCTTCAGTAGAGATTA	1335
OY		1351	TTTATTTTACCCTTCACTGTGACCTTGAGAGA	1383
Db		1336	TTTATTTTACCCTTCACTGTGACCTTGAGAGA	1368
 RESULT 5 US-09-949-016-223 ; Sequence 223, Application US/09949016 ; Patent No. 6812319 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: CLO01307 ; CURRENT APPLICATION NUMBER: US/09/949, 016 ; PRIOR FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO: 223 ; LENGTH: 4039 ; TYPE: DNA ; ORGANISM: Human US-09-949-016-223				
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Db		77	GCCTGTCTCTCTCGCCGCCGCGCGGGGCGGGGCGGGGCGCGGCGCTTACGGAACCT	136
OY		151	CAGCCACTGTGACAAATTGAGTGTCTCTGTTGAAAICTCTGCAACGTAAATATGACA	210
Db		137	CAGCCACTGTGACAAATTGAGTGTCTCTGTTGAAAICTCTGCAACGTAAATATGACA	196
OY		211	TGGAATCACCCGAGGGGAGCAGCTCAAATTGTAGTCTATGATTTTATGACTTTGGC	270
Db		197	TGGAATCACCCGAGGGGAGCAGCTCAAATTGTAGTCTATGATTTTATGACTTTGGC	256
OY		271	GACAAACAAGTAAAGAAATAGCTCCGGAACCTCGTCGTTCAATAGAAATACCCCTGAT	330
Db		257	GACAAACAAGTAAAGAAATAGCTCCGGAACCTCGTCGTTCAATAGAAATACCCCTGAT	316
OY		331	GAGAGATTTGTCTGCAAGTGGGGTCCCAGTGTAGACCAATAGAGTGAAGAGCTTAGC	390
Db		317	GAGAGATTTGTCTGCAAGTGGGGTCCCAGTGTAGACCAATAGAGTGAAGAGCTTAGC	376
OY		391	ATTTGGTTGAAAAATCATCTCACCCCAAGAGGTGATCCTGAGTCTGCTGTGACTGAA	450
Db		377	ATTTGGTTGAAAAATCATCTCACCCCAAGAGGTGATCCTGAGTCTGCTGTGACTGAG	436
OY		451	CTTCATGCAATTTGGCAACCTGAGCTACATGAAGTTCCTTGGCTCCCTGGAAGGAT	510
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QY	811	AATTATATAGCAGATGCTATTTATTAAGAGTAAAGCAATTAACAGCCAACTGACGA	870
Db	797	AATTATATAGCAGATGCTATTTATTAAGAGTAAAGCAATTAACAGCCAACTGACGA	856
QY	871	CATAATGTTTCTACGTCAGAGGCTAAATGTGAATCCAGAAATTTGAGAAATGTG	930
Db	857	CATAATGTTTCTACGTCAGAGGCTAAATGTGAATCCAGAAATTTGAGAAATGTG	916
QY	931	GAGAAATACATCTGTGTTTATAGTGCTCCGTGTGTTCTCTGATACCTTAACAACGTGCA	990
Db	917	GAGAAATACATCTGTGTTTATAGTGCTCCGTGTGTTCTCTGATACCTTAACAACGTGCA	976
QY	991	ATPAAGAGTCAAAAACAATPAAGTTATGCTATGAGATGACAACTCGAGTAATTGAGC	1050
Db	977	ATPAAGAGTCAAAAACAATPAAGTTATGCTATGAGATGACAACTCGAGTAATTGAGC	1036
QY	1051	CAAGAAATGAGTATAGTATGATGAAGCGCAATTCACACTCTACATPAACATGTTACTATT	1110
Db	1037	CAAGAAATGAGTATAGTATGATGAAGCGCAATTCACACTCTACATPAACATGTTACTATT	1096
QY	1111	GTTCCAGTCATCGTGCAGAGTGTCATCATATGATCCTGCTTACTTAAAGAGGCTCAAG	1170
Db	1097	GTTCCAGTCATCGTGCAGAGTGTCATCATATGATCCTGCTTACTTAAAGAGGCTCAAG	1156
QY	1171	ATTATTAATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTGAGAC	1230
Db	1157	ATTATTAATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTGAGAC	1216
QY	1231	CAGAAATGATGATCTCTGCTGCTGAGAAAGATACCATCTATGAGAACCAACCAAGAG	1290
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Db	1277	GAAACCGACTCTGTAGTCTGATGAAAACTGAAGAAAGCCTCAGATGATGAGATTA	1336
QY	1351	TTTATTTTACCTTCACCTGTAAGCTTGAAGA	1383
Db	1337	TTTATTTTACCTTCACCTGTAAGCTTGAAGA	1369
RESULT 7			
US-09-543-679A-2903			
Sequence 2903, Application US/09543679A			
Patent No. 7034007			
GENERAL INFORMATION:			
APPLICANT: NVCE, Jonathan W.			
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,			
COMPOSITIONS, KIT & METHOD FOR TREATMENT			
OF AIRWAY DISORDERS ASSOCIATED WITH			
BRONCHOCONSTRICTION, LUNG INFLAMMATION,			
NUMBER OF SEQUENCES: 3111			
CORRESPONDENCE ADDRESS:			
ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.			
STREET: 7 Clarke Drive			
CITY: Cranbury			
STATE: NJ			
COUNTRY: USA			
ZIP: 08512			
COMPUTER READABLE FORM:			
MEDIUM TYPE: CD-R			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: N/A			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/543.679A			
FILING DATE: 13-Apr-2000			
CLASSIFICATION: UNKNOWN			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 60/127,958			
FILING DATE: 1998-08-03			
ATTORNEY/AGENT INFORMATION:			
NAME: Amzel, Viviana			

[illegible]

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:10:57 ; Search time 1701 Seconds
(without alignments)
9990.476 Million cell updated/sec

Title: US-09-051-843D-3

Perfect score: 1383
Sequence: 1 gagctcaaccgacgacgaag.....tcactgtcacttgagaaga 1383

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11E_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11F_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1376.6	99.5	1383	6 US-10-036-568-3	Sequence 3, Appli
2	1333.8	96.4	4009	15 US-11-185-230-3	Sequence 3, Appli
3	1333.8	96.4	4009	16 US-11-182-384A-3	Sequence 3, Appli
4	1333.8	96.4	4009	16 US-11-183-599A-3	Sequence 3, Appli
5	1333.8	96.4	4038	8 US-10-671-697-8	Sequence 8, Appli
6	1333.8	96.4	4039	3 US-09-962-832-160	Sequence 160, App
7	1333.8	96.4	4039	3 US-09-880-107-3856	Sequence 186, App
8	1333.8	96.4	4039	7 US-10-172-118-633	Sequence 633, App
9	1333.8	96.4	4039	8 US-10-342-887-633	Sequence 633, App
10	1333.8	96.4	4039	10 US-10-843-641A-6046	Sequence 6046, App
11	1333.8	96.4	4466	3 US-09-971-392-58	Sequence 58, Appli
12	1330.6	96.2	1572	9 US-10-278-698-6	Sequence 6, Appli
13	1330.6	96.2	1572	9 US-10-278-698-6	Sequence 520, App
14	1264.8	91.5	1284	10 US-10-850-270-3	Sequence 3, Appli
15	1238.4	89.5	3880	3 US-09-822-846-109	Sequence 109, Appli
16	1236.8	89.4	3906	12 US-10-745-586-32	Sequence 32, Appli
17	1181.4	85.4	1680	3 US-09-822-846-110	Sequence 110, App

18	1012.8	73.2	2343	3 US-09-935-868-33	Sequence 33, Appli
19	1012.8	73.2	2343	6 US-10-287-035-33	Sequence 33, Appli
20	1012	73.2	1547	3 US-09-828-995B-49	Sequence 49, Appli
21	1012	73.2	1547	3 US-09-828-995B-51	Sequence 51, Appli
22	1012	73.2	1547	8 US-10-753-159-49	Sequence 49, Appli
23	1012	73.2	1547	8 US-10-753-159-51	Sequence 51, Appli
24	1011.2	73.1	2343	3 US-09-935-868-37	Sequence 37, Appli
25	1011.2	73.1	2343	6 US-10-287-035-17	Sequence 37, Appli
26	1011.2	73.1	2349	6 US-09-935-868-51	Sequence 51, Appli
27	1011.2	73.1	2349	6 US-10-287-035-51	Sequence 51, Appli
28	1011.2	73.1	2349	6 US-10-287-035-57	Sequence 57, Appli
29	1009.8	73.0	2382	3 US-09-313-942-31	Sequence 31, Appli
30	1009.8	73.0	2382	3 US-09-935-868-31	Sequence 31, Appli
31	1009.8	73.0	2382	6 US-10-287-035-11	Sequence 31, Appli
32	1009.8	73.0	2382	7 US-10-282-162-31	Sequence 31, Appli
33	1009.8	73.0	2382	13 US-11-134-114-31	Sequence 31, Appli
34	1008	72.9	2343	3 US-09-935-868-41	Sequence 41, Appli
35	1008	72.9	2343	6 US-10-287-035-41	Sequence 41, Appli
36	1008	72.9	2349	3 US-09-935-868-47	Sequence 47, Appli
37	1008	72.9	2349	6 US-10-287-035-47	Sequence 47, Appli
38	1008	72.9	2349	6 US-10-287-035-53	Sequence 53, Appli
39	983	71.1	1215	3 US-09-828-995B-52	Sequence 52, Appli
40	983	71.1	1215	3 US-09-828-995B-53	Sequence 53, Appli
41	983	71.1	1215	8 US-10-753-159-52	Sequence 52, Appli
42	983	71.1	1215	8 US-10-753-159-53	Sequence 53, Appli
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44	959.4	69.4	2355	3 US-09-935-868-29	Sequence 29, Appli
45	959.4	69.4	2355	6 US-10-287-035-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-10-036-568-3
Sequence 3, Application US/10036568
Publication No. US20020090682A1
GENERAL INFORMATION:
APPLICANT: Willson, Tracy
APPLICANT: Nicola, Nicols A.
APPLICANT: Hilton, Douglas J.
APPLICANT: Metcalf, Donald
APPLICANT: Zhang, Jian G.
TITLE OF INVENTION: NOVEL HAEMOPLETIN RECEPTOR AND GENETIC SEQUENCES
TITLE OF INVENTION: ENCODING SAME
FILE REFERENCE: Davies cc
CURRENT APPLICATION NUMBER: US/10/036,568
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US/09/051,843
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1383
TYPE: DNA
ORGANISM: Human IL-13 receptor alpha-chain
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(1338)
US-10-036-568-3

Query Match 99.5%; Score 1376.6; DB 6; Length 1383;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB 1 GAGCTTAACACGACCAAGAGATTAAACAGTCGCGCCGAGTTCGAGGAGAGGCTGC 60
QY 61 ATGAGTGGCGCGCGCGCTCTGCGGCGCTGTGGCGCTGCTCTGCTGCGCGCGCGG 120
DB 61 ATGAGTGGCGCGCGCGCTCTGCGGCGCTGTGGCGCTGCTGCTGCTGCGCGCGG 120

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OY		181	GTTGAAAACCTCTGCACAGTAATATGACATGGAATCCACCAGGGAGCCAGCTCAAT	240
Dd		181	GTTGAAAACCTCTGCACAGTAATATGACATGGAATCCACCAGGGAGCCAGCTCAAT	240
OY		241	TGTAGTCATAGGTATTATTTAGTCATTTTTGGCCACAACAAGATAGAATAATAGCTCCGGA	300
Dd		241	TGTAGTCATAGGTATTATTTAGTCATTTTTGGCCACAACAAGATAGAATAATAGCTCCGGA	300
OY		301	ACTGTCGTCATATGAAGTACCCCCTGAATGAGAGATTTGTCTGCAAGTGSGGGGCCAG	360
Dd		301	ACTGTCGTCATATGAAGTACCCCCTGAATGAGAGATTTGTCTGCAAGTGSGGGGCCAG	360
OY		361	TGTACACCAATGAGAGTGAAGAGCCTAGCATTTTGTGTGAATAATGATCTCACCCCCA	420
Dd		361	TGTACACCAATGAGAGTGAAGAGCCTAGCATTTTGTGTGAATAATGATCTCACCCCCA	420
OY		421	GAGGTGATCCTGAGTCTGTGTGACTGAATTCATGCAATTTGGCACAACCTGAGCTAC	480
Dd		421	GAGGTGATCCTGAGTCTGTGTGACTGAATTCATGCAATTTGGCACAACCTGAGCTAC	480
OY		481	ATGAAGTTCCTGGCTCCCTGGAGAGAAATCCAGTCCCGACACTAATATATCTCTAC	540
Dd		481	ATGAAGTTCCTGGCTCCCTGGAGAGAAATCCAGTCCCGACACTAATATATCTCTAC	540
OY		541	TATTGGCACAAGAGCCTGGAAAAAATTCATCATGTGAAAAATCTTTAGAGAGGCCCA	600
Dd		541	TATTGGCACAAGAGCCTGGAAAAAATTCATCATGTGAAAAATCTTTAGAGAGGCCCA	600
OY		601	TACTTTGGTTGTTCTTGTGATGTGACCAAAGTGAAAGATTCOAGTTTGAACAACACGT	660
Dd		601	TACTTTGGTTGTTCTTGTGATGTGACCAAAGTGAAAGATTCOAGTTTGAACAACACGT	660
OY		661	GTCCAAATPAATGAGTACAGATPATAGCAGAAAAATTAACAATCCTTCAATATAGTGCCT	720
Dd		661	GTCCAAATPAATGAGTACAGATPATAGCAGAAAAATTAACAATCCTTCAATATAGTGCCT	720
OY		721	TTAATCTTCCCGTGAAACCTGATCCTCCACATATTTAAAAACCTCTCTCCACATGAT	780
Dd		721	TTAATCTTCCCGTGAAACCTGATCCTCCACATATTTAAAAACCTCTCTCTCCACATGAT	780
OY		781	GACCTATAATGTGCAATGGGAGAAATCCACAGAAATTTTATPAGCAGATGCTTATTTGAA	840
Dd		781	GACCTATAATGTGCAATGGGAGAAATCCACAGAAATTTTATPAGCAGATGCTTATTTGAA	840
OY		841	GTAGAAATGCAATAACGCCAAATCTBAGACACATAATGTTTTCTAGTCCAGAGGCTAA	900
Dd		841	GTAGAAATGCAATAACGCCAAATCTBAGACACATAATGTTTTCTAGTCCAGAGGCTAA	900
OY		901	TGTGGAATCCAGAAATTTGAGAGAAATGTGAGAAATPACATCTGTTCATGATGCTCTGCT	960
Dd		901	TGTGGAATCCAGAAATTTGAGAGAAATGTGAGAAATPACATCTGTTCATGATGCTCTGCT	960
OY		961	GTTCTTCTGATATCTTTGAACAAGTCCAGATPAGAGTCAAAACAATAATAGTTATGCTAT	1020
Dd		961	GTTCTTCTGATATCTTTGAACAAGTCCAGATPAGAGTCAAAACAATAATAGTTATGCTAT	1020
OY		1021	GAGATGACAACTCTGAGATTAATGGAGCCCAAGAAATGAGTATGATAGTAAGAGGCAT	1080
Dd		1021	GAGATGACAACTCTGAGATTAATGGAGCCCAAGAAATGAGTATGATAGTAAGAGGCAT	1080
OY		1081	TCCAACATCTACATPACCACTGTTACTCATGTGTTCCAGTCATGCTGCGCAGGTGCATCAT	1140
Dd		1081	TCCAACATCTACATPACCACTGTTACTCATGTGTTCCAGTCATGCTGCGCAGGTGCATCAT	1140
OY		1141	GTACTCTGCTTTTAACTAAAAAGCTCAAGATTAATATATTCCTCCAAATTCCTGATCTCT	1200
Dd		1141	GTACTCTGCTTTTAACTAAAAAGCTCAAGATTAATATATTCCTCCCAATTCCTGATCTCT	1200
OY		1201	GGCAAGATTTTAAAGAAATGTTTGGAGACCAAGAAATGATGATATCTCTGCATCGAAGAG	1260

Db	1201	GGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATATGATACTCTGCATCGGAAGAG	1260
Qy	1261	TACGACATCTATGGAAGCAAAACCAAGAGAAACCGACTCTGTAGTGTGATGAAAC	1320
Db	1261	TACGACATCTATGGAAGCAAAACCAAGAGAAACCGACTGTAGTGTGATGAAAC	1320
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Db	1381	AGA 1383	
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; Sequence 3, Application US/11185230			
; Publication No. US20050282216A1			
; GENERAL INFORMATION:			
; APPLICANT: Caput, Daniel			
; APPLICANT: Ferrare, Pascual			
; APPLICANT: Laurent, Patrick			
; APPLICANT: Vitea, Natalio			
; TITLE OR INVENTION: Purified Polypeptides Having IL-13 Receptor Activity			
; FILE REFERENCE: IVD924 US CNT 1			
; CURRENT APPLICATION NUMBER: US/11/185,230			
; CURRENT FILING DATE: 2005-07-18			
; PRIOR APPLICATION NUMBER: PCT/FR96/01756			
; PRIOR FILING DATE: 1996-11-07			
; NUMBER OF SEQ ID NOS: 15			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 4009			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
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Best Local Similarity 99.6%; Score 1333.8; DB 15; Length 4009;			
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;			
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Db	7	CGGCGGGGCTCCGAGGCGAGAGGCTGCATGAGTGGCCGGGCGGCTCTGCGGGCTGTGG	66
Qy	94	GCGGTGCTGCTCTGTCGCGCGCGCGGGGGGGCGGGGGCGGGGG---CGGGCTCAGGGAACT	150
Db	67	GCGGTGCTGCTCTCTGCGCGCGGGGGGGGGGGGGCGGGGGCGGGGGCTCAGGGAACT	126
Qy	151	CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTATATGACA	210
Db	127	CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTATATGACA	186
Qy	211	TGGAATCCACCGAGGAGGCCAGCTCAAAATTGATGCTATGATATTTTATGCTATTTGGC	270
Db	187	TGGAATCCACCGAGGAGGCCAGCTCAAAATTGATGCTATGATATTTTATGCTATTTGGC	246
Qy	271	GACAAACAAAGTAAAGAAATATGCTCCGGAACCTGCTGTTCAATAGAAAGTACCCCTGAAT	330
Db	247	GACAAACAAAGTAAAGAAATATGCTCCGGAACCTGCTGTTCAATAGAAAGTACCCCTGAAT	306
Qy	331	GAGAGGATTTTCTCTGCAAGTGGGGTCCGAGTGTAGCAACAAATGAGAGTGAAGCTTAGC	390
Db	307	GAGAGGATTTTCTCTGCAAGTGGGGTCCGAGTGTAGCAACAAATGAGAGTGAAGACCTTAGC	366
Qy	391	ATTTTGGTTGAAAAATGATCTCAACCCCAAGAGTATCTGAGTCTGCTGTGACTGAA	450
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Qy	451	CTTCAATGCAATTTGGACAACCTTAGACTACATGAAGTGTCTTGGCTCCCTGGAAAGAAAT	510

Db	427	CTTCATGATTTGGCACAACCTGAGCTACAGAAATGTTCTTGGCTCCCTGGAAAGAT	486
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Db	487	ACCAATCCCGACACTAATCTACTCTCTACTATTTGGCACAAGAGCCTGGAAAAATTCAT	546
Qy	571	CAATGTGAAAAATCTTTTAGAAGAGCCAAATCTTGGTGTCTCTTGATCTTGACCAA	630
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Qy	631	GTGAAGATTCAGTTTGAACAACAAGTGCACAAATATATGGTCAAGGATATACAGA	690
Db	607	GTGAAGATTCAGTTTGAACAACAAGTGCACAAATATATGGTCAAGGATATACAGA	666
Qy	691	AAAAATTAACCATCTTCCTCAATATAGTGCCTTTAACTTCCCGTGAACCTGATCCTCA	750
Db	667	AAAAATTAACCATCTTCCTCAATATAGTGCCTTTAACTTCCCGTGAACCTGATCCTCA	726
Qy	751	CATATTAATAAACCTCTCCTCCACATATGATGCTATATGTGCAATGGAGAAATCAAG	810
Db	727	CATATTAATAAACCTCTCCTCCACATATGATGCTATATGTGCAATGGAGAAATCAAG	786
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Qy	871	CATATATGTTTTCTACGTCCAAGAGGCTAAATGTGAAATCCGAATTTGAAGAAATGTG	930
Db	847	CATATATGTTTTCTACGTCCAAGAGGCTAAATGTGAAATCCGAATTTGAAGAAATGTG	906
Qy	931	GAGAAATACATCTTGTTTCATGTGCTCCGTGATGTTCTTCTGATATCTTTGAACAAGT	990
Db	907	GAGAAATACATCTTGTTTCATGTGCTCCGTGATGTTCTTCTGATATCTTTGAACAAGT	966
Qy	991	ATAAGATGCAAAAACAATTAAGTTATAGCTATAGAGATGAACAACTCTGAGATTTGAGC	1056
Db	967	ATAAGATGCAAAAACAATTAAGTTATAGCTATAGAGATGAACAACTCTGAGATTTGAGC	1026
Qy	1051	CAAGAAATGAGATATGATPAGAAGGCGCAATTCACACTCACTACATTAACATGTTACTAT	1110
Db	1027	CAAGAAATGAGATATGATPAGAAGGCGCAATTCACACTCACTACATTAACATGTTACTAT	1086
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Db	1087	GTTCCAGTCATCTGTCGAGGTGCAATCATATAGTACTCTGCTTACCTTAACCTTAAGAGC	1146
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Db	1147	ATTATTAATATTCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAGC	1206
Qy	1231	CAGAAATGATGATCTCTGCACTGGAAGAAAGTACGACATCTATGAGAACCAACCAAGAG	1290
Db	1207	CAGAAATGATGATCTCTGCACTGGAAGAAAGTACGACATCTATGAGAACCAACCAAGAG	1266
Qy	1291	GAAACCGACTCTGTAGTGTGATGAAACCTGGAAGAAAGCTCTCACTGATGAGATTA	1356
Db	1267	GAAACCGACTCTGTAGTGTGATGAAACCTGGAAGAAAGCTCTCACTGATGAGATTA	1326
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	/	TITLE OF SEQUENCE:	Purified polypeptides having IL-13 receptor activity
	/	FILE REFERENCE:	IUD924 US DIV 2
	/	CURRENT APPLICATION NUMBER:	US/11/182, 384A
	/	CURRENT FILING DATE:	2005-07-15
	/	PRIOR APPLICATION NUMBER:	09/077, 817
	/	PRIOR FILING DATE:	1998-09-14
	/	PRIOR APPLICATION NUMBER:	PCT/FR96/01756
	/	PRIOR FILING DATE:	1996-11-07
	/	NUMBER OF SEQ ID NOS:	15
	/	SOFTWARE:	PatentIn version 3.3
	/	SEQ ID NO 3	
	/	LENGTH:	4009
	/	TYPE:	DNA
	/	ORGANISM:	Homo sapiens
	/		US-11-182-384A-3
		Query Match	96.4%; Score 133.8; DB 16; Length 4009;
		Best Local Similarity	99.6%; Pred. No. 0;
		Matches 1348; Conservative	0; Mismatches 2; Indels 3; Gaps 1
Oy		34	CGGCCGGGTTCCGAGCGCAGAGGCTGCATGTAGTGCCGGCGCGGCTTCGGCGGCTGTG 93
Dd		7	CGCGCGGGCTCCGAGGGGAGAGGCTGCATGTAGTGGCCGGCGGCTGTGGCGGCTGTGG 66
Oy		94	GCGCTGCTGCTCTGTGCGCGCGCGGGGGCGGGGGGG--CGCCCTACGGAACT 150
Dd		67	GCGCTGCTGCTCTGTGCGCGCGGGGGGGGGGGGGCGCGCGCGCTACGGAACT 126
Oy		151	CAGCACCTGTGAACAATTGATGTCTCTGTGAAAACTCTGCACGTAATAATGACA 210
Dd		127	CAGCACCTGTGAACAATTGATGTCTCTGTGAAAACTCTGCACGTAATAATGACA 186
Oy		211	TGCAATCCACCAGGAGGAGCAGCTCAAATTTAGTCTATGTTATTTAGCATTTTGGC 270
Dd		187	TGCAATCCACCAGGAGGAGCAGCTCAAATTTAGTCTATGTTATTTAGCATTTTGGC 246
Oy		271	GACAAACAATGAAGAATAATGCTCCGAAACTCGTCGTTCAATGAAGTACCCCTGAAT 330
Dd		247	GACAAACAATGAAGAATAATGCTCCGAAACTCGTCGTTCAATGAAGTACCCCTGAAT 306
Oy		331	GAGAGATTTGTCTGGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAACCTTAGC 390
Dd		307	GAGAGATTTGTCTGGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAACCTTAGC 366
Oy		391	ATTTTGGTGAATAATCATCTCAACCCCCAGAAAGTGTACTGAGTCTGCTGTACTGAA 450
Dd		367	ATTTTGGTGAATAATCATCTCAACCCCCAGAAAGTGTACTGAGTCTGCTGTACTGAA 426
Oy		451	CTTCAATGCATTTTGGCAACAACCTTAGCTACATGAAGTGTCTTGGCTCCCTGGAAGGAT 510
Dd		427	CTTCAATGCATTTTGGCAACAACCTTAGCTACATGAAGTGTCTTGGCTCCCTGGAAGGAT 486
Oy		511	ACCAAGTCCCGACATTAATCTATCTCTCTAATTTGGCAACGAGCCTGGAAAAATTCAT 570
Dd		487	ACCAAGTCCCGACATTAATCTATCTCTCTAATTTGGCAACGAGCCTGGAAAAATTCAT 546
Oy		571	CAATGTGAAAAATCTTTAGGAAGGGCAATACTTTGGTGTCTTCCCTTTGATCTGACCAA 630
Dd		547	CAATGTGAAAAATCTTTAGGAAGGGCAATACTTTGGTGTCTTCCCTTTGATCTGACCAA 606
Oy		631	GTEAAGATTCGATTTTGAACAACAAGTGTCCAATAATAGTCAAGATATGACAGA 690
Dd		607	GTEAAGATTCGATTTTGAACAACAAGTGTCCAATAATAGTCAAGATATGACAGA 666
Oy		691	AAATTTAAACATCTTCAATATATGTGCTTTAACTTCCGTGTGAAACCTGATCTTCCA 750
Dd		667	AAATTTAAACATCTTCAATATATGTGCTTTAACTTCCGTGTGAAACCTGATCTTCCA 726
Oy		751	CATATTAACAAACCTCTCTTCCACAAGATGACCTTATGTGCAATGGAGAAATCCACAG 810
Dd		727	CATATTAACAAACCTCTCTTCCACAAGATGACCTTATGTGCAATGGAGAAATCCACAG 786
Oy		811	AATTTATATGACAGATCTTATTTTATGAGTAGAGTCAATTAACGACCAACTGAGACA 870

Db	787	AAATTTATAGCAGATGCCATATTTTATAGAGAGCAATACAGCCAACTGAGACA	846
Qy	871	CATAATGTTTTCTACGTCCAAGAGCTAAATGTGGAATCCAGATTTTGAGAAATGTG	930
Db	847	CATATATGTTTTCTACGTCCAAGAGCTAAATGTGGAATCCAGATTTTGAGAAATGTG	906
Qy	931	GAGAAATACATCTGTTTCATGTGCTCCGTCGTCGTCCTCTGATPACTTTGAACAGCTCAG	990
Db	907	GAGATACATCTGTTTCATGTGCTCCGTCGTCGTCCTCTGATPACTTTGAACAGCTCAG	966
Qy	991	ATAAGAGTCAAAACAAATAGTTATGCTATGAGATGACAACTCTGAGATTAATTGAGC	1050
Db	967	ATAAGAGTCAAAACAAATAGTTATGCTATGAGATGACAACTCTGAGATTAATTGAGC	1026
Qy	1051	CAAGAAATGAGTATATGTTAAGTAGAGCGCAATTCACACTCTACATPACCATGTTACTATT	1110
Db	1027	CAAGAAATGAGTATATGTTAAGTAGAGCGCAATTCACACTCTACATPACCATGTTACTATT	1086
Qy	1111	GTTCCAGTCATCGTCGACGTCGCAATCATAGTACCTCGCTTTCACCTAAAAAGCTCAG	1170
Db	1087	GTTCCAGTCATCGTCGACGTCGCAATCATAGTACCTCGCTTTCACCTAAAAAGCTCAG	1146
Qy	1171	ATTATATATATTCCTCCCAATTCCTGATCCTGCGCAAGATTTTAAAGAAATGTTTGAGAC	1230
Db	1147	ATTATATATATTCCTCCCAATTCCTGATCCTGCGCAAGATTTTAAAGAAATGTTTGAGAC	1206
Qy	1231	CAGAAATGATGATCCTGCGCACTCGGAAGAAAGTACGACATCTATGGAACCAACCAAGAG	1290
Db	1207	CAGAAATGATGATCCTGCGCACTCGGAAGAAAGTACGACATCTATGGAACCAACCAAGAG	1266
Qy	1291	GAAACCGACCTCTGATGTCGTATAGAAACCTGGAAGAAGCCTCAGTGTGAGATTA	1350
Db	1267	GAAACCGACCTCTGATGTCGTATAGAAACCTGGAAGAAGCCTCAGTGTGAGATTA	1326
Qy	1351	TTTATATTTTACCTTCACTGTGACCTTGGAAGA	1383
Db	1327	TTTATATTTTACCTTCACTGTGACCTTGGAAGA	1359

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RESULT 4
US-11-183-599A-3
Sequence 3, Application US/11183599A
Publication No. US20060035856A1
GENERAL INFORMATION:
APPLICANT: Caput, Daniel
APPLICANT: Pettrera, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Vitta, Natalio
TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
FILE REFERENCE: IVD924 US Div 1
CURRENT APPLICATION NUMBER: US/11/183,599A
PRIORITY FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: 09/077,817
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 4009
TYPE: DNA
ORGANISM: Homo sapiens
US-11-183-599A-3

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Query Match	96.4%	Score 1333.8;	DB 16;	Length 4009;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1348;	Conservative 0;	Mismatches 2;	Indels 3;	Gaps 1;

[illegible][illegible]

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Db 1147 ATTATATATATCCCTCCCAATTCCTGATCTGCGAAGATTTTAAAGAAATGTTGGAC 1206
|||
Qy 1231 CAGATGATGATGATCTGCTGACCTGGAGAGTACGATCTATGAGAACCAACCAAGAG 1290
|||
Db 1207 CAGATGATGATGATCTGCTGACCTGGAGAGTACGATCTATGAGAACCAACCAAGAG 1266
|||
Qy 1291 GAAACCGACTCTGATGCTGATAGTAAAGAACTGAAAGAGCTCTGATGATGAGATTA 1350
1267 GAAACCGACTCTGATGCTGATAGTAAAGAACTGAAAGAGCTCTGATGATGAGATTA 1326
|||
Qy 1351 TTTATTTTACCTTCACTGCTGATGAGTGAAGA 1383
1327 TTTATTTTACCTTCACTGCTGATGAGTGAAGA 1359
|||
RESULT 5
US-10-671-697-8
; Sequence 8, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FRAGMENT TYPE: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1323
; SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-10-671-697-8
Query Match 96.4%; Score 1333.8; DB 8; Length 4038;
Best Local Similarity 99.6%; Pred No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Qy 151 CAGCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTGTGCACAGTATATGACA 210
|||
Db 136 CAGCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTGTGCACAGTATATGACA 195
|||
Qy 211 TGAATTCACCCGAGGAGGAGCCAGCTCAATTTGATGTATGATATTTTATGATTTGGC 270
196 TGAATTCACCCGAGGAGGAGCCAGCTCAATTTGATGTATGATATTTTATGATTTGGC 255
|||
Qy 271 GACAAACAAGTAAAGAAAATGCTCCGGAACCTGTCGTTCAATTTGAAGTACCTGTGAT 330
256 GACAAACAAGTAAAGAAAATGCTCCGGAACCTGTCGTTCAATTTGAAGTACCTGTGAT 315
|||
Qy 331 GAGAGATTTTGTCTGCAAGTGGGGTCCAGAGTGTACACCAATGAGAGTGAAGAGCTTGC 390
316 GAGAGATTTTGTCTGCAAGTGGGGTCCAGAGTGTACACCAATGAGAGTGAAGAGCTTGC 375
|||
Qy 391 ATTTTGGTTGAAAATGATCTCAACCCGAGAGGTGATTCCTGATGCTGTGACTGAA 450
376 ATTTTGGTTGAAAATGATCTCAACCCGAGAGGTGATTCCTGATGCTGTGACTGAG 435
|||
Qy 451 CTTCAATGCAATTTTGGCACAACCTGAGCTACATGAAGTGTCTTGGCTCTCTGGAAGAT 510
436 CTTCAATGCAATTTTGGCACAACCTGAGCTACATGAAGTGTCTTGGCTCTCTGGAAGAT 495
|||
Qy 511 ACCAGTCCCGACACTAATCTACTCTACTATTGGGACAGAGAGCTGGAAAAATTCAT 570
496 ACCAGTCCCGACACTAATCTACTCTACTATTGGGACAGAGAGCTGGAAAAATTCAT 555
|||
Qy 571 CAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTGCTTTCCTTGTGATCTGACAA 630
556 CAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTGCTTTCCTTGTGATCTGACAA 615
|||
Qy 631 GTGAAGATTCAGATTTTGAACAACAAGTGTCCAAATATGTGTCAGAGATATGACAGA 690
616 GTGAAGATTCAGATTTTGAACAACAAGTGTCCAAATATGTGTCAGAGATATGACAGA 675
|||
Qy 691 AAAATTAACCATCTTCAATATGATGCTTTAATCTCCGCTGGAAACCTGATCTCTCA 750
676 AAAATTAACCATCTTCAATATGATGCTTTAATCTCCGCTGGAAACCTGATCTCTCA 735
|||
Qy 751 CATATTAACCACTCTCTCTTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810
736 CATATTAACCACTCTCTCTTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 795
|||
Qy 811 AATTTTATTTAGAGATGCTTATTTTATGAAGTGAAGTCAATTAACGCAAACTGACACA 870
796 AATTTTATTTAGAGATGCTTATTTTATGAAGTGAAGTCAATTAACGCAAACTGACACA 855
|||
Qy 871 CATATGTTTTTCTACGTCGCAAGAGGCTTAATGTGAGAAATCCAGAAATTTGAGAAATGCTG 930
856 CATATGTTTTTCTACGTCGCAAGAGGCTTAATGTGAGAAATCCAGAAATTTGAGAAATGCTG 915
|||
Qy 931 GAGATATCATCTTGTTCATGATGCTCTGATGCTTCTCTGATATTTTGAACACAGTACA 990
916 GAGATATCATCTTGTTCATGATGCTCTGATGCTTCTCTGATATTTTGAACACAGTACA 975
|||
Qy 991 ATTAAGATCAAAACAAATTAAGTATGCTATGAGATGACAAACTGTGAGTAAATTTGAGC 1050
976 ATTAAGATCAAAACAAATTAAGTATGCTATGAGATGACAAACTGTGAGTAAATTTGAGC 1035
|||
Qy 1051 CAAAGAAATGAGTATGATGAGAAAGCCAAATTTCCACATCTATCAATCAATCAATCTTCTATT 1110
1036 CAAAGAAATGAGTATGATGAGAAAGCCAAATTTCCACATCTATCAATCAATCAATCTTCTATT 1095
|||
Qy 1111 GTTCCAGTCAATGCTGAGGAGTGAATATGATATCTCTGCTTTAATCTTAAAGAGCTCAAG 1170
1096 GTTCCAGTCAATGCTGAGGAGTGAATATGATATCTCTGCTTTAATCTTAAAGAGCTCAAG 1155
|||
Qy 1171 ATTATATATTTCCCTCCAAATTTCTGATCTGCGCAAGATTTTAAAGAAATGTTTGGAGAC 1230
1156 ATTATATATTTCCCTCCAAATTTCTGATCTGCGCAAGATTTTAAAGAAATGTTTGGAGAC 1215

[illegible]

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RESULT 6
US-09-962-832-160
; Sequence 160, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Eppner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962, 832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-160

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Query Match	96.4%	Score 133.8;	DB 3;	Length 4039;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1348; Conservative	0;	Mismatches 2;	Indels 3;	Gaps 1;

[illegible]

Db	497	ACCGTCCCGACATACTATCTCTACTATTGGCACGAAAGCTGGAAAAATTTCAT	556
Qy	571	CAATGTGAAAACATCTTTAGAGAAAGCCAACTTTGGTGTCTTTGATCTGACCAA	630
Db	557	CAATGTGAAAACATCTTTAGAGAAAGCCAACTTTGGTGTCTTTGATCTGACCAA	616
Qy	631	GTGAAGATTCGAGTTTGGAAACAACAAGTGTCCAAATAATGGTCAGAGTAATGCAGA	690
Db	617	GTGAAGATTCGAGTTTGGAAACAACAAGTGTCCAAATAATGGTCAGAGTAATGCAGA	676
Qy	691	AAATTTAAACCATGCTTCAATATATAGTCCCTTTAACTTCCCGTGGAAACCTGATCCCA	750
Db	677	AAATTTAAACCATGCTTCAATATATAGTCCCTTTAACTTCCCGTGGAAACCTGATCCCA	736
Qy	751	CATATTTAAAACTCTCTCTTCCACATATGATGACCTATATATGTGCATATGGAGAAATCCACAG	810
Db	737	CATATTTAAAACTCTCTCTTCCACATATGATGACCTATATATGTGCATATGGAGAAATCCACAG	796
Qy	811	AATTTTATATAGAGATGCGCTATTTTATGAAGTAGAAGTCATATTAACGCCAAACCTGAGACA	870
Db	797	AATTTTATATAGAGATGCGCTATTTTATGAAGTAGAAGTCATATTAACGCCAAACCTGAGACA	856
Qy	871	CATATGTTTTCTACGTCCCAAGAGGCTTAATGTGAGAAATCAGAAATTTTGAGAGAAATGTG	930
Db	857	CATATGTTTTCTACGTCCCAAGAGGCTTAATGTGAGAAATCAGAAATTTTGAGAGAAATGTG	916
Qy	931	GAGAAATACATCTTGTTCATGTGTCCTGTGGTCTTCCTGATACTTTGAAACAAGTCAGA	990
Db	917	GAGAAATACATCTTGTTCATGTGTCCTGTGGTCTTCCTGATCTTTGAAACAAGTCAGA	976
Qy	991	ATAAGAGTCAAAACAATAAGTTATGTGATAGAGATGACAAACTCTGGAGTAATTTGAGC	1050
Db	977	ATAAGAGTCAAAACAATAAGTTATGTGATAGAGATGACAAACTCTGGAGTAATTTGAGC	1036
Qy	1051	CAAGAAATGAGTATAGGTAAGAAAGCGCAATTCACACTCTACATTAACCATGTTACTATT	1110
Db	1037	CAAGAAATGAGTATAGGTAAGAAAGCGCAATTCACACTCTACATTAACCATGTTACTATT	1096
Qy	1111	GTTCAGTCACTGTCGACAGGTGCATATAGTATCTCTGCTTTAACTTAAAAAGGCTCAAG	1170
Db	1097	GTTCAGTCACTGTCGACAGGTGCATATAGTATCTCTGCTTTAACTTAAAAAGGCTCAAG	1156
Qy	1171	ATTATTTATATTCCTCCCAATTCCTGCATTCCTGGACAAAGTTTTTAAAGAAATGTTTGAGAC	1230
Db	1157	ATTATTTATATTCCTCCCAATTCCTGCATTCCTGGACAAAGTTTTTAAAGAAATGTTTGAGAC	1216
Qy	1231	CAGAAATGATGACTCTGCACTGGAAAGAGACACACTTATGAGAGCAAAACCAAGAG	1290
Db	1217	CAGAAATGATGACTCTGCACTGGAAAGAGACACACTTATGAGAGCAAAACCAAGAG	1276
Qy	1291	GAACCCGACTCTGTAGTGTGATGAAAACCTGAAAGAACCTCTCAGTATGTGAGATTA	1350
Db	1277	GAACCCGACTCTGTAGTGTGATGAAAACCTGAAAGAACCTCTCAGTATGTGAGATTA	1336
Qy	1351	TTTATTTTATCCTTCACTGTGACCTTGAGAGA	1383
Db	1337	TTTATTTTATCCTTCACTGTGACCTTGAGAGA	1369

RESULT 7
US-09-880-107-3856
; Sequence 3856, Application US/09880107
; Patent No. US20020145981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14

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:
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3856
: LENGTH: 4039
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020442981A1 Y10659
US-09-880-107-3856

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[illegible]

QY	871	CAATAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCGAATTTGAGGAATGTG	933
Db	857	CATAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCGAATTTGAGGAATGTG	916
QY	931	GAGAAATACATCTTGTTTCATGAGTGCCTGTGTCTTCTGTACTTTGAACAAGTACAGA	990
Db	917	GAGAAATACATCTTGTTTCATGAGTGCCTGTGTCTTCTGTACTTTGAACAAGTACAGA	976
QY	991	ATAAGAGTCAAACAAATTAAGTATGCTATAGAGATGACAAACTCTGAGTAATTGGAGC	1053
Db	977	ATAAGAGTCAAACAAATTAAGTATGCTATAGAGATGACAAACTCTGAGTAATTGGAGC	1038
QY	1051	CAAGAAATAGATATAGTAAAGAGCGCAATTCACACTCTACATTAACCATGTTACTCAT	1111
Db	1037	CAAGAAATAGATATAGTAAAGAGCGCAATTCACACTCTACATTAACCATGTTACTCAT	1099
QY	1111	GTTCCAGTCATCGTGCAGAGTGCAATCATAGTACTCTGCTTTTACCTTAACCAAGAGCTCAAG	1177
Db	1097	GTTCCAGTCATCGTGCAGAGTGCAATCATAGTACTCTGCTTTTACCTTAACCAAGAGCTCAAG	1155
QY	1171	ATTATTAATTTCCCTCCCAATTCCTGATCTCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC	1233
Db	1157	ATTATTAATTTCCCTCCCAATTCCTGATCTCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC	1211
QY	1231	CAGATATGATATCTCTGACCTGGAGAAAGTACGACATCTATGGAACCAACCAAGAGC	1299
Db	1217	CAGATATGATATCTCTGACCTGGAGAAAGTACGACATCTATGGAACCAACCAAGAGC	1277
QY	1291	GAAACCGACTCTGTAGTGCCTGATAGAAAACCTGAAAGAAAGCCTCTCACTGATGAGATTA	1355
Db	1277	GAAACCGACTCTGTAGTGCCTGATAGAAAACCTGAAAGAAAGCCTCTCACTGATGAGATTA	1333
QY	1351	TTTATTTTACCTTCACGTGATGAAAGCA	1383
Db	1337	TTTATTTTACCTTCACGTGATGAAAGCA	1369
RESULT 8			
US-10-172-118-633			
; Sequence 633, Application US/10172118			
; Publication No. US20030224374A1			
; GENERAL INFORMATION:			
APPLICANT: Dai, Hongyue			
APPLICANT: He, Yudong			
APPLICANT: Linsley, Peter			
APPLICANT: Mao, Mao			
APPLICANT: Roberts, Chris			
APPLICANT: Van 't Veer, Laura			
APPLICANT: Bernards, Rene			
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
FILE REFERENCE: 9301-175-999			
CURRENT APPLICATION NUMBER: US/10172.118			
CURRENT FILING DATE: 2002-06-14			
PRIOR APPLICATION NUMBER: 60/380,770			
PRIOR FILING DATE: 2002-05-14			
NUMBER OF SEQ ID NOS: 2699			
SEQ ID NO 633			
LENGTH: 4039			
TYPE: DNA			
ORGANISM: Homo sapiens			
PUBLICATION INFORMATION:			
DATABASE ACCESSION NUMBER: NM_001560			
DATABASE ENTRY DATE: 2001-06-18			
US-10-172-118-633			

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RESULT 8
US-10-172-118-633
; Sequence 633, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 633
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 001560
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-633

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Query Match	96.4%	Score 1333.8	DB 7	Length 4039
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1348	Conservative 0	Mismatches 2	Indels 3	Gaps 1

07 CGGGGGGTTCCAGGCGAGAGGCTGCATGAGAGTCCCGGCGCGGCTCTGCGGGCTGTGC 93
 |||||

Db	317	GAGAGGATTTGTCGTGAATGGGGGTCCAGGTGAGACCAATGAGAGTGAAAGCTAC	376
QY	391	ATTTTGGTTGAAAAATGCATCTCACCCAGAAAGTGATCTGAGTCTGCTGTGATGAA	450
Db	377	ATTTTGGTTGAAAAATGCATCTCACCCAGAAAGTGATCTGAGTCTGCTGTGATGAA	436
QY	451	CTTCANATGATTTGGCACAACCTGAGCTCATGAAGTGTCTTGGCTCCTTGGAAAGAT	510
Db	437	CTTCANATGATTTGGCACAACCTGAGCTCATGAAGTGTCTTGGCTCCTTGGAAAGAT	496
QY	511	ACCACTCCGACACTAATACTCTCTACTTATTTGGCAGAGAAGCCTGGAAAAATTCAT	570
Db	497	ACCACTCCGACACTAATACTCTCTACTTATTTGGCAGAGAAGCCTGGAAAAATTCAT	556
QY	571	CAATGTGAAAACATCTTTTAGAGAGGCCAATACCTTTGGTGTCTTGGATCTGACAA	630
Db	557	CAATGTGAAAACATCTTTTAGAGAGGCCAATACCTTTGGTGTCTTGGATCTGACAA	616
QY	631	GTGAAGAGTTCAGTTTGAACAACAAGTGTCCAAATPATGTCAAGATATATCAGAGA	690
Db	617	GTGAAGAGTTCAGTTTGAACAACAAGTGTCCAAATPATGTCAAGATATATCAGAGA	676
QY	691	AAAAATTAACCATCTCTCAATATATAGTGCCTTAACTTCGCCGTGAAACCTGATCTCA	750
Db	677	AAAAATTAACCATCTCTCAATATATAGTGCCTTAACTTCGCCGTGAAACCTGATCTCA	736
QY	751	CATATTTAAAAACCTCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGATATCAAG	810
Db	737	CATATTTAAAAACCTCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGATATCAAG	796
QY	811	AATTTTATTAAGACAGATGGCTATTTTATGAAGTGAAGTCAATTAACGCCAATGAGACA	870
Db	797	AATTTTATTAAGACAGATGGCTATTTTATGAAGTGAAGTCAATTAACGCCAATGAGACA	856
QY	871	CATAATGTTTTCTACGTCCAGAGGCTTAATGTGGAATCCAGAAATTTGAGAGAAATG	930
Db	857	CATAATGTTTTCTACGTCCAGAGGCTTAATGTGGAATCCAGAAATTTGAGAGAAATG	916
QY	931	GAGAAATACATCTTGTTCATGATGATGCCGTGTCTTCTCGATATCTTGAACACAGTCA	990
Db	917	GAGAAATACATCTTGTTCATGATGATGCCGTGTCTTCTCGATATCTTGAACACAGTCA	976
QY	991	ATAAGAGTCAAAAACAATPATGTATGATAGAGATGACAACTGTGAGTATTTGGAGC	1050
Db	977	ATAAGAGTCAAAAACAATPATGTATGATAGAGATGACAACTGTGAGTATTTGGAGC	1036
QY	1051	CAAGAAATGAGATPATGTATGAAGGCAATTCACACTCTACATPAACATGTACTCTATT	1110
Db	1037	CAAGAAATGAGATPATGTATGAAGGCAATTCACACTCTACATPAACATGTACTCTATT	1096
QY	1111	GTTCCAGTCACTGTGACAGTGCATCATATGATCCTCGCTTACCTTAAAGAGCTCAAG	1170
Db	1097	GTTCCAGTCACTGTGACAGTGCATCATATGATCCTCGCTTACCTTAAAGAGCTCAAG	1156
QY	1171	ATTATATATTTCCCTCAATCTCTGATCTGTGGCAAGATTTTAAAGAAATGTTTGAAC	1230
Db	1157	ATTATATATTTCCCTCAATCTCTGATCTGTGGCAAGATTTTAAAGAAATGTTTGAAC	1216
QY	1231	CAGAAATGATATCTGTGACACTGGAAGAAAGTACATCTATGTGAAGCAACAAGAG	1290
Db	1217	CAGAAATGATATCTGTGACACTGGAAGAAAGTACATCTATGTGAAGCAACAAGAG	1276
QY	1291	GAAACCGACTCTGTAGTGTCTGATAGAAAACCTGGAAGAAAGCTCTCAGTGTGAGATTA	1350
Db	1277	GAAACCGACTCTGTAGTGTCTGATAGAAAACCTGGAAGAAAGCTCTCAGTGTGAGATTA	1336
QY	1351	TTTATTTTACCCTTCACTGTGACCTTGAAGA	1383
Db	1337	TTTATTTTACCCTTCACTGTGACCTTGAAGA	1369

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US-10-843-641A-6046
; Sequence 6046, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;   APPLICANT: Avalon Pharmaceuticals, Inc.
;   TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;   TITLE OF INVENTION: Signature Gene Sets
;   FILE REFERENCE: 689290-189
;   CURRENT APPLICATION NUMBER: US/10/843,641A
;   CURRENT FILING DATE: 2004-05-12
;   PRIOR APPLICATION NUMBER: US/09/873,367
;   PRIOR FILING DATE: 2001-06-05
;   PRIOR APPLICATION NUMBER: US/09/954,531
;   PRIOR FILING DATE: 2001-09-18
;   PRIOR APPLICATION NUMBER: US/09/954,456
;   PRIOR FILING DATE: 2001-09-25
;   PRIOR APPLICATION NUMBER: US/09/962,436
;   PRIOR FILING DATE: 2001-09-25
;   PRIOR APPLICATION NUMBER: US/09/962,832
;   PRIOR FILING DATE: 2001-09-25
;   PRIOR APPLICATION NUMBER: US/09/964,824
;   PRIOR FILING DATE: 2001-09-27
;   PRIOR APPLICATION NUMBER: US/09/967,768
;   PRIOR FILING DATE: 2001-09-28
;   PRIOR APPLICATION NUMBER: US/09/968,007
;   PRIOR FILING DATE: 2001-10-02
;   PRIOR APPLICATION NUMBER: US/09/969,347
;   PRIOR FILING DATE: 2001-10-02
;   PRIOR APPLICATION NUMBER: US/09/969,708
;   PRIOR FILING DATE: 2001-10-03
;   Remaining SEQ ID Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 8447
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 6046
;   LENGTH: 4039
;   TYPE: DNA
;   ORGANISM: Homo sapiens
; US-10-843-641A-6046

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RESULT 10

Query Match	96.4%	Score 133.8	DB 10	Length 4039
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1348	Conservative 0	Mismatches 2	Indels 3	Gaps 1
QY	34	CGGCGGGGTTCCGAGCGGAGGCGTGATGAGTGGCGGCGCGGCTCTGCGGGCTGTGG	93	
Db	17	CGGCGGGGCTCCGAGGCGAGAGCGTGATGAGTGGCGGCGGGCTCTGCGGGCTGTGG	76	
QY	94	GCGCTGCTGCTCTGCGCGCGCGGCGGGGCGGGGGCGGGG--CGCGCTTACGGAACT	150	
Db	77	GCGCTGCTGCTCTGCGCGCGCGGCGGGGCGGGGGCGGGGGCGCGCGCTTACGGAACT	136	
QY	151	CAGCACCTGTGACCAATTTGAGTGTCTCTGTTGAAACCTCTGCAAGTAATATGACA	210	
Db	137	CAGCACCTGTGACCAATTTGAGTGTCTCTGTTGAAACCTCTGCAAGTAATATGACA	196	
QY	211	TGGAATCACCCGAGGAGCGAGCTCAAAATTGTAGTCTATGATATTTAGTCATTTGGC	270	
Db	197	TGGAATCACCCGAGGAGCGAGCTCAAAATTGTATGTCTATGATATTTAGTCATTTGGC	256	
QY	271	GACAAACAAATAGAAATAGCTCCGGAACTCGTCTTCAATAGAAAGTACCCCTGAT	330	
Db	257	GACAAACAAATAGAAATAGCTCCGGAACTCGTCTTCAATAGAAAGTACCCCTGAT	316	
QY	331	GAGAGATTTTGTCTGCAAGTGGGTCCTCACTGTAGACAACATGAGTGGAGAACCTTAGC	390	
Db	317	GAGAGATTTTGTCTGCAAGTGGGTCCTCACTGTAGACAACATGAGTGGAGAACCTTAGC	376	
QY	391	ATTTGGTTGAAAAATGATCTACCCCCAGAAAGTATCCTGATCTGCTGTACTGAA	450	
Db	377	ATTTGGTTGAAAAATGATCTACCCCCAGAAAGTATCCTGATCTGCTGTACTGAG	436	
QY	451	CTTCAATGCAATTTGGCAACCTGAGTACATGAAGTGTCTTGGCTCCTGGAAAGAT	510	

Db	437	CTTCATATGCAATTTGGCACAACTAGACCTACATGAAGTGTCTTGAGCTCCCTGGAAAGAAAT	496
Qy	511	ACCAATCCCGACACTAATAATCTCTACTAATTTGGCA CAGAAAGCTTGAAAAAATTCAT	570
Db	497	ACCAATCCCGACACTAATAATCTCTACTAATTTGGCA CAGAAAGCTTGAAAAAATTCAT	556
Qy	571	CAATGTGAAAACTCTTTTGAAGAAAGGCCAATNCTTGGTGTCTTTGATCTGACCAA	630
Db	557	CAATGTGAAAACTCTTTTGAAGAAAGGCCAATNCTTGGTGTCTTTGATCTGACCAA	616
Qy	631	GTGAAGATTTCCAGTTTGTGAACAA CACAGTGTCCAAATATATGTCAAGATATATGCACAGA	690
Db	617	GTGAAGATTTCCAGTTTGTGAACAA CACAGTGTCCAAATATATGTCAAGATATATGCACAGA	676
Qy	691	AAAAATTAACCACTCTTCAATATATATGTGCTTTAACTTCCCGTGTGAACCTGATCTTCCA	750
Db	677	AAAAATTAACCACTCTTCAATATATATGTGCTTTAACTTCCCGTGTGAACCTGATCTTCCA	736
Qy	751	CATATTTAAAAACCTCTCTCTTCCACATATGATGACCTATATGTGCAATGGGAATTCACAG	810
Db	737	CATATTTAAAAACCTCTCTCTTCCACATATGATGACCTATATGTGCAATGGGAATTCACAG	796
Qy	811	AATTTATATAGAGATGTGCTATTTTATGAAGTAAGTCAATTAACAGCCAACTGAGACA	870
Db	797	AATTTATATAGAGATGTGCTATTTTATGAAGTAAGTCAATTAACAGCCAACTGAGACA	856
Qy	871	CATAATGTTTTCTACGTCCAGAGGCTAAATGTGGAATTCAGAAATTTGAGAGAATTTG	930
Db	857	CATAATGTTTTCTACGTCCAGAGGCTAAATGTGGAATTCAGAAATTTGAGAGAATTTG	916
Qy	931	GAGAAATACATCTTGTTTCATGTGCTCCCTGTGTCTTCTCTGATCTTTGAACACAGTCAGA	990
Db	917	GAGAAATACATCTTGTTTCATGTGCTCCCTGTGTCTTCTCTGATCTTTGAACACAGTCAGA	976
Qy	991	ATAAAGTCAAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGGAGTAATTTGAGC	1050
Db	977	ATAAAGTCAAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGGAGTAATTTGAGC	1036
Qy	1051	CAAGAAATGAGATATGATPAAGAGCGCAATTCACACATCTACATTAACATGTACTCATTT	1110
Db	1037	CAAGAAATGAGATATGATPAAGAGCGCAATTCACACATCTACATTAACATGTACTCATTT	1096
Qy	1111	GTTCCAGTCACTGTGCGCAGGTGCAATCATAGTACTCTGTCTTAACTTAAAAAGGCTCAG	1170
Db	1097	GTTCCAGTCACTGTGCGCAGGTGCAATCATAGTACTCTGTCTTAACTTAAAAAGGCTCAG	1156
Qy	1171	ATTATTAATATCCCTCCCAATTCCTGATCCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC	1230
Db	1157	ATTATTAATATCCCTCCCAATTCCTGATCCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC	1216
Qy	1231	CAGAAATGATGATCTCTGCACTGGAAGAAGTACGACATCTATGAGAAACCAACCAAGAG	1290
Db	1217	CAGAAATGATGATCTCTGCACTGGAAGAAGTACGACATCTATGAGAAACCAACCAAGAG	1276
Qy	1291	GAACCGACTCTGTAGTCTGTATAGAAAACTTGAAAGAAAGCCTCTCACTGATGAGATTA	1350
Db	1277	GAACCGACTCTGTAGTCTGTATAGAAAACTTGAAAGAAAGCCTCTCACTGATGAGATTA	1336
Qy	1351	TTTATTTTACCTTCACTGCTGACCTTGGAAGA	1383
Db	1337	TTTATTTTACCTTCACTGCTGACCTTGGAAGA	1369
RESULT 11			
US-09-971-392-58			
; Sequence 58, Application US/09971392			
; Publication No. US20030134283A1			
; GENERAL INFORMATION:			
; APPLICANT: Pearson, Cecilia I.			
; APPLICANT: Cocks, Benjamin G.			
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION			
; FILE REFERENCE: PA-0029 US			

[illegible]

OY	811	AAATTTATATAGCAGATGCGCTATTTTATATGAAGAAAGCAATPAAACGGCAACTGAGACA	870
Db	834	AAATTTATATAGCAGATGCGCTATTTTATATGAAGAAAGCAATPAAACGGCAACTGAGACA	893
OY	871	CATAAATGTTTTCTACGTCGAAGGCGCTAAATGTGAAATCCAGAAATTTGAGAAATGTG	930
Db	894	CATAATGTTTTCTACGTCGAAGGCGCTAAATGTGAAATCCAGAAATTTGAGAAATGTG	953
OY	991	GAGAAATACATCTGTTTTTATAGTGTCCTGTCGTGTTCTTCTGATACCTTTGAAACACAGTCGA	990
Db	994	GAGAAATACATCTGTTTTTATAGTGTCCTGTCGTGTTCTTCTGATACCTTTGAAACACAGTCGA	1013
OY	991	ATPAAAGTCGAAAACAAATPAAATGATATGCTATGAGATGACAAACTCTGAGATPAAATGGAGC	1056
Db	1014	ATPAAAGTCGAAAACAAATPAAATGATATGAGATGACAAACTCTGAGATPAAATGGAGC	1073
OY	1051	CAAGAAATGAGATPAAAGTAAAGAGCGCAATTCACACTCTACATPAAACATGTTACTCATTT	1110
Db	1074	CAAGAAATGAGATPAAAGTAAAGAGCGCAATTCACACTCTACATPAAACATGTTACTCATTT	1133
OY	1111	GTTCCAGTCATCTGTCGAGGTCGATCATATGATCTCTGCTTTACTTAAAAAGCTCAAG	1170
Db	1134	GTTCCAGTCATCTGTCGAGGTCGATCATATGATCTCTGCTTTACTTAAAAAGCTCAAG	1193
OY	1171	ATTATTTATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC	1230
Db	1194	ATTATTTATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC	1253
OY	1231	CAGAAATGATGATCTCTGCTGCACTGGAAAGATPACGATCTATGAGAAACCAAGAGAG	1290
Db	1254	CAGAAATGATGATCTCTGCTGCACTGGAAAGATPACGATCTATGAGAAACCAAGAGAG	1313
OY	1291	GAAACCGGCTCTGATGTCGTGATGAAAAACCTGAAAGAAAGGCTCTCAATGATGAGATPAA	1350
Db	1314	GAAACCGGCTCTGATGTCGTGATGAAAAACCTGAAAGAAAGGCTCTCAATGATGAGATPAA	1373
OY	1351	TTTATTTTACCTTCACGTGACCTTGGAGAAGA	1383
Db	1374	TTTATTTTACCTTCACGTGACCTTGGAGAAGA	1406
RESULT 12			
US-10-278-698-6			
; Sequence 6, Application US/10278698			
; Publication No. US20050037344A1			
; GENERAL INFORMATION:			
; APPLICANT: Pathoarray GmbH			
; APPLICANT: Stuhlmüller, Bruno			
; TITLE OF INVENTION: Nucleic Acid Array			
; FILE REFERENCE: 030027US			
; CURRENT APPLICATION NUMBER: US/10/278,698			
; NUMBER OF SEQ ID NOS: 1050			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 6			
; LENGTH: 1572			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-278-698-6			

	Query Match	96.2%	Score 1330.6;	DB 9;	Length 1572;
	Best Local Similarity	99.5%;	Pred. No. 0;		
	Matches 1346;	Conservative	0;	Mismatches	4; Indels 3; Gaps 1;
Qy	34	CGGCGGGTTCGAGAGCGAGAGGCTGCATGTGAAGTGCCGCGCGGCTCTTGCGGGCTGTGCG	93		
Dd	58	CGGCGGGGCTCCGAGGCGAGAGGCTGCATGTGAAGTGCCGCGCGGCTCTTGCGGGCTGTGCG	117		
Qy	94	CGCGTGTGCTCTTGCGCGGCGCGGCCGAGGCGGGGCGGGG---CGCGCTTACGGAACA	150		
Dd	118	GCGGTGTGCTCTTGCGCGGCGCGGGCGGGGCGGGGCGGGGCGCGCTTACGGAACA	177		

QY	151	AAGCACCCTGACAAATTTGAGTGTCTCGTTGAAAACCTCGCACAGTAATATGAGACA	210
Db	178	CAGCACCCCTGTGACAAATTTGAGTGTCTCGTTGAAAACCTCGCACAGTAATATGAGACA	237
QY	211	TGGAATCCACCCTGAGGGAGCCAGCTCAAAATTGAGTCTATGTAATTTTATGACTTTGGC	270
Db	238	TGGAATCCACCCTGAGGGAGCCAGCTCAAAATTGATGTAATGTAATTTTATGACTTTTGGC	297
QY	271	GACAAACAAAGTAAGAAAATAGCTCCGGAAAACCTGCTGTTCAATAGAACTACCCCTGAT	330
Db	298	GACAAACAAAGTAAGAAAATAGCTCCGGAAAACCTGCTGTTCAATAGAACTACCCCTGAT	357
QY	331	GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAGAAGCCTTAC	390
Db	358	GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAGAAGCCTTAC	417
QY	391	ATTTTGGTTGAAAAATGCAATCTCACCCCGAAGGATGATCTGAGTCTGCTGACTGAA	450
Db	418	ATTTTGGTTGAAAAATGCAATCTCACCCCGAAGGATGATCTGAGTCTGCTGATTTGAG	477
QY	451	CTTCAATGCAATTTGGGCACAACCTGAGATTCATGAACTGTCTTGGCTCCCTGGAAGGAT	510
Db	478	CTTCAATGCAATTTGGGCACAACCTGAGATTCATGAACTGTCTTGGCTCCCTGGAAGGAT	537
QY	511	ACCAAGTCCCGACACTAATCTACTCTCTACTATTTGGCAGAGAAGCCTGGAAAAAATTCAT	570
Db	538	ACCAAGTCCCGACACTAATCTACTCTCTACTATTTGGCAGAGAAGCCTGGAAAAAATTCAT	597
QY	571	CAATGTGAAAAATCTTTTAGAAGAGCCAAATCTTTGTTGTTTCTTTGATCTGACCAA	630
Db	598	CAATGTGAAAAATCTTTTAGAAGAGCCAAATCTTTGTTGTTTCTTTGATCTGACCAA	657
QY	631	GTGAAGGATTCAGATTTTGAACAACAACAGTGTCCAATATAGGTCAAGGATATATGACAGA	690
Db	658	GTGAAGGATTCAGATTTTGAACAACAACAGTGTCCAATATAGGTCAAGGATATATGACAGA	717
QY	691	AAAAATTAAACCATCTTCAATATAGTGCCTTTAACTTCCGTTGTAACCTGATCTCTCCA	750
Db	718	AAAAATTAAACCATCTTCAATATAGTGCCTTTAACTTCCGTTGTAACCTGATCTCTCCA	777
QY	751	CATATTTAAAAACCTCTCCCTCCCAATGATGACCTTATGTGCAATGGAGAAATCCACAG	810
Db	778	CATATTTAAAAACCTCTCCCTCCCAATGATGACCTTATGTGCAATGGAGAAATCCACAG	837
QY	811	AATTTTATTTAGCAGATGCCATTTTATGAAAGTAGAAGTCAATPAACAGCAAACTGAGACA	870
Db	838	AATTTTATTTAGCAGATGCCATTTTATGAAAGTAGAAGTCAATPAACAGCAAACTGAGACA	897
QY	871	CATPATGTTTTTCTAAGTCCAAAGGCTAAATGTGAGAAATCCGAATTTGAGAAATGTG	930
Db	898	CATPATGTTTTTCTAAGTCCAAAGGCTAAATGTGAGAAATCCGAATTTGAGAAATGTG	957
QY	931	GAGAAATCATCTTGTTTCAATGAGCCCTGGGTCTTCCGATACCTTGAACACAGTCCAGA	990
Db	958	GAGAAATCATCTTGTTTCAATGAGCCCTGGGTCTTCCGATACCTTGAACACAGTCCAGA	1017
QY	991	ATAAGAGTCAAAAACAATAAGTATGCTATGAGATGACAAACTGTGAGTAATTGGAGC	1050
Db	1018	ATAAGAGTCAAAAACAATAAGTATGCTATGAGATGACAAACTGTGAGTAATTGGAGC	1077
QY	1051	CAAGAAATGAGTATAGTAAAGAAAGGCCAATTCACACTAATPAACCTGTTACTCATTT	1110
Db	1078	CAAGAAATGAGTATAGTAAAGAAAGGCCAATTCACACTAATPAACCTGTTACTCATTT	1137
QY	1111	GTTTCCAGTCAATGCTGACAGGTGCAATCATAGTACTCTGCTTTTACCTTAAAAAGCTCAAG	1170
Db	1138	GTTTCCAGTCAATGCTGACAGGTGCAATCATAGTACTCTGCTTTTACCTTAAAAAGCTCAAG	1197
QY	1171	ATATATATATATCCCTCCCAATCTCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAAAC	1230
Db	1198	ATATATATATATCCCTCCCAATCTCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAAAC	1257

QY 1231 CAGAAATGATGATCTCTGCACTGGAAGAGTACGACATCTATGAAAGCAACCAAGAG 1290
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|
|
Db 1258 CAGAAATGATGATCTCTGCACTGGAAGAGTACGACATCTATGAAAGCAACCAAGAG 1317

QY 1291 GAAACCGACTCTGAGTGTGATAGAAAACCTGAAAGAAAGCTCTGAGTGTGAGATTA 1350
|
|
|
Db 1318 GAAACCGACTCTGAGTGTGATAGAAAACCTGAAAGAAAGCTCTCTGAGTGTGAGATTA 1377

QY 1351 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
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|
|
Db 1378 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1410

RESULT 13

US-10-278-698-520
; Sequence 520, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoTray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupt, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 03002705
; CURRENT APPLICATION NUMBER: US/10/278, 698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-520

Query Match 96.2%; Score 1330.6; DB 9; Length 1572;
Best Local Similarity 99.5%; Pred. No. 0;

Matches 1346; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 34 CGGCCGGGTTCCGAGGCGAGAGGCTGCATGAGTGCAGGCGCGGCTCTGCGGGCTGTGG 93
|
|
|
Db 58 CGGCCGGGCTCCGAGGCGAGAGGCTGCATGAGTGCAGGCGCGGCTCTGCGGGCTGTGG 117

QY 94 GGGCTCTGCTCTGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 150
|
|
|
Db 118 GGGCTCTGCTCTGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 177

QY 151 CAGCCACTGTGCAAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACA 210
|
|
|
Db 178 CAGCCACTGTGCAAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACA 237

QY 211 TGGATTCACCCGAGGAGGAGCTCAATTTGATGATGATATTTTACTCAATTTTGGC 270
|
|
|
Db 238 TGGATTCACCCGAGGAGGAGCTCAATTTGATGATGATATTTTACTCAATTTTGGC 297

QY 271 GACAAACAGATTAAGAAATAGCTCCGGAACCTCGTCTTCATATGAAAGTACCCCTGAAT 330
|
|
|
Db 298 GACAAACAGATTAAGAAATAGCTCCGGAACCTCGTCTTCATATGAAAGTACCCCTGAAT 357

QY 331 GAGAGATTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCTTACG 390
|
|
|
Db 358 GAGAGATTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCTTACG 417

QY 391 ATTTTGGTTGAAAAATGATCTTCAACCCCGAAGAGGTATCTGAGTCTGCTGACTGAA 450
|
|
|
Db 418 ATTTTGGTTGAAAAATGATCTTCAACCCCGAAGAGGTATCTGAGTCTGCTGACTGAA 477

QY 451 CTTCATGATTTTGGACAACTGACCTACATGAAGTGTCTTGGCTCCCTCGAAGGAAT 510
|
|
|
Db 478 CTTCATGATTTTGGACAACTGACCTACATGAAGTGTCTTGGCTCCCTCGAAGGAAT 537

QY 511 ACCAGTCCGACACTAATACTCTACTATTTGGACAAGAGCTGAAAAAATTCAT 570
|
|
|
Db 538 ACCAGTCCGACACTAATACTCTACTATTTGGACAAGAGCTGAAAAAATTCAT 597

QY 571 CAATGGAACAATCTTTAGAGAGGCCAATACTTTGTTGTTCTTTGATCTGACCAA 630
|
|
|
Db 598 CAATGGAACAATCTTTAGAGAGGCCAATACTTTGTTGTTCTTTGATCTGACCAA 657

QY 631 GTGAAGATTTCCGTTTGAACAACAGTGTCCAATATATGTTCAAGGTAATGACGA 690
|
|
|
Db 658 GTGAAGATTTCCGTTTGAACAACAGTGTCCAATATATGTTCAAGGTAATGACGA 717

QY 691 AAAATTAACCAATCTTCAATATATGAGCTTTAACTTCCGTTGAACCTGATCTCCA 750
|
|
|
Db 718 AAAATTAACCAATCTTCAATATATGAGCTTTAACTTCCGTTGAACCTGATCTCCA 777

QY 751 CATATTAACCAATCTTCTTCCCAATGATGACCTATATGTCATATGGAATTCACAG 810
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|
|
Db 778 CATATTAACCAATCTTCTTCCCAATGATGACCTATATGTCATATGGAATTCACAG 837

QY 811 AATTTATTAAGAGAGCTTATTTTGAAGTGAAGTCAATATACGCCCAACTGAGACA 870
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|
|
Db 838 AATTTATTAAGAGAGCTTATTTTGAAGTGAAGTCAATATACGCCCAACTGAGACA 897

QY 871 CATATGTTTTCTACCTCCAGAGGCTAAATGTGAATTCAGAAATTTGAGAAATGTG 930
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|
|
Db 898 CATATGTTTTCTACCTCCAGAGGCTAAATGTGAATTCAGAAATTTGAGAAATGTG 957

QY 931 GAGATATCATCTTTGTTTATGTCCTCGTGTCTTCTGATATCTTTGAAACAGTCACA 990
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|
|
Db 958 GAGATATCATCTTTGTTTATGTCCTCGTGTCTTCTGATATCTTTGAAACAGTCACA 1017

QY 991 ATTAGAGTCAAAACAAATAGTTATGCTATGAGAGTACAAATCTGAGATTAATGGAGC 1050
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|
|
Db 1018 ATTAGAGTCAAAACAAATAGTTATGCTATGAGAGTACAAATCTGAGATTAATGGAGC 1077

QY 1051 CAGAAATGATATAGTAAAGAGCCCAATTCACACTACATTAACAATGTTACTATT 1110
|
|
|
Db 1078 CAGAAATGATATAGTAAAGAGCCCAATTCACACTACATTAACAATGTTACTATT 1137

QY 1111 GTTCCAGTCACTGTCCAGAGTCAATCATATATATCTCTGTTAACTTAAAGGCTCAAG 1170
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|
|
Db 1138 GTTCCAGTCACTGTCCAGAGTCAATCATATATATCTCTGTTAACTTAAAGGCTCAAG 1197

QY 1171 ATTATATATTCCTCCCAATTCCTGATCCCTGGCAAGATTTTAAAGAAATGTTGGAGC 1230
|
|
|
Db 1198 ATTATATATTCCTCCCAATTCCTGATCCCTGGCAAGATTTTAAAGAAATGTTGGAGC 1257

QY 1231 CAGAAATGATATCTCTGCACTGGAAGAGTACGACATCTATGAGAGCAACCAAGAG 1290
|
|
|
Db 1258 CAGAAATGATATCTCTGCACTGGAAGAGTACGACATCTATGAGAGCAACCAAGAG 1317

QY 1291 GAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTCTCAGTGATGAGATTA 1350
|
|
|
Db 1318 GAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTCTCAGTGATGAGATTA 1377

QY 1351 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
|
|
|
Db 1378 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1410

RESULT 14

US-10-850-270-3

; Sequence 3, Application US/10850270
; Publication No. US20050058645A1

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)

; APPLICANT: Dunlop, Felicity (US only)

; APPLICANT: Baca, Manuel (US only)

; APPLICANT: Nash, Andrew (US only)

; APPLICANT: Fabril, Louis (US only)

; TITLE OF INVENTION: Novel peptides

; FILE REFERENCE: 12175890/BJH

; CURRENT APPLICATION NUMBER: US/10/850,270

; CURRENT FILING DATE: 2004-05-20

; PRIOR APPLICATION NUMBER: AU PS1301

; PRIOR FILING DATE: 2002-03-22

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? PRIOR APPLICATION NUMBER: AU 2003900437
? PRIOR FILING DATE: 2003-02-03
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3
? LENGTH: 1284
? TYPE: DNA
? ORGANISM: human
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1284)
? OTHER INFORMATION:
US-10-850-270-3

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Query Match		91.5%	Score 1264.8	DB 10	Length 1284	
Best Local Similarity		99.6%	Pred. No. 0			
Matches 1279		Conservative	0	Mismatches	2	Indels
					3	Gaps
QY	61	ATGAGATGGCGGCGCGGCTCTGCGGGCTGTGGCGCTGCTGCGCGCGCGCGG	120			
DB	1	ATGAGATGGCGGCGCGGCTCTGCGGGCTGTGGCGCTGCTGCGCGCGCGCGG	60			
QY	121	GGCGGGGGGGGGGGG---GGCGCTACGGAACTCAGCCACTGTGACAAATTTAGTGTG	177			
DB	61	GGCGGGGGGGGGGGGCGCGCGCTACGGAACTCAGCCACTGTGACAAATTTAGTGTG	120			
QY	178	TCTGTGAAAACTCTGCACAGTATATAGACATGGAATCCAGCGAGGACGACTCA	237			
DB	121	TCTGTGAAAACTCTGCACAGTATATAGACATGGAATCCAGCGAGGACGACTCA	180			
QY	238	AATTGTAGTCATAGGTATTTTATGTCAATTTTGCGCAACAAGATAGAAAATAGCTCG	297			
DB	181	AATTGTAGTCATAGGTATTTTATGTCAATTTTGCGCAACAAGATAGAAAATAGCTCG	240			
QY	298	GAAACTGTCGTCAATAGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCC	357			
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QY	538	TACTATTGGCAGAGAGCTTGGAAAAATTCATCAATGTGAAAAATCTTTTAGAAGAGC	597			
DB	481	TACTATTGGCAGAGAGCTTGGAAAAATTCATCAATGTGAAAAATCTTTTAGAAGAGC	540			
QY	598	CAATACTTTGGTGTCTCTTGATCTGACCAAGAGGAAGATTCAGTTTGGACAACAC	657			
DB	541	CAATACTTTGGTGTCTCTTGATCTGACCAAGAGGAAGATTCAGTTTGGACAACAC	600			
QY	658	AGTGTCCAAATATATGTCAAGATATGCAAGAAAAATTAACCATCTTCAATATAGTG	717			
DB	601	AGTGTCCAAATATATGTCAAGATATGCAAGAAAAATTAACCATCTTCAATATAGTG	660			
QY	718	CCTTTAACTCCCGGTGAAACCTGATCTCCACATATTAATAAATCTTCTTCCACAT	777			
DB	661	CCTTTAACTCCCGGTGAAACCTGATCTCCACATATTAATAAATCTTCTTCCACAT	720			
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DB	781	GAAGTAAAGTCATTAACGCCAAATGAGACATATATGTTTTCTAGCTCCAAAGAGCT	840			

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Oy	958	GGTGTCTTCTCGATCTTTGAACACAGTCAGAAATAAGTCAAAACAATAAGTTATGC	1017
Db	901	GGTGTCTTCTCGATCTTTGAACACAGTCAGAAATAAGTCAAAACAATAAGTTATGC	960
Oy	1018	TATGAGATGACAAACTCTGAGATTAATGAGCCAAATAATGATATAGTATGAACCGC	1077
Db	961	TATGAGATGACAAACTCTGAGATTAATGAGCCAAATAATGATATAGTATGAACCGC	1020
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RESULT 15
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; Sequence 109, Application US/09822846
; Publication No. US2003027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 3880
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-109
Query Match      89.5%; Score 1238.4; DB 3; Length 3880;

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Searched: 844069 seqs, 650066433 residues

Total number of hits satisfying chosen parameters: 1688138

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1333.8	96.4	2139	US-11-266-748A-25722	Sequence 25722, A
2	1333.8	96.4	4006	US-11-266-748A-56241	Sequence 56241, A
3	1011	73.1	2741	US-11-266-748A-185183	Sequence 185183, A
4	978.2	70.7	1016	US-11-266-748A-54658	Sequence 54658, A
5	972.4	70.3	975	US-11-266-748A-192679	Sequence 192679, A
6	972.4	70.3	975	US-11-266-748A-226550	Sequence 226550, A
7	927.6	67.1	1294	US-11-266-748A-73628	Sequence 73628, A
8	927.6	67.1	1294	US-11-266-748A-107924	Sequence 107924, A
9	927.6	67.1	1294	US-11-266-748A-126439	Sequence 126439, A
10	601	43.5	902	US-11-266-748A-54614	Sequence 54614, A
11	334.4	24.2	1297	US-11-266-748A-73627	Sequence 73627, A
12	334.4	24.2	1297	US-11-266-748A-107923	Sequence 107923, A
13	334.4	24.2	1297	US-11-266-748A-126438	Sequence 126438, A
14	63	4.6	583	US-11-266-748A-51095	Sequence 51095, A
15	44.6	3.2	2566	US-11-266-748A-26705	Sequence 26705, A
16	41.8	3.0	642	US-11-266-748A-219120	Sequence 219120, A
17	41.4	3.0	1332	US-10-449-902-2328	Sequence 2328, Ap
18	41.4	3.0	1377	US-10-449-902-21352	Sequence 21352, A
19	41.4	3.0	152331	US-11-175-714-86	Sequence 86, Appl
20	41.2	3.0	4620	US-11-266-748A-30060	Sequence 30060, A
21	41.2	3.0	4620	US-11-266-748A-27561	Sequence 27561, A
22	41.1	3.0	2601	US-10-449-902-17145	Sequence 17145, A
23	40.6	2.9	1045	US-11-218-305-11663	Sequence 11663, A
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C	25	40.4	2.9	1000	US-11-266-748A-481838	Sequence 481838, A
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C	27	39.8	2.9	8079	US-11-266-748A-56474	Sequence 56474, A
C	28	39.6	2.9	923	US-10-449-902-3516	Sequence 3516, Ap
C	29	39.6	2.9	4563	US-10-196-749-311	Sequence 311, App
C	30	39.4	2.8	1211	US-11-174-307B-3379	Sequence 3379, Ap
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C	38	38.4	2.8	3913	US-11-266-748A-29031	Sequence 29031, A
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C	40	38	2.7	1507	US-10-449-902-11785	Sequence 11785, A
C	41	37.8	2.7	1817	US-10-449-902-20981	Sequence 20981, A
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C	43	37.6	2.7	1152	US-10-449-902-14304	Sequence 14304, A
C	44	37.6	2.7	1597	US-10-449-902-12119	Sequence 12119, A
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ALIGNMENTS

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US-11-266-748A-25722
; Sequence 25722, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Hartkin, Paul
; APPLICANT: Johnson, Patrick
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 25722
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25722

Query Match      96.4%; Score 1333.8; DB 8; Length 2139;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
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Db 994 AGAAGCCTCTCAGTGTAGTGAATATTTTACCTTCACTGTGACCTTGAAGAA 1052

RESULT 4
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ. ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192679
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-192679

Query Match 70.3%; Score 972.4; DB 8; Length 975;
Best Local Similarity 99.9%; Pred. No. 4,5e-278;
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGGCCCTACGGAACCTGACCACTGTGACAAATTTAGAGTCTCTGTGAAAACTCTG 194
Db 2 CGGGCCCTACGGAACCTGACCACTGTGACAAATTTAGAGTCTCTGTGAAAACTCTG 61
Qy 195 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATATGATGATGTA 254
Db 62 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATATGATGATGTA 121
Qy 255 TTTTATGATTTTGGGCAAAACAAATTAAGAAATAGCTCCGAAAACCTGCTTCAAT 314
Db 122 TTTTATGATTTTGGGCAAAACAAATTAAGAAATAGCTCCGAAAACCTGCTTCAAT 181
Qy 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCAACATGA 374
Db 182 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCAACATGA 241
Qy 375 GAGTGAGAGCCTTAGCATTTTGGTTGAAAAATGCATCTACCCCAAGAGGTGATCTGA 434

Db 242 GAGTGAGAGCCTAGCATTTTGTGAAAAATGATCTCACCCCAAGAGGTGATCTGA 301
Qy 435 GTCTGCTGATCTAATCTTCAATGATCTTTGGCAACCTGATCAATGAGTGTCTTG 494
Db 302 GTCTGCTGATCTAATCTTCAATGATCTTTGGCAACCTGATCAATGAGTGTCTTG 361
Qy 495 GCTCCCTGAGAGAAATCCAGTCCCGACACATTAATCTCTACTATTTGGACAGAG 554
Db 362 GCTCCCTGAGAGAAATCCAGTCCCGACACATTAATCTCTACTATTTGGACAGAG 421
Qy 555 CTTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGCCCAATACCTTGTGTTTC 614
Db 422 CTTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGCCCAATACCTTGTGTTTC 481
Qy 615 CTTGATCTGACCAATGAGAGATTCAGTTTGAACACACAGTGTCCAAATATGAT 674
Db 482 CTTGATCTGACCAATGAGAGATTCAGTTTGAACACACAGTGTCCAAATATGAT 541
Qy 675 CAAGATATATGACAGAAAAATTAACCATCTTCAATATATGCTTAACTTCCCGT 734
Db 542 CAAGATATATGACAGAAAAATTAACCATCTTCAATATATGCTTAACTTCCCGT 601
Qy 735 GAAACCTGATCTCCACATATTAATAAACCTCTCTCCACATATGATGATCTATATGCA 794
Db 602 GAAACCTGATCTCCACATATTAATAAACCTCTCTCCACATATGATGATCTATATGCA 661
Qy 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGATGAGAGTCAAT 854
Db 662 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGAGAGTCAAT 721
Qy 855 CAGCCAACTGAGACACATATATGTTTCTAGTCCAGAGAGCTAAATGAGATCCAGA 914
Db 722 CAGCCAACTGAGACACATATATGTTTCTAGTCCAGAGAGCTAAATGAGATCCAGA 781
Qy 915 ATTGAGAGAAATGTGAGATATACATCTTGTTCATGCTCCGTGTTCTCTGATAC 974
Db 782 ATTGAGAGAAATGTGAGATATACATCTTGTTCATGCTCCGTGTTCTCTGATAC 841
Qy 975 TTTGACACACGTCAATTAAGATCAAAACAAATTAAGTATGATGATGATCAAACT 1034
Db 842 TTTGACACACGTCAATTAAGATCAAAACAAATTAAGTATGATGATGATCAAACT 901
Qy 1035 CTGAGTAATTTGAGCCCAAGAAATGATATGTAAGAGGCAATCCACATCTCAT 1094
Db 902 CTGAGTAATTTGAGCCCAAGAAATGATATGTAAGAGGCAATCCACATCTCAT 961
Qy 1095 AACCATGTACTCA 1108
Db 962 AACCATGTACTCA 975

RESULT 6
US-11-266-748A-226550
; Sequence 226550, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
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; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 226550
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-226550

Query Match      70.3%; Score 972.4; DB 8; Length 975;
Best Local Similarity 99.9%; Pred. No. 4,5e-278;
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CCGGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAAACTCTG 194
DB 2 CCGGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAAACTCTG 61

QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGTATGTGTA 254
DB 62 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGTATGTGTA 121

QY 255 TTTTATGATTTTGGGACAAACAAGATAGAAAAATAGTCCGGAAAACTGTGGTTCAAT 314
DB 122 TTTTATGATTTTGGGACAAACAAGATAGAAAAATAGTCCGGAAAACTGTGGTTCAAT 181

QY 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374
DB 182 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 241

QY 375 GAGTGAAGACCTTAGCATTTTGTGTTAAAAATGATCTACCCCGAGAGGTATCTCTGA 434
DB 242 GAGTGAAGACCTTAGCATTTTGTGTTAAAAATGATCTACCCCGAGAGGTATCTCTGA 301

QY 435 GTCTGCTGATGCACTGAACTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTCTTG 494
DB 302 GTCTGCTGATGCACTGAACTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTCTTG 361

QY 495 GCTCCCTGGAAGGAATACAGTCCCGACACTAACTATACTCTACTATTGGACAGAAAG 554
DB 362 GCTCCCTGGAAGGAATACAGTCCCGACACTAACTATACTCTACTATTGGACAGAAAG 421

QY 555 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAAAGGCCAATCTTTGGTGTTC 614
DB 422 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAAAGGCCAATCTTTGGTGTTC 481

QY 615 CTTTATGCTGACCAAGATGGAAGATTCAGTTTGTGAACAACAGAGTCCCAATTAATGCT 674
DB 482 CTTTATGCTGACCAAGATGGAAGATTCAGTTTGTGAACAACAGAGTCCCAATTAATGCT 541

QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATAGTGCCTTTAACTCCGCTG 734
DB 542 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATAGTGCCTTTAACTCCGCTG 601

QY 735 GAAACTGATCTCCACATTTAAAACTCTCTCTCCACCAATGATGACCTATATGTGCA 794
DB 602 GAAACTGATCTCCACATTTAAAACTCTCTCTCCACCAATGATGACCTATATGTGCA 661

QY 795 ATGGGGAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAGTAAAGTCAATA 854
DB 662 ATGGGGAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAGTAAAGTCAATA 721

QY 855 CAGCCAAACTGAGACACATTAATGTTTCTAGTCCAGAGAGCTAAATGTGAGATCCAGA 914
DB 722 CAGCCAAACTGAGACACATTAATGTTTCTAGTCCAGAGAGCTAAATGTGAGATCCAGA 781

QY 915 ATTGAGAGAAATGTGAGAAATACATCTTCTTCAATGCTCCCTGGGTGTCTCTCTGATAC 974
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DB 782 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCCTGGGTGTCTCTCTGATAC 841
QY 975 TTGGAACAGAGTCAGATTAAGAGTCAAAACAATTAAGTTATGCTATAGAGATGACAAACT 1034
DB 842 TTGGAACAGAGTCAGATTAAGAGTCAAAACAATTAAGTTATGCTATAGAGATGACAAACT 901
QY 1035 CTGAGTAATTTGGAGCCCAAGAAATGATATAGTAAAGAACGCAATTCACACTTACAT 1094
DB 902 CTGAGTAATTTGGAGCCCAAGAAATGATATAGTAAAGAACGCAATTCACACTTACAT 961
QY 1095 AACCATGTTACTCA 1108
DB 962 AACCATGTTACTCA 975

RESULT 7
US-11-266-748A-73628/c
; Sequence 73628, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73628
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-73628

Query Match      67.1%; Score 927.6; DB 8; Length 1294;
Best Local Similarity 98.4%; Pred. No. 1.1e-264;
Matches 990; Conservative 0; Mismatches 9; Indels 7; Gaps 5;

QY 385 CTTAGCATTTTGGTTGAAAAA--TGCATCTACCCCCAGAGGTGATCCTGAGTCTGCTG 442
DB 1294 CTTAGCATTTTGGTTGAAAAAAGTGCATCTACCCCAAGTGTGATCCGAGTTCTGCTG 1235
QY 443 TGACTGAATCTTCA--TGCATTTGGCAACAACCTGACTACATGAATGTCTTGCT-CC 499
DB 1234 TGACTGAATCTTCAATAGGATGGGCAACAACCTGACTACATGAATGTCTTGCTGCC 1175
QY 500 CTGGAAGAAATACAGATCCCGACACTAATATATCTCTC-TACTATTGGACAGAAAGCTG 558
DB 1174 CTGGAAGAAATACAGATCCCGACACTAATATATCTCTC-TACTATTGGACAGAAAGCTG 1115
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QY 559 GAAAAATTCATCA-ATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 617
 Db 1114 GAGAAAAATTCATCATATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 1055
 QY 618 TGATCTGACCAAAATGAAAGATTCAGTTTGAACACAGGTGCTCAAAATATAGTCTCA 677
 Db 1054 TGATCTGACCAAAATGAAAGATTCAGTTTGAACACAGGTGCTCAAAATATAGTCTCA 995
 QY 678 GATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGGCTTTAACTTCCGTGAA 737
 Db 994 GATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGGCTTTAACTTCCGTGAA 935
 QY 738 ACTGATCTTCCATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTGCAATG 797
 Db 934 ACTGATCTTCCATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTGCAATG 875
 QY 798 GAGAAATCCACAGAAATTTTATAGCAATGCTTATTTATAGAAATGATCAATTAACAG 857
 Db 874 GAGAAATCCACAGAAATTTTATAGCAATGCTTATTTATAGAAATGATCAATTAACAG 815
 QY 858 CCAAACTGAGACACATTAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCAGAAAT 917
 Db 814 CCAAACTGAGACACATTAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCAGAAAT 755
 QY 918 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTGTCCTTCTCTGATACCTT 977
 Db 754 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTGTCCTTCTCTGATACCTT 695
 QY 978 GAAACACGTCAAGATTAAGATCAAAACAAATAGTTATGCTATGAGATGACAAACTGTG 1037
 Db 694 GAAACACGTCAAGATTAAGATCAAAACAAATAGTTATGCTATGAGATGACAAACTGTG 635
 QY 1038 GAGTAATTTGAGCCCAAGAAATAGTATAGGTAAGAAAGCAATTCACACCTTACATTAAC 1097
 Db 634 GAGTAATTTGAGCCCAAGAAATAGTATAGGTAAGAAAGCAATTCACACCTTACATTAAC 575
 QY 1098 CATGTTACTCATTTGTCAGTCACTGTCGAGGTGACATCATAGTACTCTGCTTTACCT 1157
 Db 574 CATGTTACTCATTTGTCAGTCACTGTCGAGGTGACATCATAGTACTCTGCTTTACCT 515
 QY 1158 AAAAAGGCTCAAGATTAATTAATTCCTTCAATTCCTGATCTGTGCAAGATTTTAAAGA 1217
 Db 514 AAAAAGGCTCAAGATTAATTAATTCCTTCAATTCCTGATCTGTGCAAGATTTTAAAGA 455
 QY 1218 AATGTTTGAGACAGAGATGATATCTGCACTGGAAGAAAGCAATCTATAGTGA 1277
 Db 454 AATGTTTGAGACAGAGATGATATCTGCACTGGAAGAAAGCAATCTATAGTGA 395
 QY 1278 GCAAAACCAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTCTCA 1337
 Db 394 GCAAAACCAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTCTCA 335
 QY 1338 GTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAA 1393
 Db 334 GTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAA 289
 RESULT 8
 US-11-266-748A-107924/c
 ; Sequence 107924, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266, 748A
 ; PRIOR FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 48396
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO 107924
 ; LENGTH: 1294
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (30)..(30)
 ; OTHER INFORMATION: n is a, c, g, or t
 US-11-266-748A-107924
 Query Match 67.1%; Score 927.6; DB 8; Length 1294;
 Best Local Similarity 98.4%; Pred. No. 1.1e-264;
 Matches 990; Conservative 0; Mismatches 9; Indels 7; Gaps 5;
 QY 385 CTTAGCATTTTGGTTGAAAA--TGCACTCTACCCCGAAGGTGATCTGAGTCTGCTG 442
 Db 1294 CTTAGCATTTTGGTTGAAAAAGTCACTCACCCAGTAAAGTATCCGGATTCTGCTG 1235
 QY 443 TGACTGAATCTTCAA--TGCACTTTGGCAACCTGAGCTAATGAAGTCTTGGCT-CC 499
 Db 1234 TGACTGAATCTTCAAATGGCATGGGGCACAACTGAGCTAATGAAGTCTTGGCTGCC 1175
 QY 500 CTGGAAGGAATACAGTCCCGACACTATATCTCTC-TACTATTGGCAAGAGGCTG 558
 Db 1174 CTGGAAGGAATACAGTCCCGACACTATATCTCTCGTATCTATTGGCAAGAGGCTG 1115
 QY 559 GAAAAATTCATCA-ATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 617
 Db 1114 GAAAAATTCATCATATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 1055
 QY 618 TGATCTGACCAAGATGAAAGATTCAGTTTGAACACAGGTGCTCAAAATATAGTCTCA 677
 Db 1054 TGATCTGACCAAGATGAAAGATTCAGTTTGAACACAGGTGCTCAAAATATAGTCTCA 995
 QY 678 GATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGGCTTTAACTTCCGTGAA 737
 Db 994 GATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGGCTTTAACTTCCGTGAA 935
 QY 738 ACTGATCTTCCATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTGCAATG 797
 Db 934 ACTGATCTTCCATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTGCAATG 875
 QY 798 GAGAAATCCACAGAAATTTTATAGCAATGCTTATTTATAGAAATGATCAATTAACAG 857
 Db 874 GAGAAATCCACAGAAATTTTATAGCAATGCTTATTTATAGAAATGATCAATTAACAG 815
 QY 858 CCAAACTGAGACACATTAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCAGAAAT 917
 Db 814 CCAAACTGAGACACATTAATGTTTCTACGTCCAAAGAGCTAAATGTGAAATCCAGAAAT 755
 QY 918 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTGTCCTTCTCTGATACCTT 977
 Db 754 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTGTCCTTCTCTGATACCTT 695
 QY 978 GAAACACGTCAAGATTAAGATCAAAACAAATAGTTATGCTATGAGATGACAAACTGTG 1037
 Db 694 GAAACACGTCAAGATTAAGATCAAAACAAATAGTTATGCTATGAGATGACAAACTGTG 635

OY	1038	GAGTAATTTGGACCAAGAATAAGAGTAAATGTAAGAAAGGCCAATTCCACTCTACATPAC	1097
Db	634	GAGTAATTTGGACCAGAAATGAAGTAAGTAAGAAAGGCACAATTCACACTCTACATPAC	575
OY	1098	CATGTACTCATTTGTTCCAGTCATCGTGCAAGGTGCATCATAGTACTCTGCTTTACT	1157
Db	574	CATGTACTCATTTGTTCCAGTCATCGTGCGAGGTGCATCATAGTACTCTGCTTTACT	515
OY	1158	AAAAAGGCTCAAGATTATTAATTCCTCCCAATTCCTGATCTCGGCAAGATTTTTAAGA	1217
Db	514	AAAAAGGCTCAAGATTATTAATTCCTCCCAATTCCTGATCTCGGCAAGATTTTTAAGA	455
OY	1218	AATGTTTGAGACCAGAAATGATGATCTCTGCACTGGAAGAATPACGACATCTATGAAA	1277
Db	454	AATGTTTGAGAACCCAGATGATGATCTCTGCACTGGAAGAATPACGACATCTATGAAA	395
OY	1278	GCAAACCAAGGAGGAAACCGACTCTGTATGTCGTGATTAAGAAACCTGAAAGAAAGCCTCCA	1337
Db	394	GCAAACCAAGGAGGAAACCGACTCTGTATGTCGTGATTAAGAAACCTGAAAGAAAGCCTCCA	335
OY	1338	GTGATGAGATPAATTTATTTTTTACCTTCACTGTGACCTTTGAGAAGA	1383
Db	334	GTGATGAGATPAATTTATTTTTTACCTTCACTGTGACCTTTGAGAAGA	289

443 TGACGTGACTTCA--TGACTTTGGGCAACAAGCTGACTGATGAAGTGTCTTTGGCT -CC 459
Db TGACTGACCTTCAATGAGCATGGGGGACAACTGGAGTCAATGAAGTGTCTGGGCTCCC 120
Qy CTGGAAGAATTAACACAGTCCCGACATAACTACTCTC-TACTATTGGGACAGAAAGCTG 558
Db CTGGAAGAATTAACAGTCCCGACATAACTACTCTCTGACTATTGGGACAGAAAGCTG 180
Qy 500
121 CTGGAAGAATTAACAGTCCCGACATAACTACTCTCTGACTATTGGGACAGAAAGCTG 180
Qy 559 GAAAAAATTCAATCA-ATGTGAAGACATCTTTAGAGAGGCCAATACTTTGGTTGCTTT 617
Db 181 GAGAAAAATTCAATCATATGAGAAAAATCTTTAGAGAGGCCAATACTTTGGTTGCTTT 240
Qy 618 TGATGTGACCAAGAGGAGATTCAGATTTGGAACAACAACATGTGCCAATAATAGTCAA 677
Db 241 TGATGTGACCAAGAGGAGATTCAGATTTGGAACAACAACATGTGCCAATAATAGTCAA 300
Qy 678 GGATATATCAGAGAAATTTAAACCATCTCTCAATATAGGCTTATTAATTCCTCCGTGAA 737
Db 301 GGATATATCAGAGAAATTTAAACCATCTCTCAATATAGGCTTATTAATTCCTCCGTGAA 360
Qy 738 ACGTGATCTTCACATATTTAAACCATCTCTCTTCACAAATGATGACCTTATATGTGCAATG 797

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RESULT 9
US-11-266-748A-126439
; Sequence 126439, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
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; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126439
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1265)..(1265)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-126439

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OY	798	GGAGAAATCCACAGATTTTATTATAGAGATGCTTATTTATGAAAGTAGAAGTCAATTAACG	857
Db	421	GGAGAAATCCACAGATTTTATTATYAGAGATGCTTATTTATGAAAGTAGAAGTCAATTAACG	480
OY	858	CCAAACTGAGACACATATGTTTTTCTAGGTCACAGAGGCTTAATGTAAGATCCAAAT	917
Db	481	CCAAACTGAGACACATATGTTTTTCTAGGTCACAGAGGCTTAATGTAAGATCCAAAT	540
OY	918	TGAGGAAATGTGAGAAATACACTGTGTTCAATGCTCCGCGTGTTCTTCTGATACCTT	977
Db	541	TGAGGAAATGTGAGAAATACACTGTGTTCAATGCTCCGCGTGTTCTTCTGATACCTT	600
OY	978	GAACACAGTCAGAAATPAAGAGTCCAAACAAATPAAGTTATGCTATGAGATGACAACTCTG	1033
Db	601	GAACACAGTCAGAAATPAAGAGTCCAAACAAATPAAGTTATGCTATGAGATGACAACTCTG	660
OY	1038	GAGTATTTGAGGCCCAAGAAATGAGTATAGGTAAAGAGGCAATTCACACTTACCTAAC	1099
Db	661	GAGTATTTGAGGCCCAAGAAATGAGTATAGGTAAAGAGGCAATTCACACTTACCTAAC	720
OY	1098	CATGTTACTCAATGTTCCAGTCATCGTGGCAGGTCCAAATCAATAGTACTCTGCTTAACCT	1155
Db	721	CATGTTACTCAATGTTCCAGTCATCGTGGCAGGTCCAAATCAATAGTACTCTGCTTAACCT	780
OY	1158	AAAAAGCTCAAGATTATTTATATTCCTCCCAATTCCTGTAATCCGCGCAAGATTTTAAAG	1211
Db	781	AAAAAGCTCAAGATTATTTATATTCCTCCCAATTCCTGTAATCCGCGCAAGATTTTAAAG	840
OY	1218	AATGTTTGAGAACCGAATGATGATCTCTGCACCTGGAAGAAAGTACGACATCTATGAGAA	1277
Db	841	AATGTTTGAGAACCGAATGATGATCTCTGCACCTGGAAGAAAGTACGACATCTATGAGAA	900
OY	1278	GCAAAACCAAGAGGAACCGACTCTGTATGCTGTATAGAAAACCTGAAGAAAACCTCTCA	1333
Db	901	GCAAAACCAAGAGGAACCGACTCTGTATGCTGTATAGAAAACCTGAAGAAAACCTCTCA	960
OY	1338	GTGATGAGATPAATTTATTTTACCTTCACTGTGACTCTTGAGAGA	1383
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	Query Match	67.1%	Score 927.6;	DB: 8;	Length 1294;
	Best Local Similarity	98.4%	Prod. NO. 1.1e-264;		
	Matches 990;	Conservative 0;	Mismatches 26;	Indels 7;	Gaps 5;
QY	385	CCTAGCATTTTGGTGTAAAAA--TGCATCTACCCCCGAAAGGTGATCCTGAGTCTGCTG	442		
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RESULT 10
US-11-266-748A-54614
; Sequence, 54614, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Hartson, Paul
; APPLICANT: Johnston, Patrick

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? APPLICANT: Mulligan, Karl
? TITLE OF INVENTION: Transcriptome Microarray Technology and
? FILE REFERENCE: 55815-0102 (319189)
? CURRENT APPLICATION NUMBER: US/11/266,748A
? CURRENT FILING DATE: 2005-11-03
? PRIOR APPLICATION NUMBER: EP 04105479.2
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105482.6
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105483.4
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105507.0
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105485.9
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105484.2
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: US 60/662,276
? PRIOR FILING DATE: 2005-03-14
? PRIOR APPLICATION NUMBER: US 60/700,293
? PRIOR FILING DATE: 2005-07-18
? NUMBER OF SEQ ID NOS: 483996
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 54614
? LENGTH: 902
? TYPE: DNA
? ORGANISM: Homo Sapiens
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? OTHER INFORMATION: n is a, c, g, or t
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? OTHER INFORMATION: n is a, c, g, or t
? US-11-266-748A-54614

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Best Local Similarity 99.8%; Pred. No. 7.6e-168;
Matches 612; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      772 CACAAATGATGACCTATATATGCAAT--GGGAGAAATCCACAGAAATTTTATGACAGATCCT 830
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QY      831 ATTTATGAAGTAAAGTCAATAAAGCAAGCAAACTGAGACACATTAATGTTTCTAAGTCCA 890
DB      61 ATTTATGAAGTAAAGTCAATAAAGCAAGCAAACTGAGACACATTAATGTTTCTAAGTCCA 120

QY      891 AGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATCATCTGTTTCAT 950
DB      121 AGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATCATCTGTTTCAT 180

QY      951 GGTCCCTGGTCTCTCTCTGATACCTTTGAACACAGTCAGATTAAGTCAAAACAAATTA 1010
DB      181 GGTCCCTGGTCTCTCTCTGATACCTTTGAACACAGTCAGATTAAGTCAAAACAAATTA 240

QY      1011 GTTATGCTATGAGATGACAAACTCTGAGTAATTTGAGCAAGAAATGATAGGTAA 1070
DB      241 GTTATGCTATGAGATGACAAACTCTGAGTAATTTGAGCAAGAAATGATAGGTAA 300

QY      1071 GAAGCGCAATTCACACTCTACATTAACATGTTACTATGTTCCAGTCACTGCGGAGG 1130
DB      301 GAAGCGCAATTCACACTCTACATTAACATGTTACTATGTTCCAGTCACTGCGGAGG 360

QY      1131 TGGCAATCATAGTACTCTGCTTACCTAAAGGCTCAAGATATTTATTCCTCCAAAT 1190
DB      361 TGGCAATCATAGTACTCTGCTTACCTAAAGGCTCAAGATATTTATTCCTCCAAAT 420

QY      1191 TCCTGATCTCGGCAAGATTTTAAAGAAATGTTTGAGACCAAGATGATATCTCTGCA 1250
DB      421 TCCTGATCTCGGCAAGATTTTAAAGAAATGTTTGAGACCAAGATGATATCTCTGCA 480
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QY      1251 CTGAGAAAGTACGACATCTATGAGAGCAAAACGAGAAACCGACTCTGATGCT 1310
DB      481 CTGAGAAAGTACGACATCTATGAGAGCAAAACGAGAAACCGACTCTGATGCT 540

QY      1311 GATGAGAAACCTGAGAAAGCTCTCAGTATGAGATTAATTTTATTCCTTCACTGT 1370
DB      541 GATGAGAAACCTGAGAAAGCTCTCAGTATGAGATTAATTTTATTCCTTCACTGT 600

QY      1371 GACCTTGAGAGA 1383
DB      601 GACCTTGAGAGA 613

RESULT 11
US-11-266-748A-73627
? Sequence 73627, Application US/11266748A
? Publication No. US20060134663A1
? GENERAL INFORMATION:
? APPLICANT: Harkin, Paul
? APPLICANT: Johnston, Patrick
? APPLICANT: Mulligan, Karl
? TITLE OF INVENTION: Transcriptome Microarray Technology and
? FILE REFERENCE: 55815-0102 (319189)
? CURRENT APPLICATION NUMBER: US/11/266,748A
? CURRENT FILING DATE: 2005-11-03
? PRIOR APPLICATION NUMBER: EP 04105479.2
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105482.6
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105483.4
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105507.0
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105485.9
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: EP 04105484.2
? PRIOR FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: US 60/662,276
? PRIOR FILING DATE: 2005-03-14
? PRIOR APPLICATION NUMBER: US 60/700,293
? PRIOR FILING DATE: 2005-07-18
? NUMBER OF SEQ ID NOS: 483996
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 73627
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1156 CTA AAAAAGGCTC

	Query Match	Best local Similarity	Score	DB	Length
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			Pred. No. 1,3e-88;		
	Matches 346;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
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OY	1156	CTAAAAAGGCTCAAGATTATTATATTCCTCCCAATTCCTGATCTCGCAAGATTTTAA	1215		

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:23:01 ; Search time 950 Seconds
(without alignments)
10150.126 Million cell updates/sec

Title: US-09-051-843D-3

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: N_Geneseq_8:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1198	86.6	3999	3	AAAS5213
3	1198	86.6	3999	3	AAAF21335
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5	1198	86.6	3999	11	ABD20878
6	1198	86.6	4006	13	ACF87407
7	1198	86.6	4006	14	AEC15897
8	1198	86.6	4009	2	AAT85827
9	1198	86.6	4038	4	AAAS8907
10	1198	86.6	4038	12	ADL71811
11	1198	86.6	4038	12	ADN62574
12	1198	86.6	4039	3	AAAS5214
13	1198	86.6	4039	3	AAAF21336
14	1198	86.6	4039	6	ABK67709
15	1198	86.6	4039	6	ABK84753
16	1198	86.6	4039	6	ABN97361
17	1198	86.6	4039	10	AB297030
18	1198	86.6	4039	11	ABD20879

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20	1198	86.6	4039	12	ADN04503	Adn04503 Antipoxi
21	1198	86.6	4039	13	ADR24772	Adr24772 Breast ca
22	1198	86.6	4039	13	ACN41073	Acn41073 Tumour-as
23	1198	86.6	4039	13	ADX97460	Adx97460 Pancreat1
24	1198	86.6	4466	10	ADB47358	Adb47358 Human CDN
25	1198	86.6	11927	2	AAK77356	AAK77356 Polynucle
26	1198	86.6	11927	3	AAA90388	AAa90388 Plaemid p
27	1198	86.6	14978	3	AAA35216	AAa35216 Human ade
28	1198	86.6	14978	3	AAF21338	AAf21338 Human low
29	1198	86.6	14978	10	AB297032	ABz97032 Human nuc
30	1198	86.6	14978	11	ABD20881	ABd20881 Human pul
31	1198	86.6	3880	6	ABK35718	ABk35718 CDNA sequ
32	1156	82.3	1284	14	ADV42774	Adv42774 Human psy
33	1138	83.6	3906	5	AAF98394	AAf98394 Human CDN
34	1105	79.9	1284	10	ADP17834	Adp17834 Human IL-
35	901	65.1	966	6	AAD22979	AAd22979 Human sol
36	901	65.1	2355	3	AAA09049	AAa09049 IL-13/IL-
37	901	65.1	2355	10	AAD63743	AAd63743 Human IL-
38	901	65.1	2382	3	AAA09050	AAa09050 IL-13/IL-
39	901	65.1	1995	10	AAD63744	AAd63744 Human IL-
40	900	65.1	1389	12	ADP17840	Adp17840 CDNA enco
41	882	63.8	1389	12	ADO26893	Ado26893 CDNA enco
42	839	60.7	2331	14	AEC31481	Aec31481 Human IL-
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44	839	60.7	2331	14	AEC31477	Aec31477 Human IL-
45	839	60.7	2331	14	AEC31479	Aec31479 Human IL-

ALIGNMENTS

RESULT 1	
ID	AAT66165 standard; DNA; 1383 BP.
AC	AAT66165;
DT	15-JUL-1997 (first entry)
XX	
DE	Human interleukin-12 receptor alpha chain NR4 DNA.
XX	
KW	NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine;
KW	allergy; asthma; therapy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	sig_peptide
FT	mat_peptide
XX	
PN	W09715663-AL.
XX	
PD	01-MAY-1997.
XX	
PF	23-OCT-1996; 96WO-AU000668.
XX	
PR	23-OCT-1995; 95AU-00006135.
PR	22-DEC-1995; 95AU-00007276.
PR	09-SEP-1996; 96AU-00002208.
XX	
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
PI	Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX	
DR	WPI, 1997-259018/23.
DR	P-PSDB; AA009822.
XX	
PT	DNA encoding animal haemopoietin receptor which interacts with

PT interleukin-13 - useful to treat asthma, allergy or condition exacepbated
 PT by IGE production.

XX Claim 6; Page 52-54; 93pp; English.

CC DNA sequences (AA166164 and AA166165) respectively code for novel mouse
 CC and human haemopoietin receptors (AAW09821 and AAW09822) designated NR4
 CC that comprise the interleukin-13 (IL-13) receptor alpha-chain. A human
 CC bone marrow cDNA library was screened with probes comprising nucleotides
 CC 82-840 and 840-1270 of murine NR4 cDNA, and a composite sequence for
 CC human NR4 was produced from isolated clones. The availability of genetic
 CC sequences for NR4 permits the development of a range of agents capable of
 CC modulating the activity of IL-13 and related cytokines such as
 CC interleukin-4 for the treatment of allergy, asthma and other conditions
 CC relating to IGE. The genetic sequences can also be used in prodn. of
 CC recombinant NR4 or fusion proteins including NR4

XX Sequence 1383 BP; 421 A; 292 C; 319 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 1383; DB 2; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCAACACGACCAAGAGATTAAACAGTGCAGCCGGGTTCCGAGCGAAGGCTGC 60
 DB 1 GAGCTCAACACGACCAAGAGATTAAACAGTGCAGCCGGGTTCCGAGCGAAGGCTGC 60
 QY 61 ATGAGATGCGCGCGCGGCTCTGCGGGCTGTGGGCGCTGCTGCTGCGCGCGGCGGG 120
 DB 61 ATGAGATGCGCGCGCGGCTCTGCGGGCTGTGGGCGCTGCTGCTGCGCGCGGCGGG 120
 QY 121 GCGGCGGGGCGGGGCGCGCTCAAGAACTCAAGCACTGTGACAAATTTGAGTGTCTC 180
 DB 121 GCGGCGGGGCGGGGCGCGCTCAAGAACTCAAGCACTGTGACAAATTTGAGTGTCTC 180
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 QY 181 GTTGAACAACTCTGACAGTAATATGACATGTGATTCACCCGAGGGAGCCAGTCAAT 240
 DB 181 GTTGAACAACTCTGACAGTAATATGACATGTGATTCACCCGAGGGAGCCAGTCAAT 240
 QY 241 TGTAGCTATGATGATTTTATGATCATTTTGGGCAACAAATGAAGAAATAGCTCCGGAA 300
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 QY 301 ACTCGTCTGTTCAATAGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAG 360
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 QY 361 TGTAGCAACCAATGAGAGTGAAGAGCTTGAATTTTGGTGAAGAAATGCACTCCCA 420
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 QY 481 ATGAGATGTTCTTGGCTCCCTGGAAGAAATACAGTCCGACACTAATTAATCTCTTAC 540
 DB 481 ATGAGATGTTCTTGGCTCCCTGGAAGAAATACAGTCCGACACTAATTAATCTCTTAC 540
 QY 541 TATTGGCACAAGAGCTCTGAAAAAATTCATCAATGTGAAGAAATCTTTAAGAGAGCCAA 600
 DB 541 TATTGGCACAAGAGCTCTGAAAAAATTCATCAATGTGAAGAAATCTTTAAGAGAGCCAA 600
 QY 601 TACTTGGTTGTTCTTGTGATCTGACCAAGTGAAGATTCAGTTTGAACAACACAGT 660
 DB 601 TACTTGGTTGTTCTTGTGATCTGACCAAGTGAAGATTCAGTTTGAACAACACAGT 660
 QY 661 GTTCAATATATGCTCAAGATTAATGACAGAAAAATTAACCAATCTTCAATATATGTCCT 720
 DB 661 GTTCAATATATGCTCAAGATTAATGACAGAAAAATTAACCAATCTTCAATATATGTCCT 720
 QY 721 TTACTTTCCGCTGTGAACCTGATCTCTCAATTTAAAAAAGCTCTCTTCCACATGAT 780
 DB 721 TTACTTTCCGCTGTGAACCTGATCTCTCAATTTAAAAAAGCTCTCTTCCACATGAT 780

DB 721 TTACTTTCCGCTGTGAACCTGATCTCTCAATTTAAAAAAGCTCTCTTCCACATGAT 780
 QY 781 GACCTATATGTCATATGAGAGATCCACAGAAATTTATTAGAGATGCTAATTTATGAA 840
 DB 781 GACCTATATGTCATATGAGAGATCCACAGAAATTTATTAGAGATGCTAATTTATGAA 840
 QY 841 GTTGAAGTCAATPACAGCCAACTGAGACACATATGTTTCTACGTCAGAGGCTTAA 900
 DB 841 GTTGAAGTCAATPACAGCCAACTGAGACACATATGTTTCTACGTCAGAGGCTTAA 900
 QY 901 TGTGAAGATCCGAATTTGAGAAATGAGAAATACATCTGTTTCAATGAGTCCCTGAT 960
 DB 901 TGTGAAGATCCGAATTTGAGAAATGAGAAATACATCTGTTTCAATGAGTCCCTGAT 960
 QY 961 GTTCTTCTGATATCTTGAACACAGTCAAGATTAAGTCAAAACAATTAAGTTATCTAT 1020
 DB 961 GTTCTTCTGATATCTTGAACACAGTCAAGATTAAGTCAAAACAATTAAGTTATCTAT 1020
 QY 1021 GAGGATGACAACTCTGAGTAATTTGAGCCCAAGAAATGATATGATTAAGAGCCCAAT 1080
 DB 1021 GAGGATGACAACTCTGAGTAATTTGAGCCCAAGAAATGATATGATTAAGAGCCCAAT 1080
 QY 1081 TCCACACTTACATTAACCAATGTTACTCATGTTTCCAGTATGTCAGAGTGCATCATTA 1140
 DB 1081 TCCACACTTACATTAACCAATGTTACTCATGTTTCCAGTATGTCAGAGTGCATCATTA 1140
 QY 1141 GTACTCTCTTACCTTAATAAAGGCTCAAGATTAATTAATTCCTTCAATTCCTGATCCT 1200
 DB 1141 GTACTCTCTTACCTTAATAAAGGCTCAAGATTAATTAATTCCTTCAATTCCTGATCCT 1200
 QY 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTGTGACCTGGAAG 1260
 DB 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTGTGACCTGGAAG 1260
 QY 1261 TACGACATCTATGAGAGAGAAACCAAGAGAAACCAAGTCTGTATGCTGATGAGAAAC 1320
 DB 1261 TACGACATCTATGAGAGAGAAACCAAGAGAAACCAAGTCTGTATGCTGATGAGAAAC 1320
 QY 1321 CTGAAGAAAGCCTCTGATGATGAGATTAATTTTACCTTCACTGTGACCTTGAGA 1380
 DB 1321 CTGAAGAAAGCCTCTGATGATGAGATTAATTTTACCTTCACTGTGACCTTGAGA 1380
 QY 1381 AGA 1383
 DB 1381 AGA 1383

RESULT 2
 AAA35213
 ID AAA35213 standard; DNA; 3999 BP.
 XX
 XX AAA35213;
 DT 28-JUL-2000 (first entry)
 XX
 XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO: 87.
 DE
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatoxy;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200009525-A2.
 PN
 XX
 XX 24-FEB-2000.
 PD
 XX
 XX 03-AUG-1999; 99MO-US017712.
 PF

XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX NYCE JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.
XX Disclosure; Page 1252-1253; 1343pp; English.
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antispasmodic, cytoskeletal and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impeded respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasize to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ON reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA3233 to AAA5312 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2333 to
XX AAA3392) are specifically claimed ONs from the present invention. N.B.
XX Sequences given in the disclosure of the present invention do not match
XX up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
XX
XX Query Match 86.6%; Score 1198; DB 3; Length 3999;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 135 CGGCGCTACGGAACCTGAGCACTGACCAATTTGAGTGTCTGTGAAAACCTCTG 194
DB |||||
DB 111 CGGGCTACGGAACCTGAGCACTGACCAATTTGAGTGTCTGTGAAAACCTCTG 170
QY 195 CACAGTAATATGACATGAGATCCACCGAGGAGGAGCAGCTCAATTTGATGATGATA 254
DB |||||
DB 171 CACAGTAATATGACATGAGATCCACCGAGGAGGAGCAGCTCAATTTGATGATGATA 230
QY 255 TTTTAGCATTTTGGCGACAAACAAGATAGAAAATAGCTCCGAAATCGTGCTCAAT 314
DB |||||
DB 231 TTTTAGCATTTTGGCGACAAACAAGATAGAAAATAGCTCCGAAATCGTGCTCAAT 290
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 374
DB |||||
DB 291 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 350
QY 375 GAGTGAGAACCTTACGATTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA 434
DB |||||
DB 351 GAGTGAGAACCTTACGATTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA 410
QY 435 GTCTGCTGACGAGCACTTCAATGCACTTTGGGCAACCACTGACATCAATGAAGCTTTTG 494
DB |||||
DB 411 GTCTGCTGACGAGCACTTCAATGCACTTTGGGCAACCACTGACATCAATGAAGCTTTTG 470
QY 495 GCTCCCTGGAAGAAATCAAGTCCCGACACTAATCTACTATTTGGGACAGAG 554

DB 471 GCTCCCTGGAAGAAATCAAGTCCCGACACTAATCTACTATTTGGGACAGAG 530
QY 555 CCTGGAATAAATTTATCATATGTAATAACATCTTTAGAGAGGCCAATCTTTGTTGTC 614
DB |||||
DB 531 CCTGGAATAAATTTATCATATGTAATAACATCTTTAGAGAGGCCAATCTTTGTTGTC 590
QY 615 CTTGATCTGACCAAGAGTAAGATTCAGTTTGAACACACAGGTGCCAATAATAGT 674
DB |||||
DB 591 CTTGATCTGACCAAGAGTAAGATTCAGTTTGAACACACAGGTGCCAATAATAGT 650
QY 675 CAAGATATATGACAGAAAATAATTAACATCTTCAATATAGTGCCTTTAATCCCGGT 734
DB |||||
DB 651 CAAGATATATGACAGAAAATAATTAACATCTTCAATATAGTGCCTTTAATCCCGGT 710
QY 735 GAAACCTGATCTTCCATATATTAATAAATCTCTCTTCCACATATGATGACCTATATGCA 794
DB |||||
DB 711 GAAACCTGATCTTCCATATATTAATAAATCTCTCTTCCACATATGATGACCTATATGCA 770
QY 795 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAGCAATTA 854
DB |||||
DB 771 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAGCAATTA 830
QY 855 CAGCCAAACTGAGACACATATATGTTTCTACGTCCAAAGAGCTAAATGTGAATCCAGA 914
DB |||||
DB 831 CAGCCAAACTGAGACACATATATGTTTCTACGTCCAAAGAGCTAAATGTGAATCCAGA 890
QY 915 ATTTGAAGAAATGTGAGAAATATACATCTTTGATGATGCTCCGTGTTCTCTGATAC 974
DB |||||
DB 891 ATTTGAAGAAATGTGAGAAATATACATCTTTGATGATGCTCCGTGTTCTCTGATAC 950
QY 975 TTTGAACAGATGAGAAATATAGAGCAAAATTAATGATATGATAGAGAGAGCAAACT 1034
DB |||||
DB 951 TTTGAACAGATGAGAAATATAGAGCAAAATTAATGATATGATAGAGAGAGCAAACT 1010
QY 1035 CTGAGATATTTGAGAGCAAAATATAGATATGATAGAGAGCAATTCACACTCTACAT 1094
DB |||||
DB 1011 CTGAGATATTTGAGAGCAAAATATAGATATGATAGAGAGCAATTCACACTCTACAT 1070
QY 1095 AACCATGTTACTACTATTTGTTCCAGTCATGCTGCGAGGTGCAATCATATGACTCTGCTTTA 1154
DB |||||
DB 1071 AACCATGTTACTACTATTTGTTCCAGTCATGCTGCGAGGTGCAATCATATGACTCTGCTTTA 1130
QY 1155 CCTAAAAGGCTCAAGATTTATATATCCCTCCCAATTCGATCTGCGCAAGATTTTAA 1214
DB |||||
DB 1131 CCTAAAAGGCTCAAGATTTATATATCCCTCCCAATTCGATCTGCGCAAGATTTTAA 1190
QY 1215 AGAATGTTTGGAGACAGATGATGATCTGCTGACCTGGAAGAATGACATCTATGA 1274
DB |||||
DB 1191 AGAATGTTTGGAGACAGATGATGATCTGCTGACCTGGAAGAATGACATCTATGA 1250
QY 1275 GAAGCAAAACCAAGAGAGAAACCGACTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1334
DB |||||
DB 1251 GAAGCAAAACCAAGAGAGAAACCGACTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1310
QY 1335 TCAGTGAATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB |||||
DB 1311 TCAGTGAATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAGA 1359

RESULT 3
AAF21335
ID AAF21335 standard; DNA; 3999 BP.
XX
XX AAF21335;
XX AC
XX XX
XX DT
XX 14-MAR-2001 (first entry)
XX
XX Human low adenosine antisense oligonucleotide related sequence #2902.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;

immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; sufficient hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

MO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

06-APR-1999; 99US-0127958P.

(UYEC-) UNIV EAST CAROLINA.

(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure, Page 1336-1337; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiepileptic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulin and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other; XX XX

Query Match 86.6%; Score 1198; DB 3; Length 3999; Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

135 CGGCGCTACGAACTCAGCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 194
111 CGGCGCTACGAACTCAGCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 170
195 CACAGTAATGTGACATGCAATCCACCGAGGAGCCAGCTCAATTGTGTATGTGTA 254

171 CACAGTAATGTGACATGCAATCCACCGAGGAGCCAGCTCAATTGTGTATGTGTA 230
255 TTTTACGATTTTGGGACAAACAAGATAGAGTCCGGAAGCTGTGTTCAAT 314
231 TTTTACGATTTTGGGACAAACAAGATAGAGTCCGGAAGCTGTGTTCAAT 230
315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374
291 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 350
375 GAGTGAAGAGCCCTAGATTTTGGTTGAAATAATGATCTCAACCCCGAAGGTGATCTCTGA 434
351 GAGTGAAGAGCCCTAGATTTTGGTTGAAATAATGATCTCAACCCCGAAGGTGATCTCTGA 410
435 GTCTGCTGTGACGTAAGTCAATGCAATTTGGGCAACCTGAGCTACATGAGTGTCTTG 494
411 GTCTGCTGTGACGTAAGTCAATGCAATTTGGGCAACCTGAGCTACATGAGTGTCTTG 470
495 GCTCCCTGGAAGAGATACAGTCCGACACTAACTTACTCTCTACTATTTGGCAGAGAG 554
471 GCTCCCTGGAAGAGATACAGTCCGACACTAACTTACTCTCTACTATTTGGCAGAGAG 530
555 CCTGGAATAAATTCATCAATGCAATTTGGGCAACCTGAGCTACATGAGTGTCTTG 614
531 CTTGGAATAAATTCATCAATGCAATTTGGGCAACCTGAGCTACATGAGTGTCTTG 590
615 CTTTGAATGTGACCAAGTGAAGATTCAGTTTGAACAACACAGTGTCCAAATAATGTG 674
591 CTTTGAATGTGACCAAGTGAAGATTCAGTTTGAACAACACAGTGTCCAAATAATGTG 650
675 CAAAGTAATGACAGGAAATTAACCATCTTCAATATATATGTCCTTTAACTTCCGTGT 734
651 CAAAGTAATGACAGGAAATTAACCATCTTCAATATATATGTCCTTTAACTTCCGTGT 710
735 GAAACCTGATCCCTCCCATATTAATAAAGCTCTTCCCAATGATGACCTATATATGCA 794
711 GAAACCTGATCCCTCCCATATTAATAAAGCTCTTCCCAATGATGACCTATATATGCA 770
795 ATGGAGAAATCCACAGAAATTTTATGACAGATGCTATTTTATGAGTGAAGTCAATGA 854
771 ATGGAGAAATCCACAGAAATTTTATGACAGATGCTATTTTATGAGTGAAGTCAATGA 830
855 CAGCCAACTGAGACACATATATTTTCTACGTCGAAGGCTAAATGTGAGATTCAGA 914
831 CAGCCAACTGAGACACATATATTTTCTACGTCGAAGGCTAAATGTGAGATTCAGA 890
915 ATTTGAGAAATATGAGAAATATATATCTGTTCAATGATCCCTGGTGTCTCTGATAC 974
891 ATTTGAGAAATATGAGAAATATATCTGTTCAATGATCCCTGGTGTCTCTGATAC 950
975 TTTGAACACAGTCAGATATGAGTCAAAACAATAATGATATGATGAGATGACAAACT 1034
951 TTTGAACACAGTCAGATATGAGTCAAAACAATAATGATATGATGAGATGACAAACT 1010
1035 CTTGAGTAATTTGAGGCAAGAAATGATATGATTAAGAAAGCGCAATTTCAACTTACAT 1094
1011 CTTGAGTAATTTGAGGCAAGAAATGATATGATTAAGAAAGCGCAATTTCAACTTACAT 1070
1095 AACCATGTTATTCATGTTTCCAGTCAATGTCGAGAGTGAATCATATGATCTCTGCTTTA 1154
1071 AACCATGTTATTCATGTTTCCAGTCAATGTCGAGAGTGAATCATATGATCTCTGCTTTA 1130
1155 CCTAATAAGGCTCAAGATTTATATATTCCTCCATTCCTGATCCCTGGAAGATTTTAA 1214
1131 CCTAATAAGGCTCAAGATTTATATATTCCTCCATTCCTGATCCCTGGAAGATTTTAA 1190
1215 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAAGATGACATCTATGA 1274
1191 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAAGATGACATCTATGA 1250
1275 GAAAGCAACCAAGAGAGAAACCGACTCTGATAGTGTGATGAAACCTGAAGAAAGCTTC 1334
1251 GAAAGCAACCAAGAGAGAAACCGACTCTGATAGTGTGATGAAACCTGAAGAAAGCTTC 1310

QY 1335 TCAGTGTGAGATTAATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB 1311 TCAGTGTGAGATTAATTTTACCTTCACTGTGACCTTGAGAGA 1359

RESULT 4
AB297029 standard; DNA; 3999 BP.
ID AB297029
XX
AC AB297029;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cytosolic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPiG-) EPiGENESIS PHARM INC.
XX
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12271; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cytosolic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
Query Match 86.6%; Score 1198; DB 10; Length 3999;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTGAAAACTCTG 194
DB 111 CGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTGAAAACTCTG 170

QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATATTGACTATGAGTA 254
DB 171 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATATTGACTATGAGTA 230

QY 255 TTTTAGTCAATTTGGGCAACAAGATTAAGAAATATGCTCCGGAACTCGTCCGTCAAT 314
DB 231 TTTTAGTCAATTTGGGCAACAAGATTAAGAAATATGCTCCGGAACTCGTCCGTCAAT 290

QY 315 AGAAGTACCCCTGAATGAGAGATTTTGTCTGCAAGTGGGTCCTCAGTGTAGCAACAAATGA 374
DB 291 AGAAGTACCCCTGAATGAGAGATTTTGTCTGCAAGTGGGTCCTCAGTGTAGCAACAAATGA 350

QY 375 GAGTGAAGCTTAGCATTTTGTGTAATAATGATCTCACCCGAGAGGTGATCTCTGA 434
DB 351 GAGTGAAGCTTAGCATTTTGTGTAATAATGATCTCACCCGAGAGGTGATCTCTGA 410

QY 435 GTCTGCTGTGACTGAATCTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAGTGTCTTG 494
DB 411 GTCTGCTGTGACTGAATCTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAGTGTCTTG 470

QY 495 GCTCCCTGGAAGGAATACCAAGTCCCGACATCACTACTCTACTATTGGCACAAGAG 554
DB 471 GCTCCCTGGAAGGAATACCAAGTCCCGACATCACTACTCTACTATTGGCACAAGAG 530

QY 555 CTTGGAATAAATTCATCATGTGTAACAATCTTTTGAAGAGGCCAATACTTTGGTGTTC 614
DB 531 CTTGGAATAAATTCATCATGTGTAACAATCTTTTGAAGAGGCCAATACTTTGGTGTTC 590

QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGAGTGTCCAAATATAGGT 674
DB 591 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGAGTGTCCAAATATAGGT 650

QY 675 CAAGGATATGACAGGAATAAATTAACCATCTTCATATATGTGCTTTAACTCCGGT 734
DB 651 CAAGGATATGACAGGAATAAATTAACCATCTTCATATATGTGCTTTAACTCCGGT 710

QY 735 GAAACCTGATCTCTCACAATATTAATAAATCTCTCTTCCACAAATGATGACCTATATGTGA 794
DB 711 GAAACCTGATCTCTCACAATATTAATAAATCTCTCTTCCACAAATGATGACCTATATGTGA 770

QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTGAAGTGAAGTCAATAA 854
DB 771 ATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTGAAGTGAAGTCAATAA 830

QY 855 CAGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGGCTAAATGTGAGAAATCCAGA 914
DB 831 CAGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGGCTAAATGTGAGAAATCCAGA 890

QY 915 ATTTGAGAGAAATGTGAGAAATCATCTTTTCATGTCCTGTGTCTCTCTGATAC 974
DB 891 ATTTGAGAGAAATGTGAGAAATCATCTTTTCATGTCCTGTGTCTCTCTGATAC 950

QY 975 TTTGACACAGTCAAGTAATAGTCAAAACAATAATAGTATGCTATGAGATGCAAACT 1034
DB 951 TTTGACACAGTCAAGTAATAGTCAAAACAATAATAGTATGCTATGAGATGCAAACT 1010

QY 1035 CTGGAGTAATTTGAGCAAAATATGATATAGGTAAAGCGCAATTCACACCTCTCAT 1094
DB 1011 CTGGAGTAATTTGAGCAAAATATGATATAGGTAAAGCGCAATTCACACCTCTCAT 1070

QY 1095 AACCATGTTTACTGATTTTCCAGTCACTGTGAGGTCACATCATAGTACTCTGCTTTA 1154
DB 1071 AACCATGTTTACTGATTTTCCAGTCACTGTGAGGTCACATCATAGTACTCTGCTTTA 1130

QY 1155 CTTAAAAAGGCTCAAGATTTATATTTCTCTCAATTTCTGATCTCTGGCAAGATTTTAA 1214
DB 1131 CTTAAAAAGGCTCAAGATTTATATATTTCTCTCAATTTCTGATCTCTGGCAAGATTTTAA 1190

OY		1215	AGAAATGTTTGAGACCCGAATGANGATCACTCGACCTGGAAAAGAAGTACGCATCTGTGA	1274
Dd		1191	AGAAATGTTTGAGACCCGAATGANGATCACTCGACCTGGAAAAGAAGTACGCATCTGTGA	1250
OY		1275	GAGCAAAACCAGAGGAGAACCCGACTCTGTAGTCGTATATAAAAACTGGAAGAAAGCCTC	1334
Dd		1251	GAGCAAAACCAGAGGAGAACCCGACTCTGTAGTCGTATATAAAAACTGGAAGAAAGCCTC	1310
OY		1335	TCACTGATGAGAGATTAATTATTTTTTACCTTGACCTTGACCTTGAGAGA	1383
Dd		1311	TCAGTGATGAGAGATTAATTATTTTTTACCTTGACCTTGACCTTGAGAGA	1359
RESULT 5				
ABD20878	ID	ABD20878	standard; DNA; 3999 BP.	
XX	AC	ABD20878;		
DT		29-JUL-2004	(first entry)	
DE	XX		Human pulmonary and inflammatory target DNA #489.	
XX	XX		Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
KM	KM		respiratory tract inflammation; adenosine sensitivity; lung; cancer;	
KM	KM		surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;	
KM	KM		anaesthetic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;	
KM	KM		beta-adrenergic agonist; respiratory disease; pulmonary vasocostriction;	
KM	KM		respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;	
KM	KM		emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;	
KM	KM		pulmonary transplantation rejection; ds.	
OS	XX		Homo sapiens.	
XX	PN		WO200285309-A2.	
PD		31-OCT-2002.		
PF	XX	23-APR-2002;	2002WO-US013143.	
PR	XX	24-APR-2001;	2001US-0286036P.	
PA	XX	(EPFG-) EPIGENESIS PHARM INC.		
PI	XX	Nyce JW, Li Y, Sandraesgra A, Katz E, Pabalan J, Aguilar D;		
PT	XX	Miller S, Tang L, Shahabuddin S;		
DR	XX	WPI; 2003-093058/08.		
PT	XX		Pharmaceutical composition for treating asthma, has antisense	
PT	XX		oligonucleotide containing less percentage of adenosine, targeted to	
PT	XX		nucleic acids associated with lung airway or lung dysfunction, and	
PT	XX		bronchodilating agent.	
XX		Claim 15; SEQ ID NO 12271; 763bp; English.		
PS	XX		This invention describes a novel composition (a) a first active agent,	
CC	CC		comprising oligonucleotides, effective for alleviating	
CC	CC		bronchoconstriction, respiratory tract inflammation, allergies and	
CC	CC		reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,	
CC	CC		surfactant depletion or hyposecretion, when administered to a mammal. The	
CC	CC		oligonucleotides are derived from a gene encoding or regulating	
CC	CC		expression of a target polypeptide associated with lung airway or lung	
CC	CC		dysfunction or cancer and can be anti-sense to the corresponding mRNA.	
CC	CC		The invention also describes a kit, that comprises: (a) a delivery	
CC	CC		device, in separate containers, (b) the oligonucleotides, (c)	
CC	CC		instructions for adding a carrier and for use of the kit. The composition	
CC	CC		of the invention has anti-allergic, anti-inflammatory, antiasthmatic,	
CC	CC		analgesic, hypotensive, immunosuppressive and cytostatic activity, is a	
CC	CC		beta-adrenergic agonist. The composition is useful for preventing or	
CC	CC		treating a respiratory, lung or malignant disease. The administered	
CC	CC		composition comprises oligo and is administered to reduce the production	
CC	CC		or availability, or to increase the degradation of the target mRNA or to	

CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
XX	Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
Query Match	86.6%; Score 1198; DB 11; Length 3999;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1248; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	135 CGCGCTTACGAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAACCTCTG 194
DB	111 CGCGCTTACGAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAACCTCTG 170
QY	195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGCTATGTGA 254
DB	171 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGCTATGTGA 230
QY	255 TTTTAGTATTTTGGCGCAACAAGATPAAGAAAATBACTCCGGAAATCCGTCGTTCAAT 314
DB	231 TTTTAGTATTTTGGCGCAACAAGATPAAGAAAATBACTCCGGAAATCCGTCGTTCAAT 290
QY	315 AGAAGTACCCCTGATGAGAGATTTTGTCTCAAGTGGGTGCCAGTGTAGCCACCAATGA 374
DB	291 AGAAGTACCCCTGATGAGAGATTTTGTCTCAAGTGGGTGCCAGTGTAGCCACCAATGA 350
QY	375 GAGTGAGAGCCTTAGCATTTTGGTTGAAAAATGCATCTCACCCCGAAGGTGCTCTGA 434
DB	351 GAGTGAGAGCCTTAGCATTTTGGTTGAAAAATGCATCTCACCCCGAAGGTGCTCTGA 410
QY	435 GTCTGCTGTGCTGAACCTTCAATGATTTGGCAACAACCTGAGCTACATGAAGTGTCTTG 494
DB	411 GTCTGCTGTGCTGAACCTTCAATGATTTGGCAACAACCTGAGCTACATGAAGTGTCTTG 470
QY	495 GCTCCCTGGAAGAAATACCAAGTCCGACACTPACTATCTCTATCTATTGGCAGAGAG 554
DB	471 GCTCCCTGGAAGAAATACCAAGTCCGACACTPACTATCTCTATCTATTGGCAGAGAG 530
QY	555 CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATACTTTGGTGTTC 614
DB	531 CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATACTTTGGTGTTC 590
QY	615 CTTTGATCTGACCAAGTGAAGGATTCAGTTTGAACAACAAGTGTCCAAATATGTGT 674
DB	591 CTTTGATCTGACCAAGTGAAGGATTCAGTTTGAACAACAAGTGTGTCAAAATATAGT 650
QY	675 CAAGGATATGACAGAAAAATTTAAACCATCTTCAATATATGAGCTTTAACTTCCCGGT 734
DB	651 CAAGGATATGACAGAAAAATTTAAACCATCTTCAATATATGAGCTTTAACTTCCCGGT 710
QY	735 GAAACCTGATCCTCCACATATTTAAACCATCTCTCTTCCACATATGATGATGATGCA 794
DB	711 GAAACCTGATCCTCCACATATTTAAACCATCTCTCTTCCACATATGATGATGATGCA 770
QY	795 ATGGAGAAATCAACGAATTTTATATGAGATGCTATTTTATGAAATGAAATGCAATPA 854
DB	771 ATGGAGAAATCAACGAATTTTATATGAGATGCTATTTTATGAAATGAAATGCAATPA 830
QY	855 CAGCCAAATGAGACATATATGTTTCTACGTCCAAAGGCTAAATGTGAAATCCGAGA 914
DB	831 CAGCCAAATGAGACATATATGTTTCTACGTCCAAAGGCTAAATGTGAAATCCGAGA 890
QY	915 ATTGAGAGAAATGTGGAATPACATCTGTGTTCAATGCTCCCTGGTGTCTTCCTGATAC 974

|||||
DB 891 ATTGAGAGAAATGTGAGATATACATCTGTTTCATGGTCCCTGGTGTCTTCTGATAC 950
QY 975 TTGGAACAGAGTCAGATTAAGAGTCAAAACAAATAGTATGCTATGAGGTGCAACT 1034
DB 951 TTGGAACAGAGTCAGATTAAGAGTCAAAACAAATAGTATGCTATGAGGTGCAACT 1010
QY 1035 CTGAGATTAATGAGCCAGAAATAGTATAGTATAGAGGCAATTCACACTCTACAT 1094
DB 1011 CTGAGATTAATGAGCCAGAAATAGTATAGTATAGAGGCAATTCACACTCTACAT 1070
QY 1095 AACCATGTTACTACTGTTCCAGTCATGTCGAGGTGCAATCATTAAGTACTCTGCTTTA 1154
DB 1071 AACCATGTTACTACTGTTCCAGTCATGTCGAGGTGCAATCATTAAGTACTCTGCTTTA 1130
QY 1155 CCTAAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCCTGCAAGATTTTAA 1214
DB 1131 CCTAAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCCTGCAAGATTTTAA 1190
QY 1215 AGAAATGTTGAGACCAAGATGATGATCTGCACTGGAAGAGTACGATCTATGA 1274
DB 1191 AGAAATGTTGAGACCAAGATGATGATCTGCACTGGAAGAGTACGATCTATGA 1250
QY 1275 GAAGCAAAACCAAGAGGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334
DB 1251 GAAGCAAAACCAAGAGGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1310
QY 1335 TCAGTGTGAGATTAATTTATTTTACCTTCACTGATACCTTGAGAGA 1383
DB 1311 TCAGTGTGAGATTAATTTATTTTACCTTCACTGATACCTTGAGAGA 1359

RESULT 6

ACF87407
ID ACF87407 standard; DNA; 4006 BP.

AC ACF87407;

DT 02-JUN-2005 (first entry)

DE Human SIRS/sepsis diagnostic marker DNA fragment 6267.

XX Systemic inflammatory response syndrome; SIRS; antibacterial;

KW immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.

OS Homo sapiens.

PN WO2004087949-A2.

PD 14-OCT-2004.

PF 31-MAR-2004; 2004MO-EP003419.

PR 02-APR-2003; 2003DE-01015031.

PR 08-AUG-2003; 2003DE-01036511.

PR 02-SEP-2003; 2003DE-01040395.

XX (SIRS-) SIRS LAB GMBH.

XX Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;

PI WPI; 2004-748070/73.

DR In vitro detection of systemic inflammatory response syndrome and related

PT conditions, for e.g. monitoring progression, comprises detecting abnormal

PT expressions of disease-related genes.

PS Disclosure; Page; 75pb; German.

XX The invention relates to a novel method for in vitro detection of

CC systemic inflammatory response syndrome (SIRS). The method comprises

CC detecting abnormal expression of disease-related genes, or their

CC associated peptides. The method of the invention demonstrates

CC antibacterial, immunosuppressive and antiinflammatory applications and
CC may be used for early differential diagnosis, monitoring progression,
CC assessing risk, assessing the likely response to treatment and for post
CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and
CC sepsis-like conditions. The recombinant or synthetic nucleic acid
CC sequences of the invention, or derived proteins or peptides, may be
CC useful as calibrants in assays for the specified diseases, for evaluating
CC activity or toxicity in screening for active agents and/or for
CC preparation of agents for treatment or prevention of the specified
CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic
CC marker DNA fragment of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at ftd.wipo.int/pub/published
CC pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
CC disclosed within the specification, however, these have not been taken
CC into account during indexing due to inconsistencies in application and
CC format

XX Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

SO Query Match 86.6%; Score 1198; DB 13; Length 4006;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACCGAAACTCAGCCACCTGTGACAAATTTGATGTCCTGTGAAACCTCTG 194

DB 121 CGGCGCTACCGAAACTCAGCCACCTGTGACAAATTTGATGTCCTGTGAAACCTCTG 180

QY 195 CACAGTAATATGACATGATATCCACCGAGGAGCCAGCTCAATTTGATGTCCTGTA 254

DB 181 CACAGTAATATGACATGATATCCACCGAGGAGCCAGCTCAATTTGATGTCCTGTA 240

QY 255 TTTTATGATTTTGGCGACAAACAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 314

DB 241 TTTTATGATTTTGGCGACAAACAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 300

QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 374

DB 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 360

QY 375 GAGTGAGAACCTAGACATTTTGGTTGAAAATGATCTACCCCGAGAGGTGATCTGTA 434

DB 361 GAGTGAGAACCTAGACATTTTGGTTGAAAATGATCTACCCCGAGAGGTGATCTGTA 420

QY 435 GTCTGCTGTGACTGAACTTCAATGCAATTTGGGACAACTGATCACTGAAGTCTTGG 494

DB 421 GTCTGCTGTGACTGAACTTCAATGCAATTTGGGACAACTGATCACTGAAGTCTTGG 480

QY 495 GCTCCCTGGAAGGATATACAGTCCCGACATTAATCTCTACTATTTGGGACAGAG 554

DB 481 GCTCCCTGGAAGGATATACAGTCCCGACATTAATCTCTACTATTTGGGACAGAG 540

QY 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTTTC 614

DB 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTTTC 600

QY 615 CTTTGTATCTGACCAAGAGTATTCAGTTTGAACAACAAGTCTCCAAATATAGT 674

DB 601 CTTTGTATCTGACCAAGAGTATTCAGTTTGAACAACAAGTCTCCAAATATAGT 660

QY 675 CAAGATTAATGACGAAAAATTAACCATCTTCAATATATGTCCTTTAACTCCGCTGT 734

DB 661 CAAGATTAATGACGAAAAATTAACCATCTTCAATATATGTCCTTTAACTCCGCTGT 720

QY 735 GAAACCTGATCTTCCATATTAATAAACCCTCTCTTCCAAATGATGACCTATATGTA 794

DB 721 GAAACCTGATCTTCCATATTAATAAACCCTCTCTTCCAAATGATGACCTATATGTA 780

QY 795 ATGGAGAAATCCACAGATTTTATAGAGATGCTATATTTATGAGATGAAGTCAATTA 854

DB 781 ATGGAGAAATCCACAGATTTTATAGAGATGCTATATTTATGAGATGAAGTCAATTA 840

QY 855 CAGCCAAACTGACACATTAATGTTTCTACGTCCAAGAGCTAAATGTGAGATCCAGA 914

|||||
Db 841 CAGCCAACTGAGACACATATCTTTCTACGTCACAAAGAGCTAAATGTGAGATCCAGA 900
|||||
Qy 915 ATTTGAGAGAAATGTGGAGAAATCATCTGTGTTTCAAGGTCCCGTGTCTTCTCTGATAC 974
|||||
Db 901 ATTTGAGAGAAATGTGGAGAAATCATCTGTGTTTCAAGGTCCCGTGTCTTCTCTGATAC 960
|||||
Qy 975 TTTGAAACACAGTCAGATTAAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1034
|||||
Db 961 TTTGAAACACAGTCAGATTAAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1020
|||||
Qy 1035 CTGAGATTAATTTGAGCCAGAAATGAGTATAGGTAGAGACGCAATTCACACTTCATCAT 1094
|||||
Db 1021 CTGAGATTAATTTGAGCCAGAAATGAGTATAGGTAGAGACGCAATTCACACTTCATCAT 1080
|||||
Qy 1095 AACCATGTTACTGATTTCTCAGTCATCGTCGAGGAGCAATCATAGTACTCTCGCTTTA 1154
|||||
Db 1081 AACCATGTTACTGATTTCTCAGTCATCGTCGAGGAGCAATCATAGTACTCTCGCTTTA 1140
|||||
Qy 1155 CCTAAAAAGGCTCAGATTAATTTATTTCCCTCCAAATTCCTGATCTGGCAAGATTTTAA 1214
|||||
Db 1141 CCTAAAAAGGCTCAGATTAATTTATTTCCCTCCAAATTCCTGATCTGGCAAGATTTTAA 1200
|||||
Qy 1215 AGAAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAGATGACATCTATGA 1274
|||||
Db 1201 AGAAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAGATGACATCTATGA 1260
|||||
Qy 1275 GAGCAAAACCAAGAGAAACCGACTCTGATGCTGATGAGAAAACCTGAAAGAGCTC 1334
|||||
Db 1261 GAGCAAAACCAAGAGAAACCGACTCTGATGCTGATGAGAAAACCTGAAAGAGCTC 1320
|||||
Qy 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAGA 1383
|||||
Db 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAGA 1369
|||||
RESULT 7
AEC15897
ID AEC15897 standard; RNA; 4006 BP.
XX
AC AEC15897;
XX
DT 20-OCT-2005 (first entry)
XX
DE Human interleukin-13 receptor alpha 1 (IL-13RA1) cDNA.
XX
KW RNA interference; gene silencing; cancer; hyperproliferation; neoplasm;
cytostatic; viral infection; infection; virucide; inflammation;
antiinflammatory; autoimmune disease; immune disorder; immunosuppressive;
KW pulmonary disease; respiratory disease; respiratory-gen.;
cardiovascular disease; cardiovascular-gen.; neurological disease;
neuroprotective; renal disease; endocrine disease; gastrointestinal disease;
nephrotropic; endocrine-gen.; liver disease; gastrointestinal disease;
hepatotropic; ocular disease; ophthalmological; reproductive disorder;
infertility; antiinfertility; gynecology and obstetrics; andrology;
KW mitochondrial disease; prion disease; degeneration;
interleukin-13 receptor alpha 1; IL-13 receptor alpha 1; gene; ss.
XX
XX OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 44..1327
FT /tag= a
FT /product= "Interleukin-13 receptor alpha 1 (IL-13RA1)"
XX
PN US2005182007-A1.
XX
PD 18-AUG-2005.
XX
PF 20-AUG-2004; 2004US-009222675.
XX
PR 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.

PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 17-MAY-2002; 2002US-05015875.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 14-FEB-2003; 2003US-05004566.
PR 20-FEB-2003; 2003US-05005028.
PR 20-FEB-2003; 2003US-05005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826566.
PR 30-APR-2004; 2004US-05013456.
PR 24-MAY-2004; 2004US-05013390.
PR 09-JUN-2004; 2004US-00863973.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Meswigen J, Beigelman L;
XX
DR WPI; 2005-581759/59.
XX
DR REFSEQ; NM_001560.
XX
PT New chemically synthesized double stranded siNA molecule that directs
PT cleavage of an Interleukin-13 receptor (IL-13R) RNA via RNA interference,
PT useful in preparing a composition for treating e.g., inflammatory
PT disorders.
XX
PS Claim 32; Page; 127pp; English.
XX
CC The invention relates to chemically synthesized short interfering nucleic
CC acids (siNAs) which downregulate expression of receptors for interleukin-
CC 13 (e.g., IL-13 receptor (IL-13R), IL-4 receptor (IL-4R) and IL-2
CC receptor gamma (IL-2RG)) by RNA interference. The invention also relates
CC to similar siNAs which interfere with the expression of the ligands for
CC these receptors, namely IL-13 and IL-4. The siNAs of the invention may or
CC may not comprise ribonucleotides, can contain deoxyribonucleotides, can
CC be chemically modified and may be double or single stranded. They further
CC comprise sense and antisense regions, or alternatively are assembled from
CC a sense oligonucleotide and an antisense oligonucleotide. Specifically,
CC the siNAs include short interfering RNA (siRNA), double-stranded RNA,
CC micro-RNA (miRNA) and short hairpin RNA (shRNA). The invention also
CC relates to pharmaceutical compositions comprising an siNA targeted to
CC human IL-13R (e.g., IL-13R alpha 1 (IL13RA1), see RefSeq accession number
CC NM_001560), IL-4R, IL-2RG, IL-4 or IL-13, especially the siRNAs shown in
CC AEC14082-AEC1592. The invention further discloses expression vectors and
CC host cells comprising an siNA of the invention. The siNAs exhibit
CC increased resistance to nuclease degradation compared to the prior art.
CC The siNAs of the invention can be used to modulate expression of their
CC target genes in cells, tissue explants or organisms (e.g., by ex vivo
CC gene therapy), or in grafts and transplants for the treatment of a
CC variety of interleukin-related conditions. They may be used in the
CC treatment of cancers and other proliferative conditions, viral infection,
CC inflammatory conditions, autoimmune diseases, respiratory and pulmonary
CC diseases (e.g., asthma, chronic obstructive pulmonary disease (COPD),
CC allergies), cardiovascular diseases, neurological diseases, renal
CC diseases, ocular diseases, liver diseases, mitochondrial diseases,
CC endocrine diseases, prion diseases and reproduction-related conditions.
CC The siNAs may also be used in drug screening, diagnosis, therapeutic
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents a cDNA
CC corresponding to human IL-13RA1 mRNA, which is specifically claimed as a

CC target for siRNAs of the invention. Note: The present sequence is not shown in the specification, but was obtained from RefSeq accession number CC NM_001560. Other sequence data for this patent is also available in CC electronic format directly from the US patent office at CC seqdata.uspto.gov/sequence.html?docid=20050182007.

XX Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 14; Length 4006;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 194
DB 121 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 180
QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 254
DB 181 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 240
QY 255 TTTTAGTCATTTTGGCAGCAAAACAAGATAAGAAATAGCTCCGGAATCTGCTGTTCAAT 314
DB 241 TTTTAGTCATTTTGGCAGCAAAACAAGATAAGAAATAGCTCCGGAATCTGCTGTTCAAT 300
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACCAATGA 374
DB 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACCAATGA 360
QY 375 GAGTGAAGAGCTTACGCTTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA 434
DB 361 GAGTGAAGAGCTTACGCTTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA 420
QY 435 GTCTGCTGACTGAACTTCAATGATCTTGGCAACCTGAGTACATGAAAGTCTTGTG 494
DB 421 GTCTGCTGACTGAGCTTCAATGATCTTGGCAACCTGAGTACATGAAAGTCTTGTG 480
QY 495 GCTCCCTGGAAGAAATCAAGTCCCGACACTAATCTACTTCTACTATTGGCAGAGAG 554
DB 481 GCTCCCTGGAAGAAATCAAGTCCCGACACTAATCTACTTCTACTATTGGCAGAGAG 540
QY 555 CCTGGAAGAAATTCATATGTCGAAAACATCTTTAGGAAAGCCATCTTGGTGTTC 614
DB 541 CCTGGAAGAAATTCATATGTCGAAAACATCTTTAGGAAAGCCATCTTGGTGTTC 600
QY 615 CTTTGATCTGACCAAGTGAAGGATTCAGTTTGAACAACAGGTCCAAATAATGTCT 674
DB 601 CTTTGATCTGACCAAGTGAAGGATTCAGTTTGAACAACAGGTCCAAATAATGTCT 660
QY 675 CAAGATATATGAGAAATTAATTAACCATCTTCAATATAGTGCCTTAATCTCCGCTG 734
DB 661 CAAGATATATGAGAAATTAATTAACCATCTTCAATATAGTGCCTTAATCTCCGCTG 720
QY 735 GAAACCTGATCTCCACATATTAATAAAGCTCTCTCCACATGATGACCTATATGTGCA 794
DB 721 GAAACCTGATCTCCACATATTAATAAAGCTCTCTCCACATGATGACCTATATGTGCA 780
QY 795 ATGGGGAATCCACAGAAATTTTATGACAGATGCTTATTTATGAGATGAGATCAATTA 854
DB 781 ATGGGGAATCCACAGAAATTTTATGACAGATGCTTATTTATGAGATGAGATCAATTA 840
QY 855 CAGCCAAACTGAGACATATGTTTCTACGTCCAAAGAGCTTAATATGAGATCCAGA 914
DB 841 CAGCCAAACTGAGACATATGTTTCTACGTCCAAAGAGCTTAATATGAGATCCAGA 900
QY 915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTCGATAC 974
DB 901 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTCGATAC 960
QY 975 TTGGAACACAGTACAGATTAAGATCAAAACAATAATGATTAATGATGAGATGACCAACT 1034
DB 961 TTGGAACACAGTACAGATTAAGATCAAAACAATAATGATTAATGATGAGATGACCAACT 1020
QY 1035 CTGGAATTAATTTGAGCCCAAGAAATGAGTATAGTAAGACGCAATTCACACTCTACAT 1094

DB 1021 CTGAGATTAATTTGAGCCAAAGAAATAGATATAGTAAGAGGCAATTCACACTCTACAT 1080
QY 1095 AACCATTTCTCACTTTGTCAGATCATGTCGAGGTCGATCATATAGTCTCTGCTTA 1154
DB 1081 AACCATTTCTCACTTTGTCAGATCATGTCGAGGTCGATCATATAGTCTCTGCTTA 1140
QY 1155 CCTAAAGAGCTCAAGATTAATTAATTCCTCCAAATTCGATCTCTGCAAGATTTTAA 1214
DB 1141 CCTAAAGAGCTCAAGATTAATTAATTCCTCCAAATTCGATCTCTGCAAGATTTTAA 1200
QY 1215 AGAAATGTTGAGACCAAGATGATGATCTGCTGCTGCAAGAGATGACATCTATGA 1274
DB 1201 AGAAATGTTGAGACCAAGATGATGATCTGCTGCTGCAAGAGATGACATCTATGA 1260
QY 1275 GAAGCAACCAAGAGAGAAACCACTCTGATGTCGATATGAAAACTGAAAGAAAGCTC 1334
DB 1261 GAAGCAACCAAGAGAGAAACCACTCTGATGTCGATATGAAAACTGAAAGAAAGCTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGACCTGTGAGAGA 1383
DB 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGACCTGTGAGAGA 1369

RESULT 8
AAT85827
ID AAT85827 standard; DNA; 4009 BP.
XX
AC AAT85827;
XX
DT 22-JUN-1998 (first entry)
XX
DE Human interleukin-13 alpha receptor DNA.
XX
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..1317
FT FT /*tag= a
FT /product= "IL-13_alpha_receptor"
XX
PN WO9720926-A1.
XX
PD 12-JUN-1997.
XX
PF 07-NOV-1996; 96WO-FR001756.
XX
PR 06-DEC-1995; 95FR-00014424.
XX
PA (SNFI) SANOFI SA.
XX
PI Caput D, Ferrara P, Laurent P, Vita N;
XX
DR WPI: 1997-319773/29.
XX
PT P-PSDB; AAM24973.
XX
PS Claim 12; Page 44-45; 83pp; French.
XX
CC This sequence encodes human interleukin-13 (IL-13) alpha receptor. The
CC invention relates to new purified peptides comprising 380 or 427 amino
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC affinity, but acquires high affinity when associated with the IL-4
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC diagnostic probes to identify aberrant synthesis or genetic anomalies
CC such as loss of heterozygosity and rearrangements, or chromosomal
CC anomalies. They are also used for production of recombinant IL-13R beta

CC and alpha which can be used as IL-13 antagonist, specifically to regulate IL-13-induced responses for treatment of inflammation and allergy. IL-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of IL-13 receptors; when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R

SQ Sequence 4009 BP; 1137 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;

Query Match	86.6%	Score 1198	DB 2	Length 4009
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1248; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	135	CGCGCTACGAAACTCAGCCACTGTGACAAATTGGATGTCTCTGTTGAAACCTCTG	194
Db	111	CGCGCTACGAAACTCAGCCACTGTGACAAATTGGATGTCTCTGTTGAAACCTCTG	170
QY	195	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGGTA	254
Db	171	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGGTA	230
QY	255	TTTTAGTCATTTGGCGCAAAACAAGATPAGAAATAGCTCCGAAACTCGTCGTTCAAT	314
Db	231	TTTTAGTCATTTGGCGCAAAACAAGATPAGAAATAGCTCCGAAACTCGTCGTTCAAT	290
QY	315	AGAAATACCCCTGGAATGAGAGATTTGTCTCGAAGTGGGGTCCGATGTAACAATAA	374
Db	291	AGAAATACCCCTGGAATGAGAGATTTGTCTCGAAGTGGGGTCCGATGTAACAATAA	350
QY	375	GAGTGAGAAAGCTTACCATTTTGGTTGAAAAATGCATCTCACCCCGAGAAGTGATCTGTA	434
Db	351	GAGTGAGAAAGCTTACCATTTTGGTTGAAAAATGCATCTCACCCCGAGAAGTGATCTGTA	410
QY	435	GTCTGCTGTGACTGAACTTCAATGCAATTTGGCAACAACCTGAGCTTACATGAAGTGTCTTG	494
Db	411	GTCTGCTGTGACTGAACTTCAATGCAATTTGGCAACAACCTGAGCTTACATGAAGTGTCTTG	470
QY	495	GCTCCCTGGAAGGAATACCAGTCCCGACACTPAACTTACTCTCTATTTGGCAACAGAG	554
Db	471	GCTCCCTGGAAGGAATACCAGTCCCGACACTPAACTTACTCTCTATTTGGCAACAGAG	530
QY	555	CCTGAAAAAATTCATCAATGTGAAAAATCTTTGAGAGAGGCCAATCTTGTTGTTGTC	614
Db	531	CCTGAAAAAATTCATCAATGTGAAAAATCTTTGAGAGAGGCCAATCTTGTTGTTGTC	590
QY	615	CTTTGATCTGACCAAGTGAAGGATTCAGITTTGAACAACAAGTGTCCAATATAGT	674
Db	591	CTTTGATCTGACCAAGTGAAGGATTCAGITTTGAACAACAAGTGTCCAATATAGT	650
QY	675	CAGAGTAATGAGAGAAAAATTAAACCATCTTCAATATAGTCTTTAATCTTCCCGTGT	734
Db	651	CAGAGTAATGAGAGAAAAATTAAACCATCTTCAATATAGTCTTTAATCTTCCCGTGT	710
QY	735	GAAACCTGATCTCCACATATTAATAAAACCTCTCCCTTCCACATGATGACCTATATGTGCA	794
Db	711	GAAACCTGATCTCCACATATTAATAAAACCTCTCTTCCACATGATGACCTATATGTGCA	770
QY	795	ATGGAGAAATCCACAGAAATTTTATTAGCAGATGCTATTTTATGAAAGTAGAAGTCAATPA	854
Db	771	ATGGAGAAATCCACAGAAATTTTATTAGCAGATGCTATTTTATGAAAGTAGAAGTCAATPA	830
QY	855	CAGCCAAACTGAGACACATATATGTTTTCTACGTCCTCAAGAGGCTAATATGAGAAATCCAGA	914
Db	831	CAGCCAAACTGAGACACATATATGTTTTCTACGTCCTCAAGAGGCTAATATGAGAAATCCAGA	890
QY	915	ATTGAGAGAAATGTGAGAAATACATCTGTTTCATGTGCTCCGTGTTCTTCCGTGATAC	974
Db	891	ATTGAGAGAAATGTGAGAAATACATCTGTTTCATGTGCTCCGTGTTCTTCCGTGATAC	950
QY	975	TTTGAACAACAGTCAGAAATPAGAGTCAAAAACAATPAGTTATGCTATGAGATGACAAACT	1034

Db	951	TTTGAAACACAGTCAGAAATTAAGATCAAAAACAAATTAAGTTATGCAATGAGATGACAACT	1012
Qy	1035	CTGAGATTAATTGGAGCCAGAAATGAGTATAGTAAAGCGCAATTCACACTCTACAT	1094
Db	1011	CTGGAGTAAATTGGAGCCAGAAATGAGTATAGTAAAGCGCAATTCACACTCTACAT	1070
Qy	1095	AACCATGTTACTCATMTGTCAGTCATGTCGGAGGTCGAATCATAGTACTCCGCTTTA	1154
Db	1071	AACCATGTTACTCATMTGTCAGTCATGTCGGAGGTCGAATCATAGTACTCCGCTTTA	1130
Qy	1155	CCTAAAAAGGCTCAAGATTTATTTATTTCCCTCCAAATTCCTGATCCTGGCAAGATTTTAA	1214
Db	1131	CCTAAAAAGGCTCAAGATTTATTTATTTCCCTCCAAATTCCTGATCCTGGCAAGATTTTAA	1190
Qy	1215	AGAAATGTTTGGAGACCGAATGATGATCTGCACTGGAAGAGTACGACATCTATGA	1274
Db	1191	AGAAATGTTTGGAGACCGAATGATGATCTGCACTGGAAGAGTACGACATCTATGA	1250
Qy	1275	GAAGGAAACCAAGAGGAAACCGACTCTGTATGTCGTATGAAACCTGAAGAAAGCTC	1334
Db	1251	GAAGGAAACCAAGAGGAAACCGACTCTGTATGTCGTATGAAACCTGAAGAAAGCTC	1310
Qy	1335	TCAGTGATGAGATTAATTTATTTTACCTTCACCTGACCTTGACCTTGAGAAGA	1383
Db	1311	TCAGTGATGAGATTAATTTATTTTACCTTCACCTGACCTTGACCTTGAGAAGA	1359
RESULT 9			
AAA88907			
ID	AAA88907	standard; cDNA; 4038 BP.	
XX	AAA88907;		
XX	05-MAR-2001	(first entry)	
DE	Human interleukin-13 receptor alpha-1 cDNA.		
XX			
Kw	Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;		
Kw	atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;		
Kw	dermatological; antiasthmatic; antiallergic; therapy; diagnosis; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	43..1326	
FT		/*tag= a	
FT	sig_peptide	43..120	
FT		/*tag= b	
FT	mat_peptide	121..1323	
FT		/*tag= c	
XX			
PN	US6143871-A.		
XX			
PD	07-NOV-2000.		
XX			
PF	12-NOV-1997;	97US-00969125.	
XX			
PR	13-DEC-1996;	96GB-00025899.	
XX			
PA	(GAUC/) GAUCHAT J.		
PA	(BONN/) BONNEFOY J.		
XX			
PI	Gauchat J, Bonnefoy J;		
XX			
DR	WPI: 2001-006445/01.		
DR	P-PSDB: AAB19807.		
XX			
PT	Novel polypeptide capable of binding interleukin-13 or interleukin-4		
PT	useful for treating atopy, atopic dermatitis, allergies, rhinitis,		
PT	eczema, asthma or AIDS.		
XX			
PS	Example 1; Fig 1A-B; 26pp; English.		
XX			

CC The present sequence is that of cDNA encoding a protein (see AAB19d07)
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
CC 4 (IL-4) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR
CC primers (see AAB8908-10) were designed from expressed sequence tags
CC isolated from a database using mouse IL-13 receptor alpha. The primers
CC were used to amplify human IL-13 receptor cDNA from activated tonsillar B
CC cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10
CC library of activated tonsillar B cell cDNA and sequencing of the largest
CC cDNA insert provided the present sequence. This IL-13 receptor alpha-1
CC can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells,
CC useful in the treatment of diseases where IgE or Th2 differentiation
CC plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma or AIDS. Antibodies raised against the polypeptide are useful for
CC detecting IL-13 and IL-4 receptor or parts of them which have been shed
CC from cells as a result of disease, e.g. cancer, leukemia, atopy, atopic
CC dermatitis, allergies, rhinitis, eczema, asthma, AIDS, lupus
CC erythematosus, thyroiditis, diabetes, uveitis, dermatitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel
CC disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome and
CC toxoplasmosis

XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 4; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGGCCCTACGGAACTCAGCCACTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 194
DB 120 CGGGCCCTACGGAACTCAGCCACTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 179
QY 195 CACAGTAATATGACATGAAATCCACCAGGAGGAGCCAGCTCAAAATTTGATGATGATGTA 254
DB 180 CACAGTAATATGACATGAAATCCACCAGGAGGAGCCAGCTCAAAATTTGATGATGATGTA 239
QY 255 TTTTACGATTTTGGCGACAAACAGATTAAGAAATAGCTCCGGAACCTGTCCTTCAT 314
DB 240 TTTTACGATTTTGGCGACAAACAGATTAAGAAATAGCTCCGGAACCTGTCCTTCAT 299
QY 315 AGAAGTACCCCTGATATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGACCAATGA 374
DB 300 AGAAGTACCCCTGATATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGACCAATGA 359
QY 375 GAGTGAAGAGCTTGAATTTGTTGTAAGAAATGATCTACCCCAAGGTATCTCTGA 434
DB 360 GAGTGAAGAGCTTGAATTTGTTGTAAGAAATGATCTACCCCAAGGTATCTCTGA 419
QY 435 GTCTGCTGTGACTGAATCTTCATATGATTTGGCAACAACCTGACTACATGAAGTCTTG 494
DB 420 GTCTGCTGTGACTGAATCTTCATATGATTTGGCAACAACCTGACTACATGAAGTCTTG 479
QY 495 GCTCCCTGGAAGATATCCAGTCCCGACACTAACTATATCTCTACTATTGGGACAGAG 554
DB 480 GCTCCCTGGAAGATATCCAGTCCCGACACTAACTATATCTCTACTATTGGGACAGAG 539
QY 555 CCTGGAAGAAATTCATTAATGTGAAGAAATCTTTAGGAAGGCCAATATCTTTGTTGTC 614
DB 540 CCTGGAAGAAATTCATTAATGTGAAGAAATCTTTAGGAAGGCCAATATCTTTGTTGTC 599
QY 615 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGTGAACAACAAGTGTCCAAATATATGT 674
DB 600 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGTGAACAACAAGTGTCCAAATATATGT 659
QY 675 CAAGGATATATGCGAAGAAATTTAAACCATCTTCATATATATGTGCTTTAACTCCGCT 734
DB 660 CAAGGATATATGCGAAGAAATTTAAACCATCTTCATATATATGTGCTTTAACTCCGCT 719
QY 735 GAAACCTGATCTCCACATATTAATAAATCTCTCTCCACATGATGATGATGATGATG 794
DB 720 GAAACCTGATCTCCACATATTAATAAATCTCTCTCCACATGATGATGATGATGATG 779
QY 795 ATGGAGATATCCACAGATTTTATATGAGATGCTTATTTATGAGTGAAGTCAATAA 854

DB 780 ATGGAGATATCCACAGATTTTATATGAGATGCTTATTTATGAGTGAAGTCAATAA 839
QY 855 CAGCAACATGAGACATATATGTTTCTGCTCCAGAGAGCTTAATGAGATTCAGA 914
DB 840 CAGCAACATGAGACATATATGTTTCTGCTCCAGAGAGCTTAATGAGATTCAGA 899
QY 915 ATTTGAGAGAAATGTGAGATATACATCTTGTTCATGATGCTCCGTGTTCTCTGATAC 974
DB 900 ATTTGAGAGAAATGTGAGATATACATCTTGTTCATGATGCTCCGTGTTCTCTGATAC 959
QY 975 TTGGAACACAGTCCAGATTAAGTCAAAACAAATTAAGTATGATGAGATGACAACT 1034
DB 960 TTGGAACACAGTCCAGATTAAGTCAAAACAAATTAAGTATGATGAGATGACAACT 1019
QY 1035 CTGAGATTAATTTGAGCCAAAGAAATGATATATGTAAGAGGCAATTCACATCTTACAT 1094
DB 1020 CTGAGATTAATTTGAGCCAAAGAAATGATATATGTAAGAGGCAATTCACATCTTACAT 1079
QY 1095 AACCATGTAATCTGATTTGTCAGTCACTGTCGACAGTGCATCATATGATCTGCTTAA 1154
DB 1080 AACCATGTAATCTGATTTGTCAGTCACTGTCGACAGTGCATCATATGATCTGCTTAA 1139
QY 1155 CTTAAAAAGCTCAGATTAATTAATTTCCCTCCAAATTCGATCTGAGCAAGATTTTAA 1214
DB 1140 CTTAAAAAGCTCAGATTAATTAATTTCCCTCCAAATTCGATCTGAGCAAGATTTTAA 1199
QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAGTACATCTATGA 1274
DB 1200 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAGTACATCTATGA 1259
QY 1275 GAAGCAACCAAGAGAGAAACCGACTGTAGTGTGATGAAAGAACTGAAGAAAGCTC 1334
DB 1260 GAAGCAACCAAGAGAGAAACCGACTGTAGTGTGATGAAAGAACTGAAGAAAGCTC 1319
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB 1320 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1368

RESULT 10

ADL71811
ID ADL71811 standard; cDNA; 4038 BP.

XX AC ADL71811;

XX DT 20-MAY-2004 (first entry)

XX DE Human interleukin-13 receptor alpha (IL-13 Ralpna) cDNA.

XX KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;

XX KW eczema; asthma; AIDS; gene therapy; gene; ss; interleukin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 43..1326

FT FT /*tag= b

FT FT /product= "Human IL-13 protein"

FT FT sig_peptide 43..120

FT FT /*tag= a 121..1323

FT FT /*tag= c

FT FT /product= "Human mature IL-13 protein"

FT FT /*tag= d 1321..1380

FT FT /note= "GC rich region"

US2004043921-A1.

04-MAR-2004.

29-SEP-2003; 2003US-00671697.

PR 13-DEC-1996; 96GB-00025899.
PR 12-NOV-1997; 97US-00969125.
PR 06-APR-2000; 2000US-00545002.
XX
PA (BONN/) BONNEFOY J.
PA (GAUC/) GAUCHAT J.
PI Bonnefoy J, Gauchat J;
XX
XX WPI; 2004-225726/21.
DR P-PSDB; ADL1812.
XX
PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
PS
PS Example 1; SEQ ID NO 8; 27pp; English.
XX
XX The invention relates to polypeptides capable of binding human
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
CC invention also relates to a method of treatment of a disease in which
CC IL13 and IL4 cause adverse effects. The method is useful for treating a
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
CC of the invention are useful in raising antibodies. It is also useful in
CC gene therapy. The present sequence is human interleukin-13 receptor alpha
CC (IL-13 Ralpha) cDNA.
SQ Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
Query Match 86.6%; Score 1198; DB 12; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CCGGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194
DB 120 CCGGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 179
QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGTATGTATGTA 254
DB 180 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGTATGTATGTA 239
QY 255 TTTTACTCATTTTGGGACAAACAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT 314
DB 240 TTTTACTCATTTTGGGACAAACAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT 299
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTAGCAACAATGA 374
DB 300 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTAGCAACAATGA 359
QY 375 GAGTGGAAGACCTAGCATTTTGGTGAATAATGATCTCACCCCGAAGGTATCTCTGA 434
DB 360 GAGTGGAAGACCTAGCATTTTGGTGAATAATGATCTCACCCCGAAGGTATCTCTGA 419
QY 435 GTCTGTGTGACTGAACTTCAATGCAATTTTGGCAACAACCTGAGTACATGAAGTCTTGG 494
DB 420 GTCTGTGTGACTGAACTTCAATGCAATTTTGGCAACAACCTGAGTACATGAAGTCTTGG 479
QY 495 GCTCCCTGGAAGAAATACCAAGTCCGACACTAATCTACTCTCTACATTTGGGACAGAG 554
DB 480 GCTCCCTGGAAGAAATACCAAGTCCGACACTAATCTACTCTCTACATTTGGGACAGAG 539
QY 555 CCTGGAATAAATTCATCAATGTGTAACAATCTTTAGAGAGGCCAATACTTGGTGTTC 614
DB 540 CCTGGAATAAATTCATCAATGTGTAACAATCTTTAGAGAGGCCAATACTTGGTGTTC 599
QY 615 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAATTAATGTGT 674
DB 600 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAATTAATGTGT 659
QY 675 CAAGGTAATGACAGGAATAATTAACCATCTTCATATATATGAGCTTTAACTCCGCTGT 734
DB 660 CAAGGTAATGACAGGAATAATTAACCATCTTCATATATATGAGCTTTAACTCCGCTGT 719

QY 735 GAAACCTGATCTCCACATATTAACAACTCTCTTCCACATGATGACCTATATGTGCA 794
DB 720 GAAACCTGATCTCCACATATTAACAACTCTCTTCCACATGATGACCTATATGTGCA 779
QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATCCATTTTATGAAGTGAACATTA 854
DB 780 ATGGAGAAATCCACAGAAATTTTATAGCAGATCCATTTTATGAAGTGAACATTA 839
QY 855 CAGCCAAACTGACACATATGTTTCTACGTCCAGAGGCTAAATGTGAGATCCAGA 914
DB 840 CAGCCAAACTGACACATATGTTTCTACGTCCAGAGGCTAAATGTGAGATCCAGA 899
QY 915 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTCTGTTCTTCTGATAC 974
DB 900 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTCTGTTCTTCTGATAC 959
QY 975 TTTGAACACAGTCAGAAATTAAGATCAAAACAATTAAGTATGAGGATGACAAACT 1034
DB 960 TTTGAACACAGTCAGAAATTAAGATCAAAACAATTAAGTATGAGGATGACAAACT 1019
QY 1035 CTGAGTAATTTGAGGCCAAGAAATGATAGTTAAGAAACGCAATTCACACTTACAT 1094
DB 1020 CTGAGTAATTTGAGGCCAAGAAATGATAGTTAAGAAACGCAATTCACACTTACAT 1079
QY 1095 AACCATGTTACTCATTTTCCAGTCACTGTCGAGGTGCAATCATAGTACTCTGCTTTA 1154
DB 1080 AACCATGTTACTCATTTTCCAGTCACTGTCGAGGTGCAATCATAGTACTCTGCTTTA 1139
QY 1155 CCTAAATAAGCTCAATATTAATATTCCTCCCAATTCCTGATCCGCGAAGTTTAA 1214
DB 1140 CCTAAATAAGCTCAATATTAATATTCCTCCCAATTCCTGATCCGCGAAGTTTAA 1199
QY 1215 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAGAAATAGACATCTATGA 1274
DB 1200 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAGAAATAGACATCTATGA 1259
QY 1275 GAAACAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAACCTGAGAAAGCTTC 1334
DB 1260 GAAACAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAACCTGAGAAAGCTTC 1319
QY 1335 TCAGTATGAGATTAATTTTATCTTACCTTCACTGTGACCTTGAGAGA 1383
DB 1320 TCAGTATGAGATTAATTTTATCTTCACTGTGACCTTGAGAGA 1368
RESULT 11
ID ADN62574 standard; cDNA; 4038 BP.
XX
AC ADN62574;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human cDNA encoding interleukin 13 (IL-13) receptor alpha 1 chain.
XX
XX Human; ss; gene; interleukin 13 receptor alpha 1 chain; IL-13; IL-4;
KW atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW cancer; inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
KW lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
KW Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
KW Lyme disease; tuberculosis; malaria; leishmaniasis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 43..1326
FT /*tag= b
FT /product= "IL-13 receptor alpha 1 chain"
FT 43..120
FT sig_peptide
FT /*tag= a

FT mat_peptide 121..1323
FT /*tag= C
FT /note= "Mature IL-13 receptor alpha 1 chain"
XX US6743604-B1.
XX PD 01-JUN-2004.
XX 06-APR-2000; 2000US-00545002.
XX PR 13-DEC-1996; 96GB-00025899.
XX PR 12-NOV-1997; 97US-00969125.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Bonnefoy J, Gauchat J;
XX WPI; 2004-409324/38.
XX P-PSDB; ADN62575.
XX
XX New isolated nucleic acid molecule encoding a polypeptide capable of
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in
PT diagnostics or for producing antibodies.
XX
XX Claim 1; SEQ ID NO 8; 24bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (ADN62574),
CC which encodes the mature form of a polypeptide capable of binding human
CC IL-13 (interleukin 13) and/or binding human IL-4 (designated IL-13
CC receptor alpha 1 subunit) appearing as ADN62575. Also included are a
CC vector comprising the nucleic acid molecule and a host cell comprising
CC the vector. The nucleic acids are useful as probes or primers or in the
CC analysis of allelic variation. The polypeptides are useful for binding
CC human IL-13 and/or binding human IL-4 and act as inhibitors by
CC interfering with the interaction between human IL-13 or IL-4 and their
CC natural receptors. They can also be used in medicine, e.g. for treatment
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC used for producing antibodies, which can be used for diagnosing diseases.
CC The present sequence encodes IL-13 receptor alpha 1 subunit.
XX
XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
SQ
Query Match 86.6%; Score 1198; DB 12; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 194
DB 120 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 179
QY 195 CACAGTAATTGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGTGTCATATGTA 254
DB 180 CACAGTAATTGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGTGTCATATGTA 239
QY 255 TTTTAGTCAATTTTGGCGACAAACAGATAGAAAAATAGTCCGGAATCTGTGTTCAAT 314
DB 240 TTTTAGTCAATTTTGGCGACAAACAGATAGAAAAATAGTCCGGAATCTGTGTTCAAT 299
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTTCCAGTGTGACCAATGA 374
DB 300 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTTCCAGTGTGACCAATGA 359
QY 375 GAGTGAAGAGCTAGACATTTTGGTTGAAAAAATGATCTACCCCCAGAAAGTATCTCTGA 434
DB 360 GAGTGAAGAGCTAGACATTTTGGTTGAAAAAATGATCTACCCCCAGAAAGTATCTCTGA 419
QY 435 GTCTGTGTGACGTGAACCTTCAATGATGTTGGCAACCTGAGTCAATGAAGTGTCTTG 494

DB 420 GTCTGTGTGACGTGAACCTTCAATGATGTTGGCAACCTGAGTCAATGAAGTGTCTTG 479
QY 495 GCTCCCTGGAAAGGAATCCAGTCCCGACATTAATATCTCTACTATTTGGCACAAG 554
DB 480 GCTCCCTGGAAAGGAATCCAGTCCCGACATTAATATCTCTACTATTTGGCACAAG 539
QY 555 CCTGGAATAAATTCATCAATGTGAAAAACATCTTTAGAGAAAGGCCAATACTTGTGTTTC 614
DB 540 CCTGGAATAAATTCATCAATGTGAAAAACATCTTTAGAGAAAGGCCAATACTTGTGTTTC 599
QY 615 CTTTGATCTGACCAAAATGGAAGATTCAGTTTGAACAAACAGTGTCCAAATATGTG 674
DB 600 CTTTGATCTGACCAAAATGGAAGATTCAGTTTGAACAAACAGTGTCCAAATATGTG 659
QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTCTCAATATATAGTGCCTTAATCTCCGTGT 734
DB 660 CAAGATTAATGCAAGAAAAATTAACCATCTCTCAATATATAGTGCCTTAATCTCCGTGT 719
QY 735 GAAACCTGATCCTCCACATATTAATAAACCTCTCCTCCACAATGATGACCTATATGTGCA 794
DB 720 GAAACCTGATCCTCCACATATTAATAAACCTCTCCTCCACAATGATGACCTATATGTGCA 779
QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAATGAAATCAATAA 854
DB 780 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAATGAAATCAATAA 839
QY 855 CAGCCAAATCGAGACATATATGTTTCTACAGTCCAAAGAGCTTAATGTGAAATCCAGA 914
DB 840 CAGCCAAATCGAGACATATATGTTTCTACAGTCCAAAGAGCTTAATGTGAAATCCAGA 899
QY 915 ATTTGAGAAATGTGAGAAATCATCTGTTCATGCTCCGAGTCTCTCTCTGATAC 974
DB 900 ATTTGAGAAATGTGAGAAATCATCTGTTCATGCTCCGAGTCTCTCTCTGATAC 959
QY 975 TTTGAACACAGTCAAGATTAATAGTCAAAACAAATTAATGATGATGAGATGCAAACT 1034
DB 960 TTTGAACACAGTCAAGATTAATAGTCAAAACAAATTAATGATGATGAGATGCAAACT 1019
QY 1035 CTGAGTAATTGAGACCAAGAAATGATATAGTATAGTAAGCCGCAATTCACACTCTACAT 1094
DB 1020 CTGAGTAATTGAGACCAAGAAATGATATAGTATAGTAAGCCGCAATTCACACTCTACAT 1079
QY 1095 AACCATGTTACATATGTTCCAGTCACTGTCGAGGAGGCAATATATCTCTGCTTAA 1154
DB 1080 AACCATGTTACATATGTTCCAGTCACTGTCGAGGAGGCAATATATCTCTGCTTAA 1139
QY 1155 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1214
DB 1140 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1199
QY 1215 AGAAATGTTTGGAGCCAGAAATGATATCTCTGCACTGGAAGAAATGACATCTATGA 1274
DB 1200 AGAAATGTTTGGAGCCAGAAATGATATCTCTGCACTGGAAGAAATGACATCTATGA 1259
QY 1275 GAAGCAAAACCAAGAGAAACCACTCTGTAGTGTGATGAAAACTGAAAGAAAGGCTC 1334
DB 1260 GAAGCAAAACCAAGAGAAACCACTCTGTAGTGTGATGAAAACTGAAAGAAAGGCTC 1319
QY 1335 TCAGTATGAGATTAATTTATTTTAACTTCACTGATGACCTTGAGAAAG 1383
DB 1320 TCAGTATGAGATTAATTTATTTTAACTTCACTGATGACCTTGAGAAAG 1368
RESULT 12
AAA35214
ID AAA35214 standard; DNA; 4039 BP.
XX
XX AAA35214;
AC
XX 28-JUL-2000 (first entry)
DT
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:88.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNITV EAST CAROLINA.
XX
PI Myce JW;
XX
DR MPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 1253-1254; 1343p; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGGCTTAGGAAACACGACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTC 194
DB 121 CGGGCTTAGGAAACACGACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTC 180
QY 195 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATTTGATGATGTA 254
DB 181 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATTTGATGATGTA 240

QY 255 TTTTATGTCATTTTGGCGACAAAACAAGATTAAGAAAATAGCTCCGGAACCTGCTTCAAT 314
DB 241 TTTTATGTCATTTTGGCGACAAAACAAGATTAAGAAAATAGCTCCGGAACCTGCTTCAAT 300
QY 315 AGAAGTACCCCGAATGAGAGATTTGTCTGAAGTGGGGTCCAGTGTAGACCAATGA 374
DB 301 AGAAGTACCCCGAATGAGAGATTTGTCTGAAGTGGGGTCCAGTGTAGACCAATGA 360
QY 375 GAGTGAGAACCTTAGCATTTTGGTGA AAAATATGATCTTCAACCCCGAAGAGTGATCTGA 434
DB 361 GAGTGAGAACCTTAGCATTTTGGTGA AAAATATGATCTTCAACCCCGAAGAGTGATCTGA 420
QY 435 GTCTGCTGTGACTGAATCTTAATGCAATTTGGCAACAACCTGAGCTACATGAATGTTCTTG 494
DB 421 GTCTGCTGTGACTGAATCTTAATGCAATTTGGCAACAACCTGAGCTACATGAATGTTCTTG 480
QY 495 GCTCCCTGGAAGAAATATCCAGTCCGAGCACTAATATCTCTACTATTTGGACAGAG 554
DB 481 GCTCCCTGGAAGAAATATCCAGTCCGAGCACTAATATCTCTACTATTTGGACAGAG 540
QY 555 CCTGGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAAAGCCAAATCTTTGGTGTTC 614
DB 541 CCTGGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAAAGCCAAATCTTTGGTGTTC 600
QY 615 CTTTGATCTGACCAAAAGTGAAGATTTCCAGTTTGAACAACACAGTGTCCAATATATGAT 674
DB 601 CTTTGATCTGACCAAAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAATATATGAT 660
QY 675 CAAGATATATGAGAGAAAAATTAACCATCTTCAATATATAGTCCCTTAATCTCCGCTGT 734
DB 661 CAAGATATATGAGAGAAAAATTAACCATCTTCAATATATAGTCCCTTAATCTCCGCTGT 720
QY 735 GAAACCTGATCTCCACATATTTAAAAACCTCTCTTCCAAATGATGACCTATATATGCA 794
DB 721 GAAACCTGATCTCCACATATTTAAAAACCTCTCTTCCAAATGATGACCTATATATGCA 780
QY 795 ATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTTATTTATGAAATGAAATCAATA 854
DB 781 ATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTTATTTATGAAATGAAATCAATA 840
QY 855 CAGCCAAATGAGACACATATATGTTTCTACGCTCAAGAGGCTAAATGTGAGAAATCCAGA 914
DB 841 CAGCCAAATGAGACACATATATGTTTCTACGCTCAAGAGGCTAAATGTGAGAAATCCAGA 900
QY 915 ATTTGAGAAATATGAGAAATATACATCTTTGATGATGTCCTGTGTTCTTCTGTATAC 974
DB 901 ATTTGAGAAATATGAGAAATATACATCTTTGATGATGTCCTGTGTTCTTCTGTATAC 960
QY 975 TTTGAAACACAGTCAGATATAGAGTCAAAAACAATAATGTTATGCTATGAGAGTACAAACT 1034
DB 961 TTTGAAACACAGTCAGATATAGAGTCAAAAACAATAATGTTATGCTATGAGAGTACAAACT 1020
QY 1035 CTGGAGTAATTTGGAGCCAAAGATGATATAGTATGAAGCCCAATTCACACTCTACAT 1094
DB 1021 CTGGAGTAATTTGGAGCCAAAGATGATATAGTATGAAGCCCAATTCACACTCTACAT 1080
QY 1095 AACCATGTTACTCATTTGTTCCAGTCATCTGTCCAGGTGCAATCATATGATCTCTGCTTTA 1154
DB 1081 AACCATGTTACTCATTTGTTCCAGTCATCTGTCCAGGTGCAATCATATGATCTCTGCTTTA 1140
QY 1155 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGATCTGGCAAGATTTTATA 1214
DB 1141 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGATCTGGCAAGATTTTATA 1200
QY 1215 AGAATATGTTTGGAGACCAAGATGATATCTGTGCACTGGAAGAGTACGACATCTATGA 1274
DB 1201 AGAATATGTTTGGAGACCAAGATGATATCTGTGCACTGGAAGAGTACGACATCTATGA 1260
QY 1275 GAAGCAAAACCAAGAGAAACCGACTGTGTAGTCTGATAGAAAACCTGAAGAAACCTTC 1334
DB 1261 GAAGCAAAACCAAGAGAAACCGACTGTGTAGTCTGATAGAAAACCTGAAGAAACCTTC 1320
QY 1335 TCAGTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383

Db 1321 TCAGTGTGAGATTAATTTTACCTGACGTGAGAGAGA 1369

RESULT 13

AAF21336 ID AAF21336 standard; DNA; 4039 BP.

XX AAF21336;

DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2903.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytotactic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

XX Homo sapiens.

PN W0200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

PA (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

PI NYCE JW;

DR WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

PS Disclosure; Page 1337-1338; 1592PD; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytoskeletal activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with:
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF21336 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

XX Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGCGCTACGGAACCTGAGCCAGCTGACAAATTTGAGTCTCTGTTGAAAACCTGTG 194
Db 121 CGGCGCTACGGAACCTGAGCCAGCTGAGCAAAATTTGAGTCTCTGTTGAAAACCTGTG 180
QY 195 CACGTAATATGACATGGAATCCACCGAGGGAGCCAGCTCAAAATTTAGTCTATGGA 254
Db 181 CACGTAATATGACATGGAATCCACCGAGGGAGCCAGCTCAAAATTTAGTCTATGGA 240
QY 255 TTTTAGCATTTTGGCGCAACAAGATTAAGAAATAGCTCGGAACTCGTCTCAAT 314
Db 241 TTTTAGCATTTTGGCGCAACAAGATTAAGAAATAGCTCGGAACTCGTCTCAAT 300
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCACCAGTA 374
Db 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCACCAGTA 360
QY 375 GAGTGAAGAGCTTACATTTGTTGTTGAAAATGCAATCTACCCCAAGAGTATCTCTGA 434
Db 361 GAGTGAAGAGCTTACATTTGTTGTTGAAAATGCAATCTACCCCAAGAGTATCTCTGA 420
QY 435 GTCTGCTGTGCTGAATGCAATGCAATTTGGCAACAACCTGAGTACATGAAGTGTCTTG 494
Db 421 GTCTGCTGTGCTGAATGCAATGCAATTTGGCAACAACCTGAGTACATGAAGTGTCTTG 480
QY 495 GCTTCCCTGGAAGAAATACAGTCCCGACACTTAATCTCTCTACTATTTGGCAGAGAG 554
Db 481 GCTTCCCTGGAAGAAATACAGTCCCGACACTTAATCTCTCTACTATTTGGCAGAGAG 540
QY 555 CTTGGAAGAAATTTGATCAATGTTGAAAATCTTTAGAGAGGCCAATATCTTTGGTGTTC 614
Db 541 CTTGGAAGAAATTTGATCAATGTTGAAAATCTTTAGAGAGGCCAATATCTTTGGTGTTC 600
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGCT 674
Db 601 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGCT 660
QY 675 CAAGGATTAATGAGAGAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCCGGT 734
Db 661 CAAGGATTAATGAGAGAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCCGGT 720
QY 735 GAAACCTGATCTTCCACATATTTAAACCTTCTCCACAAATGATGACCTATATGTCGA 794
Db 721 GAAACCTGATCTTCCACATATTTAAACCTTCTCCACAAATGATGACCTATATGTCGA 780
QY 795 ATGGGAATTCACAGAAATTTTATTTAGCAATGCTTATTTTAAAGTGAAGCAATTA 854
Db 781 ATGGGAATTCACAGAAATTTTATTTAGCAATGCTTATTTTAAAGTGAAGCAATTA 840
QY 855 CAGGCAAACTGAGACATATATGTTTCTAGTCCAGAGGCTAAATGTGGAATCCAGA 914
Db 841 CAGGCAAACTGAGACATATATGTTTCTAGTCCAGAGGCTAAATGTGGAATCCAGA 900
QY 915 ATTTGAGAAATGTGGAATATACATTTGTTTCATGTCCTGCTGTTCTCTGATAC 974
Db 901 ATTTGAGAAATGTGGAATATACATTTGTTTCATGTCCTGCTGTTCTCTGATAC 960
QY 975 TTTGAACACGTCAGATTAAGAGTCAAAACAAATTAAGTTATGATAGAGATGCAAACT 1034
Db 961 TTTGAACACGTCAGATTAAGAGTCAAAACAAATTAAGTTATGATAGAGATGCAAACT 1020
QY 1035 CTGAGATTAATTTGAGCCAAAGAAATGAGTATAGTTAGAGAGCAATTCACACTCTATCAT 1094

Db 1021 CTGGAGTAATTGAGCCAGAGAAATGATATAGTAAAGAGCGCAATTCACACTTACAT 1080
Qy 1095 AACCATGTTACTCATTTGTCACGTACGTCGAGGTGCATCATAGTACTCTGCTTTA 1154
Db 1081 AACCATGTTACTCATTTGTCACGTACGTCGAGGTGCATCATAGTACTCTGCTTTA 1140
Qy 1155 CCTAAAGAGGCTCAAGATTATATATTTCCCTCCAAATTCCTGATCTGGCAAGATTTTAA 1214
Db 1141 CCTAAAGAGGCTCAAGATTATATATTTCCCTCCAAATTCCTGATCTGGCAAGATTTTAA 1200
Qy 1215 AGAAATGTTTGGAGACAGATATGATCTGCACTGGAGAAAGTACATCTATGA 1274
Db 1201 AGAAATGTTTGGAGACAGATATGATCTGCACTGGAGAAAGTACATCTATGA 1260
Qy 1275 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATGAAGAACTGAAGAAAGCTC 1334
Db 1261 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATGAAGAACTGAAGAAAGCTC 1320
Qy 1335 TCAGTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAA 1383
Db 1321 TCAGTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAA 1369

RESULT 14

ABL67709
ID ABL67709 standard; DNA; 4039 BP.

XX ABL67709;

DT 15-MAY-2002 (first entry)

XX Oesophagus cancer related gene sequence SEQ ID NO:6046.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.

XX Homo sapiens.

PN MO200194629-A2.

XX 13-DEC-2001.

PF 30-MAY-2001; 2001WO-US010838.

XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.

PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.

PA (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S,

PI Sopet DR, Weaver Z;

XX MPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 6046; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour

XX Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

XX Query Match 86.6%; Score 1198; DB 6; Length 4039;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGCGCTACGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 194
Db 121 CGGCGCTACGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 180
Qy 195 CACAGTAATATGACATGGAATCCACCGAGGAGCAGCTCAAAATTTAGTCTATGTA 254
Db 181 CACAGTAATATGACATGGAATCCACCGAGGAGCAGCTCAAAATTTAGTCTATGTA 240
Qy 255 TTTTGTGATTTTGGGCAACAAGATTAAGAAATAGCTCCGGAACCTGTCGTTCAAT 314
Db 241 TTTTGTGATTTTGGGCAACAAGATTAAGAAATAGCTCCGGAACCTGTCGTTCAAT 300
Qy 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374
Db 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 360
Qy 375 GAGTGAAGGCTTAGATTTTGGTTGAAAGCATCTCAACCCCAAGAGGTGATCTCTGA 434
Db 361 GAGTGAAGGCTTAGATTTTGGTTGAAAGCATCTCAACCCCAAGAGGTGATCTCTGA 420

Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 194
DB 121 CGGGCTTAGGGAACCTCAGCCACTGTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 180
QY 195 CACAGTAATATGGAACATGGAATCCACCAGGAGGCCAGCTCAATTTGTGTATGTA 254
DB 181 CACAGTAATATGGAACATGGAATCCACCAGGAGGCCAGCTCAATTTGTGTATGTA 240
QY 255 TTTTACTCATTTTGGGAGCAACAAGATAGAAAATATGCTCCGGAAACTGTGTTCAAT 314
DB 241 TTTTACTCATTTTGGGAGCAACAAGATAGAAAATATGCTCCGGAAACTGTGTTCAAT 300
QY 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTGACCAATGA 374
DB 301 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTGACCAATGA 360
QY 375 GAGTGGAAGCCCTAGACATTTTGGTGAATAATGCATCTCACCCCCAGAGGTGATCCTGA 434
DB 361 GAGTGGAAGCCCTAGACATTTTGGTGAATAATGCATCTCACCCCCAGAGGTGATCCTGA 420
QY 435 GTCTGCTGAGCTGGAACCTTCAATGCAATTTGGCAACACCTGAGCTACATGAAAGTTCCTG 494
DB 421 GTCTGCTGAGCTGGAACCTTCAATGCAATTTGGCAACACCTGAGCTACATGAAAGTTCCTG 480
QY 495 GCTCCCTGGAAGGAATACCAAGTCCCGACACTAACTACTCTACTATTGGCACAAG 554
DB 481 GCTCCCTGGAAGGAATACCAAGTCCCGACACTAACTACTCTACTATTGGCACAAG 540
QY 555 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCAACTCTTGGTGTTC 614
DB 541 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCAACTCTTGGTGTTC 600
QY 615 CTTTGTATGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAATGTGT 674
DB 601 CTTTGTATGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAATGTGT 660
QY 675 CAAGATAATGACGAAAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCGCTG 734
DB 661 CAAGATAATGACGAAAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCGCTG 720
QY 735 GAAACCTGATCTCCATATTTAAAACTCTCTCTTCCACAATGATGACCTATATGTGCA 794
DB 721 GAAACCTGATCTCCATATTTAAAACTCTCTCTTCCACAATGATGACCTATATGTGCA 780
QY 795 ATGGAGGAATCCACAGAAATTTTATGAGAGATGCCATATTTATGAGTGAAGTCAATA 854
DB 781 ATGGAGGAATCCACAGAAATTTTATGAGAGATGCCATATTTATGAGTGAAGTCAATA 840
QY 855 CAGCCAAACTGAGACATATATGTTTCTACGTCACAGAGCTAAATGTGAGATCCAGA 914
DB 841 CAGCCAAACTGAGACATATATGTTTCTACGTCACAGAGCTAAATGTGAGATCCAGA 900
QY 915 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTGCTCTGTGTCTTCTCGATAC 974
DB 901 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTGCTCTGTGTCTTCTCGATAC 960
QY 975 TTTGACACAGTGAATAAGATCAAAAACAATAAGTTATGCTATGAGAGATGACAAACT 1034
DB 961 TTTGACACAGTGAATAAGATCAAAAACAATAAGTTATGCTATGAGAGATGACAAACT 1020
QY 1035 CTGAGATAATTTGAGCCAAAGAAATGAGTATAGTAAGAAAGCCAAATTCACACTTACAT 1094
DB 1021 CTGAGATAATTTGAGCCAAAGAAATGAGTATAGTAAGAAAGCCAAATTCACACTTACAT 1080
QY 1095 AACCATGTTATCTCATTTGTTCCAGTCACTGTCAGAGTGCATATAGTACTCTGCTTTA 1154
DB 1081 AACCATGTTATCTCATTTGTTCCAGTCACTGTCAGAGTGCATATAGTACTCTGCTTTA 1140
QY 1155 CCTAAAAAGGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCTGGCAAGATTTTAA 1214
DB 1141 CCTAAAAAGGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCTGGCAAGATTTTAA 1200

QY 1215 AGAATGTTTGGAGACCAAGATGATATCTGTGCACTGGAAGAAAGTACGACATCTATGA 1274
DB 1201 AGAATGTTTGGAGACCAAGATGATATCTGTGCACTGGAAGAAAGTACGACATCTATGA 1260
QY 1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATRGAAGAAACCTGAAGAAAGCTTC 1334
DB 1261 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATRGAAGAAACCTGAAGAAAGCTTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAAGA 1383
DB 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAAGA 1369

Search completed: July 7, 2006, 22:39:03
Job time : 955 secs

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:35:39 ; Search time 7826 Seconds
(without alignments)
11300.701 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383
Sequence: 1 gactctacacgacgacgaagg.....tcactgtcacttgagaaga 1383

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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9: gb_un: *
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11: gb_ov: *
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13: gb_in: *
14: gb_om: *
15: gb_ba: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1383	100.0	1383	2	AR691934 Sequence
2	1198	86.6	1708	5	HSU81379
3	1198	86.6	2139	5	BC009960 Homo sapi
4	1198	86.6	2153	5	BC015768 Homo sapi
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6	1198	86.6	4009	2	A63257
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9	1198	86.6	4039	2	AX335537
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13	1154	83.4	1284	8	AY893945
14	1147	82.9	3960	5	AB209849 Homo sapi
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23	901	65.1	2355	2	AX503603	AX503603 Sequence
24	901	65.1	2382	2	BD231183	BD231183 Antagonis
25	901	65.1	2382	2	CQ796435	CQ796435 Sequence
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30	839	60.7	2331	2	CS162833	CS162833 Sequence
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37	477	34.5	533	2	CQ461253	CQ461253 Sequence
38	420	30.4	569	2	CQ702691	CQ702691 Sequence
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ORGANISM	Unknown.					
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AUTHORS	Willson, T., Nicola, N.A., Hilton, D.J., Metcalf, D. and Zhang, J.G.					
TITLE	Haemopoietin receptor and genetic sequences encoding same					
JOURNAL	Patent: US 6911530-A 3 28-JUN-2005;					
AUX;	Amrad Operations, Pty., Ltd., Richmond;					
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 VERSION U81379.3 GI:5870850
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 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 1708)
 AUTHORS Wada, M., Hisano, T. and Kuwano, M.
 TITLES Direct Submission
 JOURNAL Medicine, Madoashi, Fukuoka 812-82, Japan
 REFERENCE 2 (bases 1 to 1708)
 AUTHORS Wada, M., Hisano, T. and Kuwano, M.
 TITLES Direct Submission
 JOURNAL Submitted (24-JUN-1999) Biochemistry, Kyushu University School of Medicine, Madoashi, Fukuoka 812-82, Japan
 REFERENCE 3 (bases 1 to 1708)
 AUTHORS Wada, M., Hisano, T. and Kuwano, M.
 TITLES Sequence update by submitter
 JOURNAL Submitted (13-SEP-1999) Biochemistry, Kyushu University School of Medicine, Madoashi, Fukuoka 812-82, Japan
 REMARK COMMENT Sequence update by submitter
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VERSION
BC015768.1 GI:16041774
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ORGANISM
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Hominidae; Homo.
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AUTHORS
Srausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,
Mortley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahy J., Helton E., Ketterman M., Madan A., Rodrigues S.,
Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y.,
Bouffard G.G., Blakesley R.W., Touchman D.W., Green E.D.,

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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smilus, D.E., Schnerch, A., Schein, J.F., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2153)
Strausberg, R.
Direct Submission
Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabh, Parvaneh Saeedi, JR Santos, Angeliqne Schnerch, Ursula Skalska, Duane Smilus, Jeff Stolt, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: k Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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Db	185	CACAGTAATATGACATGAGATCCACCAGGAGGCCAGCTCAATTTGATGATGATGTA	244
Qy	255	TTTATGATCTTTTGGGACAAACAGATTAAGAAATAGCTCCGGAAATCGTCTTCAAT	314
Db	245	TTTATGATCTTTTGGGACAAACAGATTAAGAAATAGCTCCGGAAATCGTCTTCAAT	304
Qy	315	AGAAGTACCCCTGATAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	374
Db	305	AGAAGTACCCCTGATAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	364
Qy	375	GAGTGAGAACCTAGCATTTTGGTGAATAATGATCTCACCCCAAGGTGATCTCTGA	434
Db	365	GAGTGAGAACCTAGCATTTTGGTGAATAATGATCTCACCCCAAGGTGATCTCTGA	424
Qy	435	GTCGTCTGTGACTGAATCTTCAATGATTTGGACAACCTGAGCTACATGAAGTCTTGG	494
Db	425	GTCGTCTGTGACTGAATCTTCAATGATTTGGACAACCTGAGCTACATGAAGTCTTGG	484
Qy	495	GCTCCCTGGAAGGAATACAGTCCCGACATACTAATCTCTCACTATTTGGACACAGA	554
Db	485	GCTCCCTGGAAGGAATACAGTCCCGACATACTAATCTCTCACTATTTGGACACAGA	544
Qy	555	CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTTC	614
Db	545	CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTTC	604
Qy	615	CTTTGATCTGACCAAGAGGATTCACGTTTGAACAAACAGTGTCCAAATATGAT	674
Db	605	CTTTGATCTGACCAAGAGGATTCACGTTTGAACAAACAGTGTCCAAATATGAT	664
Qy	675	CAAGGATTAATGACGAGAAATTTAAACATCTTCAATATAGTGTCTTAATCTCCGCTG	734
Db	665	CAAGGATTAATGACGAGAAATTTAAACATCTTCAATATAGTGTCTTAATCTCCGCTG	724
Qy	735	GAACCTGATCTCTCAATATTAATAAACTCTCTCTTCCCAATGATGACCTATATGCA	794
Db	725	GAACCTGATCTCTCAATATTAATAAACTCTCTCTTCCCAATGATGACCTATATGCA	784
Qy	795	ATGGAGAAATCCACAGAAATTTTATGACAGATCCTATTTATGAAGTAGAAGTCAATA	854
Db	785	ATGGAGAAATCCACAGAAATTTTATGACAGATCCTATTTATGAAGTAGAAGTCAATA	844
Qy	855	CAGCCAACTGACACATATATGTTTCTAGCTCAAGAGGCTTAATGTGAATCCAGA	914
Db	845	CAGCCAACTGACACATATATGTTTCTAGCTCAAGAGGCTTAATGTGAATCCAGA	904
Qy	915	ATTGAGAGAAATGTGAGAAATCATCTGTTTCATGATGCTCCGTGTTCTCTGATAC	974
Db	905	ATTGAGAGAAATGTGAGAAATCATCTGTTTCATGATGCTCCGTGTTCTCTGATAC	964
Qy	975	TTTGAACACAGTCAGATTAAGTCAAAACAAATTAATGATGATGAGATGACAACT	1034
Db	965	TTTGAACACAGTCAGATTAAGTCAAAACAAATTAATGATGATGAGATGACAACT	1024
Qy	1035	CTGAGTAAATTTGAGCCCAAGAAATGATATAGTAAAGAGCGCAATTTCCACTTACAT	1094
Db	1025	CTGAGTAAATTTGAGCCCAAGAAATGATATAGTAAAGAGCGCAATTTCCACTTACAT	1084
Qy	1095	AACCATGTTACTGATTTCCAGTCACTGTCGAGGTGCAATCATATGATCTCTGCTTAA	1154
Db	1085	AACCATGTTACTGATTTCCAGTCACTGTCGAGGTGCAATCATATGATCTCTGCTTAA	1144
Qy	1155	CCTAAAGAGCTCAGATTAATTAATTCCTTCAATTCCTGATCTGGCAAGATTTTAA	1214
Db	1145	CCTAAAGAGCTCAGATTAATTAATTCCTTCAATTCCTGATCTGGCAAGATTTTAA	1204

QY 1215 AGAATGTTTGAGACAGATGATGATCTGCACTGGAGAAGTACGACATCTATGA 1274
Db 1205 AGAATGTTTGAGACAGATGATGATCTGCACTGGAGAAGTACGACATCTATGA 1264
QY 1275 GAAGCAACCAAGAGAGAAACGACCTCTGTAGTGTGATGAAAACCTGAGAAAGCTTC 1334
Db 1265 GAAGCAACCAAGAGAGAAACGACCTCTGTAGTGTGATGAAAACCTGAGAAAGCTTC 1324
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGAGACCTGAGAGA 1383
Db 1325 TCAGTATGAGATTAATTTATTTTACCTTCACTGAGACCTGAGAGA 1373

RESULT 5
HSL13RA1 3999 bp mRNA linear PRI 26-FEB-1997
LOCUS HSL13RA1 3999 bp mRNA linear PRI 26-FEB-1997
DEFINITION H. sapiens mRNA for IL13 receptor alpha-1 chain.
ACCESSION Y09328
VERSION Y09328.1 GI:1885307
KEYWORDS alpha 1 chain; IL13RA1 gene; interleukin-13 receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Miloux,B., Laurent,F., Bonnin,O., Lupker,J., Caput,D., Vitea,N. and
Ferrara,P.
TITLE Cloning of the human IL-13R alpha1 chain and reconstruction with
the IL4R alpha of a functional IL-4/IL-13 receptor complex
JOURNAL FEBS Lett. 401 (2-3), 163-166 (1997)
PUBMED 9013879
REFERENCE 2 (bases 1 to 3999)
AUTHORS Caput,D.
TITLE Direct Submission
SUBMITTED (08-NOV-1996) D. Caput, SANOFI Recherche, BP 137, F-
JOURNAL 31676 Labège Cedex, FRANCE
TITLE Location/Qualifiers
FEATURES
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Query Match 86.6%; Score 1198; DB 5; Length 3999;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGGAAGTCTAGCCACTGTGACAAATTTGAGTGTCTGTGAAAACTCTG 194
Db 111 CGGCGCTACGGAAGTCTAGCCACTGTGACAAATTTGAGTGTCTGTGAAAACTCTG 170

QY 195 CACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAAAATTTGATCTATGTA 254
Db 171 CACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAAAATTTGATCTATGTA 230
QY 255 TTTTACTCAATTTTGGGACAAACAGATTAAGAAAATAGCTCCGGAAACTGCTGTCAT 314
Db 231 TTTTACTCAATTTTGGGACAAACAGATTAAGAAAATAGCTCCGGAAACTGCTGTCAT 290
QY 315 AGAATGATCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGATGAGCAATGA 374
Db 291 AGAATGATCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGATGAGCAATGA 350
QY 375 GAGTGAAGACCTAGCATTTTGGTTGAAAAATGCAATCTACCCCGAAGTGAATCTGA 434
Db 351 GAGTGAAGACCTAGCATTTTGGTTGAAAAATGCAATCTACCCCGAAGTGAATCTGA 410
QY 435 GTCTGCTGTGACCTGAATCTCAATGCACTTTGGGACAACTGAGCTATAGTAAGTCTTG 494
Db 411 GTCTGCTGTGACCTGAATCTCAATGCACTTTGGGACAACTGAGCTATAGTAAGTCTTG 470
QY 495 GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTACTCTACTATTGGACAGAA 554
Db 471 GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTACTCTACTATTGGACAGAA 530
QY 555 CTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTGTGTTTC 614
Db 531 CTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTGTGTTTC 590
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAATNGT 674
Db 591 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAATNGT 650
QY 675 CAAGATAATGACAGAAAAATTAACCATCTCTCAATATATAGTCCCTTAATCCCGTG 734
Db 651 CAAGATAATGACAGAAAAATTAACCATCTCTCAATATATAGTCCCTTAATCCCGTG 710
QY 735 GAAACTGATCTCTCAATATTAATAAACCCTCTCTTCCCAATGATGACCTATATGCA 794
Db 711 GAAACTGATCTCTCAATATTAATAAACCCTCTCTTCCCAATGATGACCTATATGCA 770
QY 795 ATGGAGAAATCCACAAATTTTATAGAGATGCGCATTTTATGAGTGAAGTCAATTA 854
Db 771 ATGGAGAAATCCACAAATTTTATAGAGATGCGCATTTTATGAGTGAAGTCAATTA 830
QY 855 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGGCTTAATGTGAGAAATCAGA 914
Db 831 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGGCTTAATGTGAGAAATCAGA 890
QY 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGTGTCCTGTGTTCTCTGATAC 974
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Db 951 TTTGAACACAGTCAGATTAAGTCAAAACAAATAGTATAGTATGAGAGTACAAACT 1010
QY 1035 CTGGAATTAATTTGGAGCCAAAGATAGTATAGTAAAGACGCAATTTCCACTTACAT 1094
Db 1011 CTGGAATTAATTTGGAGCCAAAGATAGTATAGTAAAGACGCAATTTCCACTTACAT 1070
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Db 1071 AACCATGTTACTCATTTGTCAGTACATCGTCGCAAGTGCATATATGTAATCTCTGCTTA 1130
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QY 1215 AGAATGTTTGAGACAGATGATGATCTGTGCACTGGAAGAAATGACGACATCTATGA 1274
Db 1191 AGAATGTTTGAGACAGATGATGATCTGTGCACTGGAAGAAATGACGACATCTATGA 1250
QY 1275 GAAGCAACCAAGAGAGAAACGACCTCTGTAGTGTGATGAAAACCTGAGAAAGCTTC 1334

Db 1251 GAACCAACCAAGAGGAAACCGACTGTGTGTGTAGAAAACTGGAAGAAAGCTC 1310
Qy 1335 TCAGTGTGAGATTAATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db 1311 TCAGTGTGAGATTAATTTTACCTTCACTGTGACCTTGAGAGAGA 1359

RESULT 6

A63257 4009 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 3 from Patent WO9720926.
ACCESSION A63257
VERSION A63257.1 GI:3717098
KEYWORDS
SOURCE

unidentified
unclassified
unclassified sequences.

REFERENCE

1 Caput, D., Ferrara, P., Laurent, P., Vita and Natalio.
AUTHORS IL-13 RECEPTOR POLYPEPTIDE
TITLE Patent: WO 9720926-A 3 12-JUN-1997;
JOURNAL SANOPI SA (FR)

COMMENT

Other publication AU 7576096 19970627
Other publication FR 2742156 19970613.

FEATURES

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ORIGIN

Query Match 86.6%; Score 1198; DB 2; Length 4009;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGCGCCACGAGAACTCAGACCACTGTGACAAATTTGAGTGTCTGTGTGAAACCTGTG 194
Db 111 CGGCGCCACGAGAACTCAGACCACTGTGACAAATTTGAGTGTCTGTGTGAAACCTGTG 170
Qy 195 CACAGTAATATGACATGATCCACCGAGGAGCAGCTCAATTTGATGTATGTATG 254
Db 171 CACAGTAATATGACATGATCCACCGAGGAGCAGCTCAATTTGATGTATGTATG 230
Qy 255 TTTTATGATCTTTTGGCGACAAAGATTAAGAAATATGCTCGGAAATCTGCTGTCAAT 314
Db 231 TTTTATGATCTTTTGGCGACAAAGATTAAGAAATATGCTCGGAAATCTGCTGTCAAT 290
Qy 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGTCGCAAGTGTAGACCAATGA 374
Db 291 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGTCGCAAGTGTAGACCAATGA 350
Qy 375 GAGTGAGAGCCTTATGATTTTGTGAAATATGATCTCAACCCGAGAGGTATCTCTGA 434
Db 351 GAGTGAGAGCCTTATGATTTTGTGAAATATGATCTCAACCCGAGAGGTATCTCTGA 410
Qy 435 GTCTGCTGTGATGATCTTCAATGCTTTGGCGACCACTGAGCTTACATGAAGTGTCTTG 494
Db 411 GTCTGCTGTGATGATCTTCAATGCTTTGGCGACCACTGAGCTTACATGAAGTGTCTTG 470
Qy 495 GCTGCCCTGGAAGGAATCCAGTCCCGACACTAATATATCTCTACATTTGGGCAAGAG 554
Db 471 GCTGCCCTGGAAGGAATCCAGTCCCGACACTAATATATCTCTACATTTGGGCAAGAG 530
Qy 555 CTTGAGAAAAATTCATCATGTGAAAAATCTTTAGAGAGGCCAATATCTTTGTTGTC 614
Db 531 CTTGAGAAAAATTCATCATGTGAAAAATCTTTAGAGAGGCCAATATCTTTGTTGTC 590
Qy 615 CTTGATCTGACCAAAATGAAAGATTTCCAGTTTGAACAACAGGTGCCAAATATAGGT 674
Db 591 CTTGATCTGACCAAAATGAAAGATTTCCAGTTTGAACAACAGGTGCCAAATATAGGT 650

Qy 675 CAAGATATATGACAGAAAAATTTAAACATCTCTCAATATATAGTCCCTTAATCCCTGT 734
Db 651 CAAGATATATGACAGAAAAATTTAAACATCTCTCAATATATAGTCCCTTAATCCCTGT 710
Qy 735 GAAACCTGATCTTCAATATTTAAACCTCTCTCTTCCATATGATGACCTATATGTGCA 794
Db 711 GAAACCTGATCTTCAATATTTAAACCTCTCTCTTCCATATGATGACCTATATGTGCA 770
Qy 795 ATGGGAGAAATCCAGAAATTTTATAGAGATGCTATTTATAGAGAGAGCAATAA 854
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Qy 1035 CTGAGATTAATTTGAGCAAGAAATAGTATGATGAGAGGCAATTCACACTCTACAT 1094
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Db 1131 CCTTAAAAAGCTCAAGATTTATATTTCCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1190
Qy 1215 AGAATGTTTGGAGACAGATGATGATCTCTGACATGGAAGATGACATCTATGA 1274
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Qy 1275 GAAGCAACCAAGAGAGAAACCGACTGTGATGCTGTATGAAAACTGGAAGAAAGCTC 1334
Db 1251 GAAGCAACCAAGAGAGAAACCGACTGTGATGCTGTATGAAAACTGGAAGAAAGCTC 1310
Qy 1335 TCAGTGTGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGAGA 1383
Db 1311 TCAGTGTGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGAGA 1359

RESULT 7

AR541611 4038 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 8 from patent US 6743604.
DEFINITION AR541611
ACCESSION AR541611
VERSION AR541611.1 GI:53933625
KEYWORDS

SOURCE

Unknown.
Unidentified.

REFERENCE

1 (bases 1 to 4038)
AUTHORS Bonnefoy, J.-Y. and Gauchat, J.-F.
TITLE Substances and their uses
JOURNAL Patent: US 6743604-A 8 01-JUN-2004;
Smithline Beecham Corporation; Philadelphia, PA;
WOX;

FEATURES

source 1. 4038
/organism="unknown"
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ORIGIN

Query Match 86.6%; Score 1198; DB 2; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	135	CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTCTGTGAAAACTCTG	194	
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QY	195	CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTGTAGTCTAGTGA	254	
Db	180	CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTGTAGTCTAGTGA	239	
QY	255	TTTTAGTCATTTTGGGACAAACAGATAAGAAAAATAGCTCCGGAAAATGTCGTTCAT	314	
Db	240	TTTTAGTCATTTTGGGACAAACAGATAAGAAAAATAGCTCCGGAAAATGTCGTTCAT	299	
QY	315	AGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA	374	
Db	300	AGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA	359	
QY	375	GAGTGAAAGCCCTAGCATTTTGGTGAATAATGCATCCACCCAGAGGTGATCTCTGA	434	
Db	360	GAGTGAAAGCCCTAGCATTTTGGTGAATAATGCATCCACCCAGAGGTGATCTCTGA	419	
QY	435	GTCTGCTGAGCACTGACCTCAATGACATTTGGGCAACCTGAGCTACATGAGTCTCTG	494	
Db	420	GTCTGCTGAGCACTGACCTCAATGACATTTGGGCAACCTGAGCTACATGAGTCTCTG	479	
QY	495	GCTCCCTGGAAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGACAGAA	554	
Db	480	GCTCCCTGGAAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGACAGAA	539	
QY	555	CCTGGAATAATTCATCATATGTGAAAAATCTCTTTAGAGAGGCCAATATCTTTGGTGTTC	614	
Db	540	CCTGGAATAATTCATCATATGTGAAAAATCTCTTTAGAGAGGCCAATATCTTTGGTGTTC	599	
QY	615	CTTTGATCTGACCAAGGTGAAGGATTCACGTTTGTGAACAACAGAGTCCAAATATATGT	674	
Db	600	CTTTGATCTGACCAAGGTGAAGGATTCACGTTTGTGAACAACAGAGTCCAAATATATGT	659	
QY	675	CAAGATAATGACAGAAAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCCGTGT	734	
Db	660	CAAGATAATGACAGAAAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCCGTGT	719	
QY	735	GAAACCTGATCTCCACATATTTAAAACTCTCTCCACAAATGATGACCTATATGTGCA	794	
Db	720	GAAACCTGATCTCCACATATTTAAAACTCTCTCTCCACAAATGATGACCTATATGTGCA	779	
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QY	915	ATTGGAAGAAATGTGAGAAATACATCTTGTTCATGTCCTCTGTGTTCTCTCTGATAC	974	
Db	900	ATTGGAAGAAATGTGAGAAATACATCTTGTTCATGTCCTCTGTGTTCTCTCTGATAC	959	
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Db	1260	GAAGCAAAACCAAGAGAGAAAACGACTCTGTAGTGTGATATGAAAACCTGAAGAAACCTC	1319	
QY	1335	TCAGTATGAGATATATTTATTTTACCTTCACTGTGACCTTGAGAGA	1383	
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RESULT 8				
LOCUS	CO894698	4039 bp	DNA	linear
DEFINITION	Sequence 8 from Patent EP1471075.			
ACCESSION	CO894698			
VERSION	CO894698.1	GI:55467447		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Bruemendorf,T.,			
TITLE	Lichtner,R., Straub,E., Roepke,S. and Li,X.I.			
JOURNAL	Human nucleic acid sequences expressed in pancreatic carcinomas			
	Patent: EP 1471075-A 8 27-OCT-2004;			
	Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian			
	(DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie			
	(DE)			
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ORIGIN				
Query Match 86.6%; Score 1198; DB 2; Length 4039;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				

QY	135	CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTCTGTGAAAACTCTG	194	
Db	121	CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTCTGTGAAAACTCTG	180	
QY	195	CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTGTAGTCTATGTA	254	
Db	181	CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTGTAGTCTATGTA	240	
QY	255	TTTTAGTCATTTTGGGACAAACAGATAAGAAATAGTCCGGAAATCTGTCGTTCAT	314	
Db	241	TTTTAGTCATTTTGGGACAAACAGATAAGAAATAGTCCGGAAATCTGTCGTTCAT	300	
QY	315	AGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA	374	
Db	301	AGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA	360	
QY	375	GAGTGAAAGCCCTAGCATTTTGGTGAATAATGATCTACCCCGAAGGTGATCTGA	434	
Db	361	GAGTGAAAGCCCTAGCATTTTGGTGAATAATGATCTACCCCGAAGGTGATCTGA	420	
QY	435	GTCTGCTGACTGAACCTTCAATGATTTTGGCAAACTGAGTACATGAAGTGTCTTG	494	
Db	421	GTCTGCTGACTGAAGCTTCAATGATTTTGGCAAACTGAGTACATGAAGTGTCTTG	480	
QY	495	GCTCCCTGGAAGGAATACAGAGTCCGACACTAATCTACTACTATTGGACAGAG	554	
Db	481	GCTCCCTGGAAGGAATACAGAGTCCGACACTAATCTACTACTATTGGACAGAG	540	

QY 555 CCTGGAAAAAATTGATCATATGTAAGAAATCTTTAGAGAGGCCAATATCTTGGTTGTC 614
DB 541 CTTGGAAAAAATTCATCATATGTAAGAAATCTTTAGAGAGGCCAATATCTTGGTTGTC 600
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AX335537 4039 bp DNA linear PAT 09-JAN-2002
LOCUS AX335537
DEFINITION Sequence 6046 from Patent WO194629.
ACCESSION AX335537
VERSION AX335537.1 GI:18126256
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature

JOURNAL gene sets
Patent: WO 0194629-A 6046 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
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Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX411212
DEFINITION Sequence 3859 from Patent WO0229103.
ACCESSION AX411212
VERSION AX411212.1 GI:21443917
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE
1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3859 11-Apr-2002;
JOURNAL GENE LOGIC INC (US)
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Best Local Similarity 99.9%; Pred. No. 0;
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LOCUS HS1113RA 4039 bp mRNA linear PRI 22-JAN-1997
DEFINITION H.sapiens IL-13Ra mRNA.
ACCESSION Y10659
VERSION Y10659.1 GI:1806035

KEYWORDS IL13ra gene; interleukin-13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Gauchat, J.F.M., Schlagenhauf, E., Feng, N.P., Moser, R., Yamage, M.,
Jaanm, P., Alouani, S., Elson, G., Notarangelo, L.D., Wells, T.,
Eugster, H.P. and Bonnefoy, J.Y.
A novel 4 kb IL-13ra mRNA expressed in human B, T and endothelial
cells, encoding for an alternate type two IL-4/IL-13R
Unpublished
2 (bases 1 to 4039)
Gauchat, J.F.M.
Direct Submission
Submitted (20-JUN-1997) J-F.M. Gauchat, Geneva Biomedical Research
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Aulx, Plan-Les-Ouates, CH1228, SWITZERLAND
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
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AR282860
LOCUS AR282860 11927 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6524792.
ACCESSION AR282860
VERSION AR282860.1 GI:29719662
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 11927)
AUTHORS Remer, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 5-25-FEB-2003;
Cytos Biotechnology; Zurich-Schlieren;
CHX;
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LOCUS AY892945
DEFINITION Synthetic construct Homo sapiens clone FHL141766.01L inter-leukin 13
ACCESSION AY892945
VERSION AY892945.1 GI:60654342
KEYWORDS Human ORF project.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1284)
AUTHORS Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
TITLE Cloning of human full-length cDNAs in Creator (TM) recombinational vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1284)
AUTHORS Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
COMMENT This cDNA clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The cDNA has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.
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ORIGIN

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SOURCE
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  Ohara, O., Nagase, T., and F. Kikuno, R.
  None Title
  Published Only in Database (2005)
  2 (bases 1 to 3960)
  Totoski, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
  Ohara, O., Nagase, T., and F. Kikuno, R.
  Direct Submission
  Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
  Department of Human Gene Research; 2-6-7 Kazusa-Kamatori, Kisarazu,
  Chiba, 292-0818, Japan (E-mail: cdnainfo@kazusa.or.jp,
  URL: http://protein.gsc.riken.go.jp/, Tel: 81-438-52-3930,
  Fax: 81-438-52-3931)
COMMENT
  This work was supported in part by the National Project on Protein
  Structural and Functional Analysis, Ministry of Education, Culture
  Sports, Science and Technology of Japan. Totoki Y, Toyoda A,
  Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences
  Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 48236798 seqs, 27959665780 residues

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Database:

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10: gb_est11:
11: gb_est12:
12: gb_est13:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	689	49.8	866	14	DQ034842 Homo sapi
5	655	47.4	842	5	CK000442 AGNCOURT
6	600	43.4	799	4	CB956372 AGNCOURT
7	587	42.1	902	4	CA488843 AGNCOURT
8	582	42.1	633	4	CA391344 AGNCOURT
9	577	41.7	580	3	CA1405 Y
10	573	41.4	573	9	DA102323
11	567	41.0	567	9	DB150552
12	565	40.1	570	9	DA757245
13	552	39.9	552	9	DA707381
14	543	39.3	543	9	DA992396
15	541	39.1	541	4	DA990183
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31	394	28.5	553	9	DA839608
32	391	28.3	552	9	DA294933
33	389	28.1	578	9	DA685427
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38	374	27.0	571	9	DB261081
39	372	26.9	532	9	DA990941
40	368	26.6	419	4	CA389226
41	355	25.7	595	3	BM763177
42	345	24.9	624	1	A1768613
43	338	24.4	561	4	CA398074
44	324	23.4	1009	2	BI464939
45	322	23.3	634	7	BE971462

ALIGNMENTS

RESULT 1
CR603161
LOCUS
DEFINITION
full-length cDNA clone CSOD1001YN10 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR603161
VERSION
CR603161.1 GI:50483968
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 1756)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Peng Liang Email: liang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1756)
Genoscope.
REFERENCE
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1756
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1001YN10"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 76.9%; Score 1063; DB 6; Length 1756;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	135	CCGCGCTACGGAAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAAACCTTG	194	
DB	78	CGCGCTACGGAAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAAACCTTG	137	
QY	195	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGATGTA	254	
DB	138	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGATGTA	197	
QY	255	TTTTTACTCATTTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT	314	
DB	198	TTTTTACTCATTTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT	257	
QY	315	AGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	374	
DB	258	AGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	317	
QY	375	GAGTGAGAAAGCTAGCATTTTGGTTGAAAAATGCATCTCACCCCAAGAGTATCTGA	434	
DB	318	GAGTGAGAAAGCTAGCATTTTGGTTGAAAAATGCATCTCACCCCAAGAGTATCTGA	377	
QY	435	GTCGTGTGACTGAACTTCAATGCATTTGGGCAACCTGAGTCAATGAAGTGTCTTG	494	
DB	378	GTCGTGTGACTGAACTTCAATGCATTTGGGCAACCTGAGTCAATGAAGTGTCTTG	437	
QY	495	GCTCCCTGGAAGGAATACGAGTCCGACACTAATCTCTACTATTGGGACAGAG	554	
DB	438	GCTCCCTGGAAGGAATACGAGTCCGACACTAATCTCTACTATTGGGACAGAG	497	
QY	555	CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATCTTGTGTTGC	614	
DB	498	CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATCTTGTGTTGC	557	
QY	615	CTTTGATCTGACCAAGTGAAGATTCAGTTTGGAAACAACAGTGTCCAATATGTGT	674	
DB	558	CTTTGATCTGACCAAGTGAAGATTCAGTTTGGAAACAACAGTGTCCAATATATGTGT	617	
QY	675	CAAGATTAATGACGAAAAATTAACCATCTTCAATATATGTGTCTTTAACTCCGCTG	734	
DB	618	CAAGATTAATGACGAAAAATTAACCATCTTCAATATATGTGTCTTTAACTCCGCTG	677	
QY	735	GAAACCTGATCTCTCAATATTAATAAACTCTCTCTTCCACAAATGATGACCTATATGCA	794	
DB	678	GAAACCTGATCTCTCAATATTAATAAACTCTCTCTTCCACAAATGATGACCTATATGCA	737	
QY	795	ATGGGGAATCCACAGAAATTTTATAGCAGATGCCATATTTTAAAGTAAGTCAATTA	854	
DB	738	ATGGGGAATCCACAGAAATTTTATAGCAGATGCCATATTTTAAAGTAAGTCAATTA	797	
QY	855	CAGCCAACTGAGACATATATTTTCTACGTCGAAGAGGCTAAATGTGAGATCCAGA	914	
DB	798	CAGCCAACTGAGACATATATTTTCTACGTCGAAGAGGCTAAATGTGAGATCCAGA	857	
QY	915	ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTGCTCGTGTCTCTCTGATAC	974	
DB	858	ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTGCTCGTGTCTCTCTGATAC	917	
QY	975	TTTTGAAACAGTACAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACT	1034	
DB	918	TTTTGAAACAGTACAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACT	977	
QY	1035	CTGAGTAATTTGGAGCAAGAAATGATATAGGTAAGAGGCAATTTCCACACTCTACAT	1094	
DB	978	CTGAGTAATTTGGAGCAAGAAATGATATAGGTAAGAGGCAATTTCCACACTCTACAT	1037	
QY	1095	AACCATGTTACTCATTTGTTCCAGTCACTGTGAGAGTGAATCATAGTACTCTCTGCTTAA	1154	
DB	1038	AACCATGTTACTCATTTGTTCCAGTCACTGTGAGAGTGAATCATAGTACTCTCTGCTTAA	1097	
QY	1155	CTTAAAAAGGCTCAAGATTTATATTTCTCTCAATTTCTGATCTCGGCAAGATTTTAA	1214	

DB	1098	CCTAAAAAGGCTCAAGATTTATATATCCCTCCAAATCTCTGATCTGGCAAGATTTTAA	1157	
QY	1215	AGAAATGTTTGGAGACCAAGATGATGATCTGTG	1248	
DB	1158	AGAAATGTTTGGAGACCAAGATGATGATCTGTG	1191	
RESULT 2				
LOCUS	AL543336	1016 bp	mRNA	linear
DEFINITION	AL543336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
ACCESSION	AL543336			
VERSION	AL543336.3			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31265183.			
Contact: Genoscope				
Genoscope - Centre National de Sequencage				
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE				
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 11048.f				
For more information about this cluster, see				
http://www.genoscope.cns.fr/cdna?b=CS0D1001D6050Plac=11048.f.				
Location/Qualifiers				
1..1016				
/organism="Homo sapiens"				
/mol_type="mRNA"				
/db_xref="taxon:9606"				
/clone="CS0D1001YN10"				
/cissue_type="PLACENTA COT 25-NORMALIZED"				
/clone_1lb="Homo sapiens PLACENTA COT 25-NORMALIZED"				
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."				
ORIGIN				
Query Match 61.2%; Score 846; DB 1; Length 1016;				
Best Local Similarity 99.9%; Pred. No. 0; Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	135	CGCGCTACGGAAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAAACCTTG	194	
DB	79	CGCGCTACGGAAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAAACCTTG	138	
QY	195	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGATGTA	254	
DB	139	CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGATGTA	198	
QY	255	TTTTTACTCATTTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT	314	
DB	199	TTTTTACTCATTTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAAACTGTGTTCAAT	258	
QY	315	AGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	374	
DB	259	AGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA	318	
QY	375	GAGTGAGAAAGCTAGCATTTTGGTTGAAAAATGCATCTCACCCCAAGAGTATCTCTGA	434	

Db 319 GAGTGAAGAGCTGATTTTGGTGAAGAAATGATCTACCCAGAGGTGATCCGCA 378
Qy 435 GTCTGCTGTAAGTGAATGATTTGGACAACTGAGCTACATGAGTGTCTTG 494
Db 379 GTCTGCTGTAAGTGAATGATTTGGACAACTGAGCTACATGAGTGTCTTG 438
Qy 495 GCTCCCTGGAAGAAATGACAGTCCGACACTACTATATCTCTTACTATTTGGACAGAG 554
Db 439 GCTCCCTGGAAGAAATGACAGTCCGACACTACTATATCTCTTACTATTTGGACAGAG 498
Qy 555 CTTGGAAAAATTTATCATATGTAAGAAATCTTTTGAAGAGCCAAATCTTTGGTGTTC 614
Db 499 CTTGGAAAAATTTATCATATGTAAGAAATCTTTTGAAGAGCCAAATCTTTGGTGTTC 558
Qy 615 CTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGCCTTGAATTTGCT 674
Db 559 CTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGCCTTGAATTTGCT 618
Qy 675 CAAGATATGACAGAAAAATTAACATCTCTCAATATATGCTTTAACTTCCGTGT 734
Db 619 CAAGATATGACAGAAAAATTAACATCTCTCAATATATGCTTTAACTTCCGTGT 678
Qy 735 GAAACCTGATCTCTCAATATTAATAAATCTCTCTTCCACATATGATGCTATATGTGA 794
Db 679 GAAACCTGATCTCTCAATATTAATAAATCTCTCTTCCACATATGATGCTATATGTGA 738
Qy 795 ATGGAGATCCACAGAAATTTTATAGACATGCTTATTTTGAAGTGAAGTCAATTA 854
Db 739 ATGGAGATCCACAGAAATTTTATAGACATGCTTATTTTGAAGTGAAGTCAATTA 798
Qy 855 CAGCCAACTGACACATATATGTTTCTACGTCACAGAGCTAAATGTGAGATCCAGA 914
Db 799 CAGCCAACTGACACATATATGTTTCTACGTCACAGAGCTAAATGTGAGATCCAGA 858
Qy 915 ATTGAGAGAAATGTGAGAAATACATTTGTTTATGATGCTGCTGCTTCTCTGATAC 974
Db 859 ATTGAGAGAAATGTGAGAAATACATTTGTTTATGATGCTGCTGCTTCTCTGATAC 918
Qy 975 TTGGAACACAGTCAAGATTAAGTCAAAACAAATTAATGATGATGAGATGCA 1031
Db 919 TTGGAACACAGTCAAGATTAAGTCAAAACAAATTAATGATGATGAGATGCA 975

RESULT 3
BM905033 951 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT_6699542 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557892
DEFINITION 5', mRNA sequence.
ACCESSION BM905033
VERSION BM905033.1 GI:19355424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 951)
REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12279 row: p column: 21
High quality sequence stop: 719.
Location/Qualifiers
1..951

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5557892"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 52.6%; Score 728; DB 3; Length 951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 778; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 166 AATTGAGTGTCTCTGTTGAAACCTCTGACAGTAATATGACATGATCCACCGAG 225
Db 13 AATTGAGTGTCTCTGTTGAAACCTCTGACAGTAATATGACATGATCCACCGAG 72
Qy 226 GGAGCCAGCTCAAAATGTAGTCTATGTATTATGCAATTTGGCGCAACAAGATTAAG 285
Db 73 GGAGCCAGCTCAAAATGTAGTCTATGTATTATGCAATTTGGCGCAACAAGATTAAG 132
Qy 286 AAATAGCTCCGGAACCTCGTCTCAATGAATGATCCCTGATGAGAGATTTGCTG 345
Db 133 AAATAGCTCCGGAACCTCGTCTCAATGAATGATCCCTGATGAGAGATTTGCTG 192
Qy 346 CAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGAGCTTACATTTTGGTGAAGAA 405
Db 193 CAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGAGCTTACATTTTGGTGAAGAA 252
Qy 406 TGCATCTACCCCGAAGGTGATCTGAGTCTGCTGTGACTGATGCAATTCATTCATTTGG 465
Db 253 TGCATCTACCCCGAAGGTGATCTGAGTCTGCTGTGACTGATGCAATTCATTCATTTGG 312
Qy 466 CACAACTGAGTCAATGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525
Db 313 CACAACTGAGTCAATGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
Qy 526 AACTATCTCTACTATTTGGACAGAGAGCTGGAAATTTTCAATGATGAAATC 585
Db 373 AACTATCTCTACTATTTGGACAGAGAGCTGGAAATTTTCAATGATGAAATC 432
Qy 586 TTGAGAGAGCCATATCTTTGTTGTTCTTTGATGTCACAAAGTGAAGATTCAGT 645
Db 433 TTGAGAGAGCCATATCTTTGTTGTTCTTTGATGTCACAAAGTGAAGATTCAGT 492
Qy 646 TTGGAACACAGTGTCCAAATATATGATGAGATATGACAGAAAAATTAACCATCC 705
Db 493 TTGGAACACAGTGTCCAAATATATGATGAGATATGACAGAAAAATTAACCATCC 552
Qy 706 TTCAATATATGCTTTAACTTCCCGTGTGAACCTGATCTCCACATATTAACCTC 765
Db 553 TTCAATATATGCTTTAACTTCCCGTGTGAACCTGATCTCCACATATTAACCTC 612
Qy 766 TCTTCCACATGATGACCTATATGTCACATGAGATCCACAGAAATTTATAGAGAGA 825
Db 613 TCTTCCACATGATGACCTATATGTCACATGAGATCCACAGAAATTTATAGAGAGA 672
Qy 826 TGCTATTTTATGAGTGAAGTCAATTAACAGCCAACTGAGACATATGTTTCTAC 885
Db 673 TGCTATTTTATGAGTGAAGTCAATTAACAGCCAACTGAGACATATGTTTCTAC 732
Qy 886 GTCCAGAGGCTAAATGTGAGATCCAGATTTTGAAGAAATGTGAGAAATACATCTTG 944
Db 733 GTCCAGAGGCTAAATGTGAGATCCAGATTTTGAAGAAATGTGAGAAATACATCTTG 791

RESULT 4
DQ034842
LOCUS DQ034842 866 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens IL13RA1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION D0034842
VERSION D0034842.1 GI:66886051
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
JOURNAL
PUBMED 15869325
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translacion starts at the beginning of
alignment.
FEATURES
source
1..866
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
<1..>866
/gene="IL13RA1"
/locus_tag="HC4262"
ORIGIN
Query Match 49.8%; Score 689; DB 14; Length 866;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 146 AAACAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 205
1 AAACAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 60
QY 206 GGCATGGAATCCACCCGAGGGGCGACGCTCAATTGTAGTCTATGTTTATGTCAT 265
61 GGCATGGAATCCACCCGAGGGGCGACGCTCAATTGTAGTCTATGTTTATGTCAT 120
QY 266 TTGGCAGCAAAACAAGATAGAAATATGCTCCGGAACCTGCTCAATGAGATGCCCC 325
121 TTGGCAGCAAAACAAGATAGAAATATGCTCCGGAACCTGCTCAATGAGATGCCCC 180
QY 326 TGAATGAGAGATTTGTCTGCAAGTGGGATCCAGTGTAGACCAATGAGAGTGAAGC 385
181 TGAATGAGAGATTTGTCTGCAAGTGGGATCCAGTGTAGACCAATGAGAGTGAAGC 240
QY 386 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGGTGATCTGAGTCTGCTGTA 445
241 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGGTGATCTGAGTCTGCTGTA 300
QY 446 CTGAATCTCAATGATTTGGCACAACCTGAGTCAATGAGTGTCTGCTCCCTGGAA 505
301 CTGAGCTTCAATGATTTGGCACAACCTGAGTCAATGAGTGTCTGCTCCCTGGAA 360
QY 506 GGAATACCAAGTCCCGACACTAATCTCTCTACTATTGGCACAAGAGCTGGAAAAA 565
361 GGAATACCAAGTCCCGACACTAATCTCTCTACTATTGGCACAAGAGCTGGAAAAA 420
QY 566 TTGATCAATGTGAAAAATCTTTAGAGAGGCAATGCTTTGTTGTTCTTTGATCTGA 625
|||||

Db 421 TTCATCAATGTGAAAAATCTTTAGAGAGGCAATGCTTTGTTGTTCTTTGATCTGA 480
QY 626 CCAAGTGAAGATTCAGTTTGAACAACAACAGTGTCCAAATTAATGCTCAAGATTAAG 685
Db 481 CCAAGTGAAGATTCAGTTTGAACAACAACAGTGTCCAAATTAATGCTCAAGATTAAG 540
QY 686 CAGAAAAATTAACCAATCTTCAATATGAGCTTTAACTCCGCTGGAACCTGATC 745
Db 541 CAGAAAAATTAACCAATCTTCAATATGAGCTTTAACTCCGCTGGAACCTGATC 600
QY 746 CTCACATATTAATAAACCTCTCTCCACAAATGATGACCTATATGCAATGGAGATC 805
Db 601 CTCACATATTAATAAACCTCTCTCCACAAATGATGACCTATATGCAATGGAGATC 660
QY 806 CACAGAAATTTTATGACAGATGCTTATTTATGAAAGTCAATTAACAGCAAACTG 865
Db 661 CACAGAAATTTTATGACAGATGCTTATTTATGAAAGTCAATTAACAGCAAACTG 720
QY 866 AGACACATTAATGTTTCTAC 885
Db 721 AGACACATTAATGTTTCTAC 740
RESULT 5
CK000442 842 bp mRNA linear EST 26-NOV-2003
LOCUS
DEFINITION AGENCOURT 1636365 NIH MGC 221 Homo sapiens CDNA clone
IMAGE:30708826 5', mRNA sequence.
ACCESSION CK000442
VERSION CK000442.1 GI:38526476
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: NDML075 row: k column: 11
High quality sequence stop: 681.
FEATURES
source
1..842
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30708826"
/lab_host="DH10B TONa"
/clone_1lb="NIH_MGC_221"
/note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI;
Site 2: NotI; Library is oligo-dT primed and directionally
cloned. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
4-5kb. Adaptors 5' (AATTGGCAGAGG) 3' and 5' d
(CCTGCTGCCG) 3'. 3' linker sequence - GGGGCGCTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd

(ATTAACTCTCACTAAAGGA)3'. 5' End: T7 promoter primer 5'd
(TAATAGCACTCACTATAGG)3'. Library was constructed in the
laboratory of M. Bento Soares. Note: this is a NIH_MGC
Library"

ORIGIN

Query Match 47.4%; Score 655; DB 5; Length 842;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

729 CCGGTGAAACCTATCTCCATATTAATAAACCCTCTCTCCCAATGATGACTTAA 788
26 CCGGTGAAACCTATCTCCATATTAATAAACCCTCTCTCCCAATGATGACTTAA 85
789 TGTCAATGGAGAAATCCAGAAATTTTATAGAGATGCTTATTTATGAAGTGAAGT 848
86 TGTCAATGGAGAAATCCAGAAATTTTATAGAGATGCTTATTTTATGAAGTGAAGT 145
849 CAATTAACAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTTAATGTGADA 908
146 CAATTAACAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTTAATGTGADA 205
909 TCCGAAATTTGAGAAATGAGAAATGACATCTTTGTTTCAATGCTGCTGTTCTTCC 968
206 TCCGAAATTTGAGAAATGAGAAATGACATCTTTGTTTCAATGCTGCTGTTCTTCC 265
969 TGATCTCTTGAACACAGTCAGATTAAGTCAAAATTAAGTATGCTATGAGATGA 1028
266 TGATCTCTTGAACACAGTCAGATTAAGTCAAAATTAAGTATGCTATGAGATGA 325
1029 CAACTCTGAGATTAATGAGCCAAAGAAATGATTAAGTAAAGAGCCAAATTCACACT 1088
326 CAACTCTGAGATTAATGAGCCAAAGAAATGATTAAGTAAAGAGCCAAATTCACACT 385
1089 CTATCATACCATGTTTACTATCTATGTTTCCAGTATGTCGAGGTGCAATCATAGTCTCT 1148
386 CTATCATACCATGTTTACTATCTATGTTTCCAGTATGTCGAGGTGCAATCATAGTCTCT 445
1149 GCTTACTCTAATAAAGGCTCAAGATTTATTTATTCCTCCCAATTCCTGCAAGAT 1208
446 GCTTACTCTAATAAAGGCTCAAGATTTATTTATTCCTCCCAATTCCTGCAAGAT 505
1209 TTTTAAAGAAATGTTTGAAGACCAAGATGATGATCTGTCATGTAAGAAAGTACGACT 1268
506 TTTTAAAGAAATGTTTGAAGACCAAGATGATGATCTGTCATGTAAGAAAGTACGACT 565
1269 CTATGAAGACCAAGCAAGAGAAACCGACTCTGTAAGTGTGATTAAGAAACCTGAAGAA 1328
566 CTATGAAGACCAAGCAAGAGAAACCGACTCTGTAAGTGTGATTAAGAAACCTGAAGAA 625
1329 AGCCTCAGATGATGAGATTAATTTTATCTTCACTGCTGACCTTGAAGAA 1383
626 AGCCTCAGATGATGAGATTAATTTTATCTTCACTGCTGACCTTGAAGAA 680

RESULT 6
CB956372 799 bp mRNA linear EST 29-APR-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 799)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: Clontech Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLI at:
<http://image.llnl.gov>
Plate: NDCM154 row: a column: 16
High quality sequence stop: 651.
Location/Qualifiers
1. 799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30353391"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_184"
/note="Organ: Pooled glandular; Vector: pDNR-LIB; Site: 1:
SfiI (ggccatcgcc); Site 2: SfiI (ggccgcccggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATATGAGC-3' and 3' adaptor sequence:
5'-ATTCTAGGCGGAGGCGGCGCATATG-3' (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES

source

Query Match 43.4%; Score 600; DB 4; Length 799;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

258 TAGCATTTTGGGCAACAAAGATTAAGAAATAGCTCCGGAACCTGCTCAATGA 317
3 TAGCATTTTGGGCAACAAAGATTAAGAAATAGCTCCGGAACCTGCTCAATGA 62
318 AGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGAACCAATGAGAG 377
63 AGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGAACCAATGAGAG 122
378 TGAGAGCTTGAATTTTGGTTGAAATATGATCTCAACCCCAAGAGTATCTGAGTC 437
123 TGAGAGCTTGAATTTTGGTTGAAATATGATCTCAACCCCAAGAGTATCTGAGTC 182
438 TGCTGTGACGAACTTGAATGCAATTTGGCAACCTGAGTACATGAAGTCTTGGCT 497
183 TGCTGTGACGAACTTGAATGCAATTTGGCAACCTGAGTACATGAAGTCTTGGCT 242
498 CCTGGAAGAAATACAGTCCCGACACTAATCTCTCTAATTTGGGCAAGAGCT 557
243 CCTGGAAGAAATACAGTCCCGACACTAATCTCTCTAATTTGGGCAAGAGCT 302
558 GGAATAAATTCATCATATGTAATAACATCTTTAAGAAAGCCAAATATCTTGTCTT 617
303 GGAATAAATTCATCATATGTAATAACATCTTTAAGAAAGCCAAATATCTTGTCTT 362
618 TGATTCGACCAAGTGAAGATTTCCAGTTTGAACAACAGATGCCAATTAATGTCGA 677
363 TGATTCGACCAAGTGAAGATTTCCAGTTTGAACAACAGATGCCAATTAATGTCGA 422
678 GGATTAATGAGAAATTAATTAACATCTTCAATATATGCTTTAATCTCCGCTGGA 737
423 GGATTAATGAGAAATTAATTAACATCTTCAATATATGCTTTAATCTCCGCTGGA 482
738 ACCGTATCTTCATATTTAAACCTCTCTTCCAAATGATGAGCTATATGTCATG 797
483 ACCGTATCTTCATATTTAAACCTCTCTTCCAAATGATGAGCTATATGTCATG 542

QY 798 GGAGAAATCCACAGATTATTTATAGCAGATCCCTATTATTTATGAAAGTAGAAGTCATAACAG 857
DB 543 GGAGAAATCCACAGAAATTTTATAGCAGATCCCTATTATTTATGAAAGTAGAAGTCATAACAG 602
QY 858 CCAAACTGAGACCATTAATGTTTCTACGCTCCAAAGAGGCTTAATGTGAGAAATCCAGAAAT 917
DB 603 CCAAACTGAGACCATTAATGTTTCTACGCTCCAAAGAGGCTTAATGTGAGAAATCCAGAAAT 662
QY 918 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTCTG 959
DB 663 TGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTCTG 704

RESULT 7
CA488843 902 bp mRNA linear EST 14-NOV-2002
LOCUS CA488843
DEFINITION AGENCOURT_10808228 MAPCL Homo sapiens cDNA clone IMAGE:6721041 5',
mRNA sequence.

ACCESSION CA488843 GI:24951634
VERSION CA488843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euteleostomi; Euteleostomi; Primates; Catarrhini;
JOURNAL Homnidae; Homo.
COMMENT 1 (bases 1 to 902)
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM4281 row: 1 column: 09
High quality sequence stop: 711.
Location/Qualifiers

FEATURES
source
1..902
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6721041"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HME1, LNCaP"
/lab_host="EMD10B"
/note="Vector: PCMV-SPT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN

Query Match 42.4%; Score 587; DB 4; Length 902;
Best Local Similarity 100.0%; Pred. No. 1.1e-307;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 GGGAGAAATCCACAGATTATTTATAGCAGATCCCTATTATTTATGAAAGTAGAAGTCATAACAG 856
DB 27 GGGAGAAATCCACAGAAATTTTATAGCAGATCCCTATTATTTATGAAAGTAGAAGTCATAACAG 86
QY 857 GCGAAACTGAGACCATTAATGTTTCTACGCTCCAAAGAGGCTTAATGTGAGAAATCCAGAAAT 916
DB 87 GCGAAACTGAGACCATTAATGTTTCTACGCTCCAAAGAGGCTTAATGTGAGAAATCCAGAAAT 146

QY 917 TTGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTCTGTTCTCTGATACCT 976
DB 147 TTGAGAGAAATGTGAGAAATACATCTGTTTCATGTCCTCTGTTCTCTGATACCT 206
QY 977 TGAACACAGTCAGAAATTAAGAGTCAAAACAAATTAAGTATGCTATGAGAGTACAACTCT 1036
DB 207 TGAACACAGTCAGAAATTAAGAGTCAAAACAAATTAAGTATGCTATGAGAGTACAACTCT 266
QY 1037 GGAGTAATTTGAGACCAAGAAATGATATAGTATGATGAAGGCCAATTCACACTACATAA 1096
DB 267 GGAGTAATTTGAGACCAAGAAATGATATAGTATGATGAAGGCCAATTCACACTACATAA 326
QY 1097 CCATGTTACTCATTTGTTCCAGTCATGTCGACAGTGCATCATAGTACTCTGCTTTACC 1156
DB 327 CCATGTTACTCATTTGTTCCAGTCATGTCGACAGTGCATCATAGTACTCTGCTTTACC 386
QY 1157 TAAAAAGGCTCAAGATTATTTATATTCCTCCCAATTCCTGATCCTGCAAGATTATTAAG 1216
DB 387 TAAAAAGGCTCAAGATTATTTATATTCCTCCCAATTCCTGATCCTGCAAGATTATTAAG 446
QY 1217 AAATGTTTGGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276
DB 447 AAATGTTTGGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 506
QY 1277 AGCAAAACCAAGAGAAACCGACTCTGTAGTCTGTATGAAAACTGAAAGAAAGCCTCTC 1336
DB 507 AGCAAAACCAAGAGAAACCGACTCTGTAGTCTGTATGAAAACTGAAAGAAAGCCTCTC 566
QY 1337 AGTGATGAGATTAATTTATTTTACCTGACCTGATGATGATGATGATGATGATGATGATGAT 1383
DB 567 AGTGATGAGATTAATTTATTTTACCTGACCTGATGATGATGATGATGATGATGATGATGAT 613

RESULT 8
CA391344 633 bp mRNA linear EST 06-NOV-2002
LOCUS CA391344
DEFINITION cs14a05.y1 Human Retinal pigment epithelium/choroid cDNA
(un-normalized, unamplified): cs Homo sapiens cDNA clone cs14a05
5', mRNA sequence.

ACCESSION CA391344 GI:24723148
VERSION CA391344
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euteleostomi; Euteleostomi; Primates; Catarrhini;
JOURNAL Homnidae; Homo.
COMMENT 1 (bases 1 to 633)
Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human RPE/choroid for the
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL
PUBMED
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gwaen@helix.nih.gov
Plate: 14 row: a column: 05
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers

FEATURES
source
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs14a05"
/issue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMD10B"

/clone_lib="Human Retinal pigment epithelium/choroid cDNA (un-normalized, unamplified): cs"
(note="Organ: Eye; Vector: PCWSPOR6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>". The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 42.1%; Score 582; DB 4; Length 633;
Best Local Similarity 99.8%; Pred. No. 5.9e-305; Mismatches 1; Indels 0; Gaps 0;
Matches 632; Conservative 0;

138 GCCACGGAACCTGACGACCTGACAAATTGAGTCTCTGTGAAAACTCTGAC 197
1 GCCTACGGAACCTGACGACCTGACAAATTGAGTCTCTGTGAAAACTCTGAC 60
198 AGTAATATGACATGACATCCAGGAGGAGCAGCTCAATGATGATGATTT 257
61 AGTAATATGACATGACATCCAGGAGGAGCAGCTCAATGATGATGATTT 120
258 TAGCTATTTGGGACAAACAGTAAGAAATAGTCCGGAACCTGCTTCAATGA 317
121 TAGCTATTTGGGACAAACAGTAAGAAATAGTCCGGAACCTGCTTCAATGA 180
318 AGTACCCCTGAATGAGAGATTTGTCGCAAGTGGGTCCTCCAGTACCATGAG 377
181 AGTACCCCTGAATGAGAGATTTGTCGCAAGTGGGTCCTCCAGTACCATGAG 240
378 TGAGAGCCTAGCATTTTGGTGAATAATGATCTCACCCAGAGGTGATCCTGAG 437
241 TGAGAGCCTAGCATTTTGGTGAATAATGATCTCACCCAGAGGTGATCCTGAG 300
438 TGCTGTGATGAACTTCAATGATGATTTGGCAAACTGATCAATGAAGTTCCTG 497
301 TGCTGTGATGAACTTCAATGATGATTTGGCAAACTGATCAATGAAGTTCCTG 360
498 CCTTGAAGGAATACCACTGCTCCGACATTAATCTCTCACTATTGGGACAGAG 557
361 CCTTGAAGGAATACCACTGCTCCGACATTAATCTCTCACTATTGGGACAGAG 420
558 GGAATAATTCATCAATGTGAAACATCTTTAGAGAGGCAATCTTTGGTGTCTT 617
421 GGAATAATTCATCAATGTGAAACATCTTTAGAGAGGCAATCTTTGGTGTCTT 480
618 TGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATGTCAA 677
481 TGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATGTCAA 540
678 GGATATGCGAGAAAAATTAACCATCTTCAATATATGTGCTTTAACTCCGTGAA 737
541 GGATATGCGAGAAAAATTAACCATCTTCAATATATGTGCTTTAACTCCGTGAA 600
738 ACCGTATCTCCCATATTAATAAACCCTCTCTT 770
601 ACCGTATCTCCCATATTAATAAACCCTCTCTT 633

RESULT 9
DA102323 580 bp mRNA linear EST 01-NOV-2005
LOCUS DA102323 BRACE3 Homo sapiens cDNA clone BRACE3014879 5', mRNA
DEFINITION
SEQUENCE
ACCESSION DA102323
VERSION DA102323.1 GI:78564889

KEYWORDS

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo.

1 (bases 1 to 580)

Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Makaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

16344560

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction;

Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing; RAB.

Location/Qualifiers

1..580

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="BRACE3014879"

/tissue_type="cerebellum"

/clone_lib="BRACE3"

/note="Vector: pME18FLJ3"

ORIGIN

Query Match 41.7%; Score 577; DB 9; Length 580;
Best Local Similarity 100.0%; Pred. No. 3.1e-302; Mismatches 0; Indels 0; Gaps 0;
Matches 577; Conservative 0;

678 GGATTAATGAGGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTCCGTGAA 737
4 GGATTAATGAGGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTCCGTGAA 63
738 ACCGTATCTCCCATATTAATAAACCCTCTTCAATATAGTGCCTTTAACTCCGTG 797
64 ACCGTATCTCCCATATTAATAAACCCTCTTCAATATAGTGCCTTTAACTCCGTG 123
798 GGAGAAATCCAGAAATTTTATGAGAGATCTTATTAAGAGTAGAGCATTAACAG 857
124 GGAGAAATCCAGAAATTTTATGAGAGATCTTATTAAGAGTAGAGCATTAACAG 183
858 CCAAACTGAGACATATATTTTCTACGTCAGAGAGGCTAAATGAGATCCAGAA 917
184 CCAAACTGAGACATATATTTTCTACGTCAGAGAGGCTAAATGAGATCCAGAA 243
918 TGAGAGAAATGTGAGAAATATCATCTTTTCAATATAGTGCCTTTAACTCCGTG 977
244 TGAGAGAAATGTGAGAAATATCATCTTTTCAATATAGTGCCTTTAACTCCGTG 303
978 GAAACAGTCCAGATTAAGATCAAAACAAATTAATGATGAGATGAGATCAAACTCTG 1037
304 GAAACAGTCCAGATTAAGATCAAAACAAATTAATGATGAGATGAGATCAAACTCTG 363
1038 GAGTAATTTGAGGCAAGAAATGAGTATGATGAAGACGCAATTCACACTTACATTAAC 1097
364 GAGTAATTTGAGGCAAGAAATGAGTATGATGAAGACGCAATTCACACTTACATTAAC 423

Oy	1098	CATGTTACTATTTGTCACGATCGATCGAGGAGCAATCATATGACTCCCGCTTACT	1157
Db	424	CATGTTACTATTTGTCACGATCGATCGAGGAGCAATCATATGACTCCCGCTTACT	483
Oy	1158	AAAAAGCTCAGATTATTTATATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGA	1217
Db	484	AAAAAGCTCAGATTATTTATATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGA	543
Oy	1218	AATGTTTGAGACCGAATGATGATATCTCTGCATCGG	1254
Db	544	AATGTTTGAGACCGAATGATGATATCTCTGCATCGG	580
RESULT 10			
DB150552			
LOCUS			
DEFINITION	DB150552 THYMJ3 Homo sapiens cDNA clone THYMJ3027195 5', mRNA	573 bp	linear EST 11-DEC-2005
ACCESSION	DB150552		
VERSION	DB150552.1	GI:8338764	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo		
AUTHORS	1 (bases 1 to 573) Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsukitani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Megatsuna,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.		
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes		
JOURNAL	Genome Res. 16 (1), 55-65 (2006)		
PUBMED	1634560		
COMMENT	Contact: Takao Isogai Fuj Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdnaenlity.com NEBO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.		
FEATURES			
source	Location/Qualifiers 1..573 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="THYMJ3027195" /tissue_type="thymus" /clone_id="THYMJ3" /note="Vector: pME18SFL3"		
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Query Match	41.4%;	Score 573;	DB 9;
Best Local Similarity	100.0%;	Prod. No. 4,7e-300;	Indels 0;
Matches	573;	Conservative 0;	Mismatches 0;
Oy	755	TTAAAAACCTCTCCTCCACAAATGATGACCTATATGTCGAATGGAGAAATC	814
Db	1	TTAAAAACCTCTCCTCCACAAATGATGACCTATATGTCGAATGGAGAAATC	60
Oy	815	TTAATTAGCAGATGCTATTTTATGAGTAGAGTCAATTAACGCCAACTGAGACACATA	874

[illegible]

FEATURES
Source
Location/Qualifiers
1..567
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="NT2RP804310"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP8"
/note="Vector: pME18SF13; mRNA from NT2 neuronal precursor cells after 5-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 41.0%; Score 567; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 8.8e-297;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 CAACACAGTGTCCAAATATAGTCAAGATATGACAGAAATTTAAACATCTTCCTCAAT 711
DB 1 CAACACAGTGTCCAAATATAGTCAAGATATGACAGAAATTTAAACATCTTCCTCAAT 60
QY 712 ATAGTGCCTTAATCTCCGTGTAACCTGATCTCCACATATTTAAACCCTCTCTTC 771
DB 61 ATAGTGCCTTAATCTCCGTGTAACCTGATCTCCACATATTTAAACCCTCTCTTC 120
QY 772 CACATATGACCTATATGTCATGAGAGATCCACAGATTTTATAGAGATGCTTA 831
DB 121 CACATATGACCTATATGTCATGAGAGATCCACAGATTTTATAGAGATGCTTA 180
QY 832 TTTTATAGATGAGATGATATACAGCCAACTGAGACACATTAATGTTTCTACGTCGA 891
DB 181 TTTTATAGATGAGATGATATACAGCCAACTGAGACACATTAATGTTTCTACGTCGA 240
QY 892 GAGGCTAATGTCGATCCAGATTTGAGAGAAATGAGAAATGATCTTGTTCATG 951
DB 241 GAGGCTAATGTCGATCCAGATTTGAGAGAAATGAGAAATGATCTTGTTCATG 300
QY 952 GTCCCTGCTGTTCTCTGATCTTGAACACAGTCCAGATTTAGAGTCAAAACAAATAG 1011
DB 301 GTCCCTGCTGTTCTCTGATCTTGAACACAGTCCAGATTTAGAGTCAAAACAAATAG 360
QY 1012 TTATGCTATGAGATGACAACTCTGAGATTTGAGAGCCAAAGATGATATAGTAA 1071
DB 361 TTATGCTATGAGATGACAACTCTGAGATTTGAGAGCCAAAGATGATATAGTAA 420
QY 1072 AAGGCGAATTCACACCTCTACATACCATGTTACTTCCAGTCATGTCGCAAGT 1131
DB 421 AAGGCGAATTCACACCTCTACATACCATGTTACTTCCAGTCATGTCGCAAGT 480
QY 1132 GCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCAAT 1191
DB 481 GCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCAAT 540
QY 1192 CTTGATCTGCGCAAGATTTTAAAGAA 1218
DB 541 CTTGATCTGCGCAAGATTTTAAAGAA 567

RESULT 12
DA707381 570 bp mRNA linear EST 13-NOV-2005
LOCUS DA707381 NT2R12 Homo sapiens cDNA clone NT2R12011802 5', mRNA
DEFINITION sequence.
ACCESSION DA707381 GI:82349574
VERSION DA707381.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 570)
REFERENCE
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,

TITLE
JOURNAL
PUBMED
COMMENT
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushiida,N.,
Yonekawa,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Megatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T., and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
Fujii Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: fiji-cdna@hri.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction;
Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing; RAB.
Location/Qualifiers
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2R12011802"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2R12"
/note="Vector: pME18SF13; majorly NT2 neuron; mRNA from
NT2 neuronal precursor cells treated 2-weeks mitotic
inhibitor after 5-weeks retinoic acid (RA) induction."

ORIGIN
Query Match 40.1%; Score 555; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 3.1e-290;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 CTATTTATAGATGAGATGATATACAGCCAACTGAGACACATTAATGTTTCTACGTC 888
DB 1 CTATTTATAGATGAGATGATATACAGCCAACTGAGACACATTAATGTTTCTACGTC 60
QY 889 CAAGAGGCTAATGTCGATCCAGATTTGAGAGAAATGTCGAAATACATCTGTTTC 948
DB 61 CAAGAGGCTAATGTCGATCCAGATTTGAGAGAAATGTCGAAATACATCTGTTTC 120
QY 949 ATGATCCCTGCTGTTCTCTGATCTTGAACACAGTCCAGATTTAGAGTCAAAACAAAT 1008
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DEFINITION sequence.
ACCESSION DA992396
VERSION DA992396.1 GI:83066687
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,U., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
JOURNAL PUBLISHED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@flj.com
NEO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
source Location/Qualifiers
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Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION sequence.
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VERSION DA990183.1 GI:82428308
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,U., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
JOURNAL PUBLISHED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@flj.com
NEO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
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Query Match 39.3%; Score 543; DB 9; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-283; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION L17N670205n1-20-D03 5', mRNA sequence.
ACCESSION CBI61269
VERSION CBI61269.1 GI:28147395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 541)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

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Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 20 row: D column: 03
High quality sequence stop: 541.
Location/Qualifiers
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Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

FEATURES

source

ORIGIN

Query Match 39.1%; Score 541; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.3e-282; Indels 0; Gaps 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1198	86.6	4038	US-08-969-125-8	Sequence 8, Appl1
4	1198	86.6	4038	US-09-545-002-8	Sequence 8, Appl1
5	1198	86.6	4039	US-09-949-016-223	Sequence 223, App
6	1198	86.6	4039	US-09-880-107-3856	Sequence 3856, Ap
7	1198	86.6	4039	US-09-543-679A-2903	Sequence 2903, Ap
8	1198	86.6	11927	US-09-193-707-5	Sequence 5, Appl1
9	1198	86.6	14978	US-09-543-679A-2905	Sequence 2905, Ap
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11	901	65.1	2355	US-09-313-942-29	Sequence 29, Appl1
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13	901	65.1	2382	US-09-313-942-31	Sequence 31, Appl1
14	901	65.1	2382	US-10-282-162-31	Sequence 31, Appl1
15	643	46.5	701	US-09-949-016-2679	Sequence 2679, Ap
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17	136	9.8	42975	US-09-949-016-11965	Sequence 11965, A
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21	71	5.1	1547	US-09-828-995B-51	Sequence 51, Appl1
22	62	4.5	1680	US-09-688-286D-1	Sequence 1, Appl1
23	48	3.5	483	US-09-828-995B-48	Sequence 48, Appl1

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31	23	1.7	12163	US-09-949-016-16030	Sequence 16030, A
32	23	1.7	12164	US-09-949-016-12202	Sequence 12202, A
33	22	1.6	30	US-08-969-125-5	Sequence 5, Appl1
34	22	1.6	30	US-09-545-002-5	Sequence 5, Appl1
35	22	1.6	30	US-09-828-034-7	Sequence 7, Appl1
36	22	1.6	50	US-08-846-020A-6	Sequence 6, Appl1
37	22	1.6	50	US-09-617-871-6	Sequence 6, Appl1
38	22	1.6	56	US-08-846-020A-4	Sequence 4, Appl1
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ALIGNMENTS

RESULT 1
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Sequence 3, Application US/09688286D
Patent No. 6911530
GENERAL INFORMATION:
APPLICANT: Willson, Tracey
APPLICANT: Nicola, Nicos
APPLICANT: Hilton, Douglas
APPLICANT: Metcalf, Donald
APPLICANT: Zhang, Jian
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding sam
FILE REFERENCE: 23199-215
CURRENT APPLICATION NUMBER: US/09/688, 286D
CURRENT FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: AU PM6135
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: AU PM7276
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: AU PM2208
PRIOR FILING DATE: 1996-09-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1383
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NAME/KEY: CDS
LOCATION: (61)..(1338)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1081	TCCACATCTACATACCATGTTACTATGTTCCAGTCATGCTGCGAGGTGCAATCATTA	1140
Db	1081	TCCACATCTACATACCATGTTACTATGTTCCAGTCATGCTGCGAGGTGCAATCATTA	1140
QY	1141	GTACTCTGCTTTTACCTTAAAAAGGCTCAAGATTAATATTCCTCCCAATTCCTGATCTCT	1200
Db	1141	GTACTCTGCTTTTACCTTAAAAAGGCTCAAGATTAATATTCCTCCCAATTCCTGATCTCT	1200
QY	1201	GGCAAGATTTTAAAGAAATGTTTGGAGCCAGAAATGATGATCTCTGCACCTGGAAGAG	1260
Db	1201	GGCAAGATTTTAAAGAAATGTTTGGAGCCAGAAATGATGATCTCTGCACCTGGAAGAG	1260

QY	1261	TACGACATCTATGGAAGCAAAACCAAGAGAGAAACGACCTGTGATGCGGATGTGA	1320
QY	1261	TACGACATCTATGGAAGCAAAACCAAGAGAGAAACGACCTGTGATGCGGATGTGA <td>1320</td>	1320
Db	1261	TACGACATCTATGGAAGCAAAACCAAGAGAGAAACGACCTGTGATGCGGATGTGA <td>1320</td>	1320
QY	1321	CTGAAGAAAGCCTCTCAGTGATGAGAGATATTTATTTTCACTCACTGATGACCTTGAG	1380
Db	1321	CTGAAGAAAGCCTCTCAGTGATGAGAGATATTTATTTTCACTCACTGATGACCTTGAG	1380
QY	1381	AGA 1383	
Db	1381	AGA 1383	

RESULT 2
US-09-543-679A-2902
; Sequence 2902, Application US/09543679A

```

1 GENERAL INFORMATION:
2 APPLICANT: NYCE, Jonathan W.
3 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
4 COMPOSITIONS, KIT & METHOD FOR TREATMENT
5 OF AIRWAY DISORDERS ASSOCIATED WITH
6 BRONCHOCONSTRICTION, LUNG INFLAMMATION,
7
8 NUMBER OF SEQUENCE ADDRESSES: 3111
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
11 STREET: 7 Clarke Drive
12 CITY: Cranbury
13 STATE: NJ
14 COUNTRY: USA
15 ZIP: 08512
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: CD-R
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: N/A
22
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/09/543,679A
25 FILING DATE: 13-Apr-2000
26 CLASSIFICATION: UNKNOWN
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 60/127,958
30 FILING DATE: 1998-08-03
31
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Amzel, Viviana
34 REGISTRATION NUMBER: 30,930
35 REFERENCE/DOCKET NUMBER: EPI-0067191b
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 609-409-3035
38 TELEFAX: 413-254-9245
39
40 TELEX: <Unknown>
41
42 INFORMATION FOR SEQ ID NO: 2902:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 3999 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48
49 SEQUENCE DESCRIPTION: SEQ ID NO: 2902:
50
51 US-09-543-679A-2902
52
53 Query Match      86.6%; Score 1198; DB 5; Length 3999;
54 Best Local Similarity 99.9%; Pred. No. 0;
55 Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
56
57 QY      135  CGCGCCTACGGAACCTCAGCCACCTGTGACAAATTGTAGTGTCTGTGTAACCTCTG 194
58      |||
59      111  CGGCCTACGGAACCTCAGCCACCTGTGACAAATTGTAGTGTCTGTGTAACCTCTG 170
60
61 QY      195  CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTGTATGTATGTA 254
62      |||
63      171  CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTGTATGTATGTA 230

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QY 255 TTTTATGATTTTGGGCAAAAGATTAAGAAAAATAGCTCCGAAAATCGTCTGTTCAAT 314
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Db 231 TTTTAGTCATTTTGGCGACAAAGATTAAGAAAAATAGCTCCGAAAATCGTCTGTTCAAT 290
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QY 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACCAATGA 374
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Db 291 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACCAATGA 350
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QY 375 GAGTGAAGGCTTGAATTTGTTGTAAGAAATGATCTCAACCCGAGAGGTATCTCTGA 434
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Db 351 GAGTGAAGGCTTGAATTTGTTGTAAGAAATGATCTCAACCCGAGAGGTATCTCTGA 410
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QY 435 GTCTGCTGTGACTGAATCTTCAATGATCTTGGCAACACCTGAGTCAATGAAGTCTTGTG 494
| | | | |
Db 411 GTCTGCTGTGACTGAATCTTCAATGATCTTGGCAACACCTGAGTCAATGAAGTCTTGTG 470
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QY 495 GCTTCCCTGGAAGAAATCCAGTCCCGACACTAATCTCTCTACTATTTGGGCAAGAG 554
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Db 471 GCTTCCCTGGAAGAAATCCAGTCCCGACACTAATCTCTCTACTATTTGGGCAAGAG 530
| | | | |
QY 555 CTGGAAGAAATTCATCAATGTGAAATCATCTTTAGAGAGAGCCCAATCTTGGTGTTC 614
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Db 531 CTGGAAGAAATTCATCAATGTGAAATCATCTTTAGAGAGAGCCCAATCTTGGTGTTC 590
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QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTCTTGAACCAACAGTGTCCAAATTAATGTG 674
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QY 675 CAAGATATGCAAGAAAAATTAACCATCTTCAATATATAGTCCCTTAACTTCCGCTGT 734
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Db 651 CAAGATATGCAAGAAAAATTAACCATCTTCAATATATAGTCCCTTAACTTCCGCTGT 710
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QY 735 GAAACCTGATCTCCCAATATTAATAAATCTCTCTCCCAAGATATGATCTTATATGTCGA 794
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Db 711 GAAACCTGATCTCCCAATATTAATAAATCTCTCTCCCAAGATATGATCTTATATGTCGA 770
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QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTGAAGATGAAGTCAATGA 854
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Db 771 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTGAAGATGAAGTCAATGA 830
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QY 855 CAGCCAACTGAGACACATATGTTTCTAAGTCCAGAGGCTTAATGTGAGAAATCCAGA 914
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Db 831 CAGCCAACTGAGACACATATGTTTCTAAGTCCAGAGGCTTAATGTGAGAAATCCAGA 890
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QY 915 ATTTGAGAAATGTGAGAAATATCAATCTTTTCAAGTCCAGAGGCTTAATGTGAGAAAT 974
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Db 891 ATTTGAGAAATGTGAGAAATATCAATCTTTTCAAGTCCAGAGGCTTAATGTGAGAAAT 950
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QY 975 TTTGAACACAGTCAAGATTAAGATCAAAACAAATTAAGTATGCTATGAGAGTCAAACT 1034
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Db 951 TTTGAACACAGTCAAGATTAAGATCAAAACAAATTAAGTATGCTATGAGAGTCAAACT 1010
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QY 1035 CTGGAATATTTGGAGCCCAAGAAATGATATAGTAAAGAGCCCAATTCACACTCTAAT 1094
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Db 1011 CTGGAATATTTGGAGCCCAAGAAATGATATAGTAAAGAGCCCAATTCACACTCTAAT 1070
| | | | |
QY 1095 AACCAATGTAATCTATGTTTCAATCTGTCGACAGTGTCAATATGATCTCTCTGCTTGA 1154
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Db 1071 AACCAATGTAATCTATGTTTCAATCTGTCGACAGTGTCAATATGATCTCTCTGCTTGA 1130
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QY 1155 CCTAATAAAGGCTCAAGATTTATATATCTCTCAATCTCTGATCTGGGCAAGATTTTGA 1214
| | | | |
Db 1131 CCTAATAAAGGCTCAAGATTTATATATCTCTCAATCTCTGATCTGGGCAAGATTTTGA 1190
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QY 1215 AGAATGTTTGGAGACCAAGATATGATATCTGCACTGGAAGAGTACAGATCTATGA 1274
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Db 1191 AGAATGTTTGGAGACCAAGATATGATATCTGCACTGGAAGAGTACAGATCTATGA 1250
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QY 1275 GAAAGCAACCAAGAGAGAAACCGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCTC 1334
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Db 1251 GAAAGCAACCAAGAGAGAAACCGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCTC 1310
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QY 1335 TCAGTATGAGATTAATTTATTTTATCTTCACTGTGACCTTGAGAGA 1383
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Db 1311 TCAGTATGAGATTAATTTATTTTATCTTCACTGTACCTTGAGAGA 1359
| | | | |
RESULT 3
US-08-969-125-8
Sequence 8, Application US/08969125B
Patent No. 6143871
GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125B
FILING DATE: 12-No. 6143871-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1323
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-08-969-125-8
Query Match 86.6%; Score 1198; DB 3; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CCGGCTACGGAACCTCAGCACCTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 194
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Db 120 CCGGCTACGGAACCTCAGCACCTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 179
| | | | |
QY 195 CACAGTAATATGACATGTGAATCCACCCGAGGAGCCAGCTCAAAATTTGATGCTATGCTGA 254
| | | | |
Db 180 CACAGTAATATGACATGTGAATCCACCCGAGGAGCCAGCTCAAAATTTGATGCTATGCTGA 239
| | | | |
QY 255 TTTTATGATTTTGGGACAAACAAGATTAAGAAATAGCTCCGGAATCTGCTTCAAT 314
| | | | |
Db 240 TTTTATGATTTTGGGACAAACAAGATTAAGAAATAGCTCCGGAATCTGCTTCAAT 299
| | | | |
QY 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACCAATGA 374
| | | | |
Db 300 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACCAATGA 359
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QY 375 GAGTGAAGACCTAGCATTTTGGTTGAAATATGATCTCAACCCCGAGAGGTATCTCGA 434
DB 360 GAGTGAAGACCTAGCATTTTGGTTGAAATATGATCTCAACCCCGAGAGGTATCTCGA 419
QY 435 GTCTGCTGAGACCTGATCAATGCAATTTGGCAACCTGAGTACATGAAAGTCTTG 494
DB 420 GTCTGCTGAGACCTGATCAATGCAATTTGGCAACCTGAGTACATGAAAGTCTTG 479
QY 495 GCTCCCTGGAGAGATACAGTCCCGACATTAATATCTCTACTATTTGGACAGAG 554
DB 480 GCTCCCTGGAGAGATACAGTCCCGACATTAATATCTCTACTATTTGGACAGAG 539
QY 555 CCTGGAAAAATTCATCATATGTGAAAAATCTTTAGAGAGCCATCTTTGGTGTTC 614
DB 540 CCTGGAAAAATTCATCATATGTGAAAAATCTTTAGAGAGCCATCTTTGGTGTTC 599
QY 615 CTTTGAATCGAACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGT 674
DB 600 CTTTGAATCGAACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGT 659
QY 675 CAAGATTAATGACAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGCT 734
DB 660 CAAGATTAATGACAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGCT 719
QY 735 GAAACCTGATCTCCCATATTAATAAACTCTCTCTCCACATGATGACCTATATGTGA 794
DB 720 GAAACCTGATCTCCCATATTAATAAACTCTCTCTCCACATGATGACCTATATGTGA 779
QY 795 ATGGAGATCCACAGATTTTATTTGACAGATGCTTATTTAGAGTAAAGTCAATA 854
DB 780 ATGGAGATCCACAGATTTTATTTGACAGATGCTTATTTAGAGTAAAGTCAATA 839
QY 855 CAGCCAACTGACACATTAATGTTTCTACGTCAGAGAGCTTAATGAGATCCAGA 914
DB 840 CAGCCAACTGACACATTAATGTTTCTACGTCAGAGAGCTTAATGAGATCCAGA 899
QY 915 ATTGAGAGAAATGTGAGACATATCTTTGTCATGTCCTGCTGCTTCTTCTGATAC 974
DB 900 ATTGAGAGAAATGTGAGACATATCTTTGTCATGTCCTGCTGCTTCTTCTGATAC 959
QY 975 TTTGAACACAGTGAAGATTAAGATCAAAATTAATGATTAAGTGAAGATCAAACT 1034
DB 960 TTTGAACACAGTGAAGATTAAGATCAAAATTAATGATTAAGTGAAGATCAAACT 1019
QY 1035 CTGAGTAATTTGAGCCCAAGAAATGATAGTAAAGACCAATTCACACTCTACAT 1094
DB 1020 CTGAGTAATTTGAGCCCAAGAAATGATAGTAAAGACCAATTCACACTCTACAT 1079
QY 1095 AACCATGTTACTGATTTTCCAGTCACTGTCGAGGTGCAATCAATGATCTCTGCTT 1154
DB 1080 AACCATGTTACTGATTTTCCAGTCACTGTCGAGGTGCAATCAATGATCTCTGCTT 1139
QY 1155 CCTAAAGAGCTCAAGATTAATTTTCCCTCAATTCCTGATCTCGGCAAGATTTTAA 1214
DB 1140 CCTAAAGAGCTCAAGATTAATTTTCCCTCAATTCCTGATCTCGGCAAGATTTTAA 1199
QY 1215 AGAAATGTTTGGAGACAGATGATGATCTGCACTGGAAGAGTACATCTATGA 1274
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QY 1275 GAAACCAACCAAGAGAGAAACGACCTCTGATGCTGATGAAACCTGGAAGAGCTC 1334
DB 1260 GAAACCAACCAAGAGAGAAACGACCTCTGATGCTGATGAAACCTGGAAGAGCTC 1319
QY 1335 TCAGTATGAGATTAATTTTATCTTCACTGATGAGTGAAGA 1383
DB 1320 TCAGTATGAGATTAATTTTATCTTCACTGATGAGTGAAGA 1368

RESULT 4
US-09-545-002-8
; Sequence 8, Application US/09545002
; Patent No. 6743604

GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/545,002
FILING DATE: 12-NO. 6743604-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125
FILING DATE: 12-NO. 6743604-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1323
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-545-002-8
Query Match 86.6%; Score 1198; DB 3; Length 4038;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTACGGAACCTCAGCGACCTGTGACAAATTTGAGTGTCTGTGAAACCTCTG 194
DB 120 CGGCGCTACGGAACCTCAGCGACCTGTGACAAATTTGAGTGTCTGTGAAACCTCTG 179
QY 195 CACAGTAATATGACATGATGATCCACCGAGGAGCCAGCTCAATTTAGTATAGTA 254
DB 180 CACAGTAATATGACATGATGATCCACCGAGGAGCCAGCTCAATTTAGTATAGTA 239
QY 255 TTTTATGCTATTTTGGGCAACAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 314
DB 240 TTTTATGCTATTTTGGGCAACAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 299
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 374
DB 300 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 359
QY 375 GAGTGAAGACCTAGCATTTTGGTTGAAATATGATCTCAACCCCGAGAGGTATCTCGA 434
DB 360 GAGTGAAGACCTAGCATTTTGGTTGAAATATGATCTCAACCCCGAGAGGTATCTCGA 419
QY 435 GTCTGCTGAGACCTGATCAATGCAATTTGGCAACCTGAGTACATGAAAGTCTTG 494

Db 420 GTCTCTGTGACGTGAGCTTCAATGATTTGGCACAACCTGAGCTAATGAAGTGTCTTG 479
Qy 495 GCTCCCTGGAAGAAATACAGTCCCGACACATACTACTACTATTGGACAGAG 554
Db 480 GCTCCCTGGAAGAAATACAGTCCCGACACATACTACTACTATTGGACAGAG 539
Qy 555 CTTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACCTTGGTTGTC 614
Db 540 CTTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACCTTGGTTGTC 599
Qy 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 674
Db 600 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 659
Qy 675 CAAGATATATGACGAGAAATTAACATCTTCAATATAGTGTCTTAACTTCCCGGT 734
Db 660 CAAGATATATGACGAGAAATTAACATCTTCAATATAGTGTCTTAACTTCCCGGT 719
Qy 735 GAAACCTGATCTTCACATATTAATAAACTCTCTCTTCACAAATGATGACCTATATGTGA 794
Db 720 GAAACCTGATCTTCACATATTAATAAACTCTCTCTTCACAAATGATGACCTATATGTGA 779
Qy 795 ATGGAGAAATCCACAGAAATTTTATAGCAAGTCCCTATTTTATGAGTAGAGTCAATAA 854
Db 780 ATGGAGAAATCCACAGAAATTTTATAGCAAGTCCCTATTTTATGAGTAGAGTCAATAA 839
Qy 855 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAGTCAAT 914
Db 840 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAGTCAAT 899
Qy 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGTTCTCTGATAC 974
Db 900 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGTTCTCTGATAC 959
Qy 975 TTTGAAACACGTGACAAATAGAGTCAAAACAATAGTTATGCTATAGAGTAGCAAACT 1034
Db 960 TTTGAAACACGTGACAAATAGAGTCAAAACAATAGTTATGCTATAGAGTAGCAAACT 1019
Qy 1035 CTGAGATATTTGAGGCAAGAAATGAGTATAGGTAAGAGCGCAATCCACACTGAT 1094
Db 1020 CTGAGATATTTGAGGCAAGAAATGAGTATAGGTAAGAGCGCAATCCACACTGAT 1079
Qy 1095 AACCATGTTACTGATTTTCCAGTCAATGTCGAGAGTCAATAGTACTCTGCTTAA 1154
Db 1080 AACCATGTTACTGATTTTCCAGTCAATGTCGAGAGTCAATAGTACTCTGCTTAA 1139
Qy 1155 CCTAAAAAGGCTCAAGATTTATATATTCCTCCAAATCTGATCTGGAAGATTTTAA 1214
Db 1140 CCTAAAAAGGCTCAAGATTTATATATTCCTCCAAATCTGATCTGGAAGATTTTAA 1199
Qy 1215 AGAAATGTTTGGAGACAGAAATGATGATCTGCACTGGAAGAGTACATCTTGA 1274
Db 1200 AGAAATGTTTGGAGACAGAAATGATGATCTGCACTGGAAGAGTACATCTTGA 1259
Qy 1275 GAAGCAAAACCAAGAGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334
Db 1260 GAAGCAAAACCAAGAGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1319
Qy 1335 TCAGTATGAGATATTTATTTTAACTTCACTGATGACCTTGAGAAAG 1383
Db 1320 TCAGTATGAGATATTTATTTTAACTTCACTGATGACCTTGAGAAAG 1368

RESULT 5
US-09-949-016-223
; Sequence 223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-223

Query Match 86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGCCCTAGGAAATCTAGCCACCTGTGACAAATTTAGTGTCTGTGAAACCTCTG 194
Db 121 CGGCCCTAGGAAATCTAGCCACCTGTGACAAATTTAGTGTCTGTGAAACCTCTG 180
Qy 195 CACAGTAATATGACATGAGATCCACCGAGGAGCCAGCTCAATTTGATGATGTA 254
Db 181 CACAGTAATATGACATGAGATCCACCGAGGAGCCAGCTCAATTTGATGATGTA 240
Qy 255 TTTTATGATTTTGGCGACAAACAGATTAAGAAATAGCTCCGGAACCTGCTCAAT 314
Db 241 TTTTATGATTTTGGCGACAAACAGATTAAGAAATAGCTCCGGAACCTGCTCAAT 300
Qy 315 AGAAGTACCCCTGAATAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 374
Db 301 AGAAGTACCCCTGAATAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 360
Qy 375 GAGTGAAGAACCTAGATTTTGGTTGAAATATGATCTCACCCCAAGGTGATCTCTGA 434
Db 361 GAGTGAAGAACCTAGATTTTGGTTGAAATATGATCTCACCCCAAGGTGATCTCTGA 420
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Db 421 GTCTGCTGTGATGAACTTCAATGATTTGGCAACAACCTGATCAATGAAGTGTCTTG 480
Qy 495 GCTCCCTGGAAGAAATACAGTCCCGACATACTAATCTCTACATATGGGACAGAG 554
Db 481 GCTCCCTGGAAGAAATACAGTCCCGACATACTAATCTCTACATATGGGACAGAG 540
Qy 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACTTTGGTTGTC 614
Db 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACTTTGGTTGTC 600
Qy 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 674
Db 601 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 660
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Db 661 CAAGATATATGACGAGAAATTAACATCTTCAATATAGTGTCTTAACTTCCCGGT 720
Qy 735 GAAACCTGATCTTCACATATTAATAAACTCTCTCTTCACAAATGATGACCTATATGTGA 794
Db 721 GAAACCTGATCTTCACATATTAATAAACTCTCTCTTCACAAATGATGACCTATATGTGA 780
Qy 795 ATGGAGAAATCCACAGAAATTTATAGCAAGTCCCTATTTTATGAGTAGAGTCAATAA 854
Db 781 ATGGAGAAATCCACAGAAATTTATAGCAAGTCCCTATTTTATGAGTAGAGTCAATAA 840
Qy 855 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAGTCAAT 914
Db 841 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAGTCAAT 900
Qy 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGTTCTCTGATAC 974

Db 901 ATTGAGAGAAATGTGAGATATACATCTGTTCATGTCCTGTGTTCTTCTGTATAC 960
QY 975 TTGGAACAGAGTCAGATTAAGATCAAAACAATAATTATGCTATGAGATGACAAACT 1034
Db 961 TTGGAACAGTCAGATTAAGATCAAAACAATAATTATGCTATGAGATGACAAACT 1020
QY 1035 CTGAGATATTGGAGCCAGAAATGAGTATAGGTAGAGACCGCAATTCACACTCTACAT 1094
Db 1021 CTGAGATATTGGAGCCAGAAATGAGTATAGGTAGAGACCGCAATTCACACTCTACAT 1080
QY 1095 AACCATGTTACTGATTTGTCCTGATCAGTCGTCGAGGTCGATCATATGATCTCCGCTTAA 1154
Db 1081 AACCATGTTACTGATTTGTCCTGATCAGTCGTCGAGGTCGATCATATGATCTCCGCTTAA 1140
QY 1155 CCTAAAGAGCTCAAGATTTATTTATTTCTCTCCATTTCTGATCTGGCAAGATTTTAA 1214
Db 1141 CCTAAAGAGCTCAAGATTTATTTATTTCTCTCCATTTCTGATCTGGCAAGATTTTAA 1200
QY 1215 AGAAATGTTTGGAGACCCAGATGATGATCTTGCACCTGGAAGATGACATCTATGA 1274
Db 1201 AGAAATGTTTGGAGACCCAGATGATGATCTTGCACCTGGAAGATGACATCTATGA 1260
QY 1275 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTTC 1334
Db 1261 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db 1321 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

RESULT 6
US-09-880-107-3856
; Sequence 3856, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880.107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3856
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Genbank Accession No. 6974667 Y10659
US-09-880-107-3856

Query Match 86.6%; Score 1198; DB 4; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTACGAACTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 194
Db 121 CGGCGCTACGAACTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 180
QY 195 CACAGTAATATGACATGGAATCCACCAGAGGAGCCAGCTCAATTTGATGCTATGCTA 254
Db 181 CACAGTAATATGACATGGAATCCACCAGAGGAGCCAGCTCAATTTGATGCTATGCTA 240
QY 255 TTTTACTGATTTTGGGAGCAACCAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 314
Db 241 TTTTACTGATTTTGGGAGCAACCAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 300

QY 315 AGAATGATCCCTGATGATGAGAGATTTGTCTGCAAGTGGGGTCCCAAGTATGACCAATGA 374
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QY 375 GAGTGAAGAGCTTACGATTTTGGTTGAAAAATGCAATCTCAACCCCGAAGGATATCTCTGA 434
Db 361 GAGTGAAGAGCTTACGATTTTGGTTGAAAAATGCAATCTCAACCCCGAAGGATATCTCTGA 420
QY 435 GTCTGCTGATGATGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 494
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QY 495 GCTCCCTGGAAGGATATGACAGTCCGACATTAATTAATTAATTAATTAATTAATTAATTAAT 554
Db 481 GCTCCCTGGAAGGATATGACAGTCCGACATTAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 555 CCTGGAAGAAATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
Db 541 CCTGGAAGAAATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 615 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
Db 601 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 675 CAAAGATTAATGACAGAAAAATTAACCATCTTCAATTAATAGCTTTAACTTCCGCTGT 734
Db 661 CAAAGATTAATGACAGAAAAATTAACCATCTTCAATTAATAGCTTTAACTTCCGCTGT 720
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Db 721 GAAACCTGATCCCTCCATTTTAAACCTTCCCTCCCAATGATGATGATGATGATGATGATGAT 780
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Db 781 ATGGAGAAATCCACAGAAATTTTATGACAGATGCTATTTTATGAGTGAAGTCAATTA 840
QY 855 CAGCCAACTGAGACATATATGTTTCTACGTCGCAAGAGCTTAAATGTGAGATCCAGA 914
Db 841 CAGCCAACTGAGACATATATGTTTCTACGTCGCAAGAGCTTAAATGTGAGATCCAGA 900
QY 915 ATTGAGAGAAATGTGAGAAATATCAATCTGTTTCAATGATGATGATGATGATGATGATGAT 974
Db 901 ATTGAGAGAAATGTGAGAAATATCAATCTGTTTCAATGATGATGATGATGATGATGATGAT 960
QY 975 TTGGAACAGTCAGATTAAGATCAAAACAATAATTATGATGATGATGATGATGATGATGAT 1034
Db 961 TTGGAACAGTCAGATTAAGATCAAAACAATAATTATGATGATGATGATGATGATGATGAT 1020
QY 1035 CTGAGATATTGGAGCCAGAAATGAGTATAGGTAGAGACCGCAATTCACACTCTACAT 1094
Db 1021 CTGAGATATTGGAGCCAGAAATGAGTATAGGTAGAGACCGCAATTCACACTCTACAT 1080
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Db 1081 AACCATGTTACTGATTTGTCCTGATCAGTCGTCGAGGTCGATCATATGATCTCCGCTTAA 1140
QY 1155 CCTAAAGAGCTCAAGATTTATTTATTTCTCTCCATTTCTGATCTGGCAAGATTTTAA 1214
Db 1141 CCTAAAGAGCTCAAGATTTATTTATTTCTCTCCATTTCTGATCTGGCAAGATTTTAA 1200
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Db 1201 AGAAATGTTTGGAGACCCAGATGATGATCTTGCACCTGGAAGATGACATCTATGA 1260
QY 1275 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTTC 1334
Db 1261 GAAGCAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db 1321 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

RESULT 7
US-09-543-679A-2903
; Sequence 2903, Application US/09543679A
; Patent No. 7034007
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LONG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; City: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2903:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4039 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2903:
US-09-543-679A-2903
Query Match 86.6%; Score 1198; DB 5; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTACGGAAGTCTGACCAATTTGAGTGTCTGTGTAACCTCTG 194
DB 121 CGGCGCTACGGAAGTCTGACCAATTTGAGTGTCTGTGTAACCTCTG 180
QY 195 CACAGTAATGTGACATGGAATCCACCCGAGGAGCCAGTCAATTTGATGTAAGTA 254
DB 181 CACAGTAATGTGACATGGAATCCACCCGAGGAGCCAGTCAATTTGATGTAAGTA 240
QY 255 TTTTATGATTTTGGGACAAACAAGATAAGAAATAGTCCGGAATCGTGGTCAAT 314
DB 241 TTTTATGATTTTGGGACAAACAAGATAAGAAATAGTCCGGAATCGTGGTCAAT 300
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DB 301 AGAAGTAACCTGATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 360
QY 375 GAGTGAGAGCTAGCATTTTGGTGAATAATGATCTACCCCGAAGATGATCTGTA 434
DB 361 GAGTGAGAGCTAGCATTTTGGTGAATAATGATCTACCCCGAAGATGATCTGTA 420
QY 435 GTCTGTGTGACTGAACCTTCATGATTTTGGCAACCTGAGTACATGAAGTGTCTTG 494

DB 421 GTCTGTGTGACTGAGCTTCATGATCTTTGGCAACCTGAGTACATGAAGTGTCTTG 480
QY 495 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATTAATCTCTACTATTTGGCAGAG 554
DB 481 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATTAATCTCTACTATTTGGCAGAG 540
QY 555 CTTGGAATAATTCATGATGTAAGAAATCATCTTTAGAGAGGCGCAATCTTGGTGTG 614
DB 541 CTTGGAATAATTCATGATGTAAGAAATCATCTTTAGAGAGGCGCAATCTTGGTGTG 600
QY 615 CTTGATCTGACCAAGATGAGATTCAGTTTGAACAACAGTGTCCAAATATATGT 674
DB 601 CTTGATCTGACCAAGATGAGATTCAGTTTGAACAACAGTGTCCAAATATATGT 660
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DB 661 CAAGATATGACAGAAATAATTAACATCTCTCAATATATGTGCTTTACTCCGTGT 720
QY 735 GAAACCTGATCTTCACATATTAATAAATCTCTCTCCACAAATGATGACCTATATGCA 794
DB 721 GAAACCTGATCTTCACATATTAATAAATCTCTCTCCACAAATGATGACCTATATGCA 780
QY 795 ATGGAGAAATCCACAGAAATTTATAGCAGATGCTATTTTATGAGTGAAGTCAATA 854
DB 781 ATGGAGAAATCCACAGAAATTTATAGCAGATGCTATTTTATGAGTGAAGTCAATA 840
QY 855 CAGCCAAATGACACATATATGTTTCTACAGTCCAAAGGCTTAATGTGAATCCAGA 914
DB 841 CAGCCAAATGACACATATATGTTTCTACAGTCCAAAGGCTTAATGTGAATCCAGA 900
QY 915 ATTGAGAGAAATGTGAGAAATCATCTTGTTCATGAGTCCGTGCTCTCTCTGATAC 974
DB 901 ATTGAGAGAAATGTGAGAAATCATCTTGTTCATGAGTCCGTGCTCTCTCTGATAC 960
QY 975 TTTGAACACAGTCAAGATTAAGTCAAAACAAATTAAGTATGCTATGAGATGACA 1034
DB 961 TTTGAACACAGTCAAGATTAAGTCAAAACAAATTAAGTATGAGATGACA 1020
QY 1035 CTGAGATTAATGAGCCAAAGAAATGAGTATAGTGAAGCGCAATTCACACTCTCAT 1094
DB 1021 CTGAGATTAATGAGCCAAAGAAATGAGTATAGTGAAGCGCAATTCACACTCTCAT 1080
QY 1095 AACCATGTTATCTATTTGTTCCAGTCAATCGTCGAGGAGTCAATATGATCTCTGCTTTA 1154
DB 1081 AACCATGTTATCTATTTGTTCCAGTCAATCGTCGAGGAGTCAATATGATCTCTGCTTTA 1140
QY 1155 CTTAAAAAGGCTCAAGATTAATTAATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1214
DB 1141 CTTAAAAAGGCTCAAGATTAATTAATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1200
QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAGTACATCTATGA 1274
DB 1201 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAGTACATCTATGA 1260
QY 1275 GAAGCAAAACCAAGAGAAACCGACCTGTGATGCTGATGAAACCTGAAAGAAAGCTC 1334
DB 1261 GAAGCAAAACCAAGAGAAACCGACCTGTGATGCTGATGAAACCTGAAAGAAAGCTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGGAAGA 1383
DB 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGGAAGA 1369
RESULT 8
US-09-193-707-5
; Sequence 5, Application US/09193707
; Patent No. 6524792
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.

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; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,  
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH  
; FILE REFERENCE: 8358-0005-999  
; CURRENT APPLICATION NUMBER: US/09/193,707  
; CURRENT FILING DATE: 1998-11-17  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 11927  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-193-707-5  
  
Query Match      86.6%; Score 1198; DB 3; Length 11927;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY      135  CCGGCTAGGAAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 134  
DB      7763  CCGGCTACGAAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG 7822  
QY      195  CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATAGTA 254  
DB      7823  CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATAGTA 7882  
QY      255  TTTTACTATTTTGGGACAAACAAGATAAGAAATAGCTCCGAAATCTGCTCAAT 314  
DB      7883  TTTTACTATTTTGGGACAAACAAGATAAGAAATAGCTCCGAAATCTGCTCAAT 7942  
QY      315  AGAAGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGTTCCAGTGTACACCAATGA 374  
DB      7943  AGAAGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGTTCCAGTGTACACCAATGA 8002  
QY      375  GAGTGAGAGCCCTAGATTTTGGTTGAAAAATGATCTACCCCGAAGGATATCTGTA 434  
DB      8003  GAGTGAGAGCCCTAGATTTTGGTTGAAAAATGATCTACCCCGAAGGATATCTGTA 8062  
QY      435  GTCTGCTGTAAGTAATCAATGATGATTTGGCAAACTGAGTACATGAGTGTCTTG 494  
DB      8063  GTCTGCTGTAAGTAATCAATGATGATTTGGCAAACTGAGTACATGAGTGTCTTG 8122  
QY      495  GCTCCCTGGAAGAAATACCAAGTCCGACATACTATCTCTACTATTGGACAGAG 554  
DB      8123  GCTCCCTGGAAGAAATACCAAGTCCGACATACTATCTCTACTATTGGACAGAG 8182  
QY      555  CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATACTTTGGTTGTC 614  
DB      8183  CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATACTTTGGTTGTC 8242  
QY      615  CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGAGTCCAAAATAATGT 674  
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QY      675  CAAAGTAATGACGAAAAATTAACCATCTTCAATATAGTCTTTAACTTCCGCTGT 734  
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QY      735  GAAACCTGATCCCTCCATTTAAAAAACCCTCTTCCACAATGATGACCTATATGCA 794  
DB      8363  GAAACCTGATCCCTCCATTTAAAAAACCCTCTTCCACAATGATGACCTATATGCA 8422  
QY      795  ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTATGAGTAGAAGTCAATA 854  
DB      8423  ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTATGAGTAGAAGTCAATA 8482  
QY      855  CAGCCAAATGAGACACATATATTTTCTAGCTCCAGAGGCTTAATGTGAGAAATCAG 914  
DB      8483  CAGCCAAATGAGACACATATATTTTCTAGCTCCAGAGGCTTAATGTGAGAAATCAG 8542  
QY      915  ATTGAGAGAAATGAGAGAAATCAATCTGTTCAAGGTCCTCGGCTTCTCTGATAC 974  
DB      8543  ATTGAGAGAAATGAGAGAAATCAATCTGTTCAAGGTCCTCGGCTTCTCTGATAC 8502
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QY      975  TTTGAACACAGTCAGATAAGTCAAAACAATAAGTTATGCTATAGAGATGACAAACT 1034  
DB      8603  TTTGAACACAGTCAGATAAGTCAAAACAATAAGTTATGCTATAGAGATGACAAACT 8662  
QY      1035  CTGAGTAATTTGAGCCAGAAATAGGTATAGGTAAAGCCCAATTCACACTCAACT 1094  
DB      8663  CTGAGTAATTTGAGCCAGAAATAGGTATAGGTAAAGCCCAATTCACACTCAACT 8722  
QY      1095  AACCATGTACTCATTTGTCAGTCACTGTCGAGGTGCAATCATATCTCTGCTTTA 1154  
DB      8723  AACCATGTACTCATTTGTCAGTCACTGTCGAGGTGCAATCATATCTCTGCTTTA 8782  
QY      1155  CCTAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGATCTGCGAAGATTTTAA 1214  
DB      8783  CCTAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGATCTGCGAAGATTTTAA 8842  
QY      1215  AGAAATGTTTGAAGACCAAGATATATCTGCACTGGAAGAAATGACATCATATGA 1274  
DB      8843  AGAAATGTTTGAAGACCAAGATATATCTGCACTGGAAGAAATGACATCATATGA 8902  
QY      1275  GAAGCAAAACCAAGAGAAACGACTCTGTAGTGTATAGAAAACCTGAAGAACCTTC 1334  
DB      8903  GAAGCAAAACCAAGAGAAACGACTCTGTAGTGTATAGAAAACCTGAAGAACCTTC 8962  
QY      1335  TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB      8963  TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 9011  
  
RESULT 9  
US-09-543-679A-2905  
; Sequence 2905, Application US/09543679A  
; Patent No. 7034007  
; GENERAL INFORMATION:  
; APPLICANT: NYCE, Jonathan W.  
; TITLE OF INVENTION: LOW ADENOSSINE ANTI-SENSE OLIGONUCLEOTIDE,  
; COMPOSITIONS, KIT & METHOD FOR TREATMENT  
; OF AIRWAY DISORDERS ASSOCIATED WITH  
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,  
; NUMBER OF SEQUENCES: 3111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-R  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: N/A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/543,679A  
; FILING DATE: 13-Apr-2000  
; CLASSIFICATION: UNKNOWN  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/127,958  
; FILING DATE: 1998-08-03  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-0067191b  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2905:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14978 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2905;
US-09-543-679A-2905

Query Match 86.6%; Score 1198; DB 5; Length 14978;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

135 CGGCGCTACGGAATCTGACCACTGTCGACAAATTTGAGTCTCTGTTGAAAACCTGTG 194
1381 CGGCGCTACGGAATCTGACCACTGTCGACAAATTTGAGTCTCTGTTGAAAACCTGTG 1440
195 CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTGAGTCTATGCTA 254
1441 CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTGAGTCTATGCTA 1500
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1501 TTTTAGTCATTTTGGCCGCAACAAAGATTAAGAAAATAGCTCCGGAATCTGCTTCAAT 1560
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1561 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGTCCTGATGACCAATGA 1620
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1621 GAGTGAGAGCCCTGACATTTTGTGTAATAATGATCTCACCCCGAGAGGTGATCTGA 1680
435 GTCTGCTGTGACTTAATCTTCAATGATTTGGCAACAACCTGACTACATGAAGTGTCTG 494
1681 GTCTGCTGTGACTTAATCTTCAATGATTTGGCAACAACCTGACTACATGAAGTGTCTG 1740
495 GCTCCCTGGAAGAAATACAGTCCCGACATCAATCTCTACTATTGGGCAACAAG 554
1741 GCTCCCTGGAAGAAATACAGTCCCGACATCAATCTCTACTATTGGGCAACAAG 1800
555 CTTGGAATAATTCATCATGTGTAATAATCTTTAGAGAGGCCAATATCTTGGTGTG 614
1801 CTTGGAATAATTCATCATGTGTAATAATCTTTAGAGAGGCCAATATCTTGGTGTG 1860
615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATATGT 674
1861 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATATGT 1920
675 CAAGATTAATGCAAGGAAATTAATTAACATCTTCAATATATGCTTAACTTCCGCTGT 734
1921 CAAGATTAATGCAAGGAAATTAATTAACATCTTCAATATATGCTTAACTTCCGCTGT 1980
735 GAAACCTGATCTTCCATATTAATAAATCTCTCTTCCACATGATGACCTATATGTGCA 794
1981 GAAACCTGATCTTCCATATTAATAAATCTCTCTTCCACATGATGACCTATATGTGCA 2040
795 ATGGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTATGAGTGAAGTCAATAA 854
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2101 CAGGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGCTTAAATGAGATCCAGA 2160
915 ATTTGAGAGAAATGAGAGATATCATCTTGTTCATGCTGCTGCTGCTTCTCTGATAC 974
2161 ATTTGAGAGAAATGAGAGATATCATCTTGTTCATGCTGCTGCTGCTTCTCTGATAC 2220
975 TTTTGAACACGTCAGATTAAGAGTCAAAACAATATGCTATGCTATGAGATGCAAACT 1034
2221 TTTTGAACACGTCAGATTAAGAGTCAAAACAATATGCTATGCTATGAGATGCAAACT 2280
1035 CTGAGATTAATGAGGCAAGAAATGAGTATAGTGAAGAGCAATTCACACTCTCAT 1094
2281 CTGAGATTAATGAGGCAAGAAATGAGTATAGTGAAGAGCAATTCACACTCTCAT 2340
1095 AACCATGTTACTCATTTGTTCCAGTCGTCGAGGTGCAATCATAGTACTCTGCTTTTA 1154

2341 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTSCAATCATAGTACTCTGCTTTA 2400
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2401 CCTAAAAAGCTCAAGATTAATATATATCCCTCCCAATTCCTGATCTGCGCAAGATTTTAA 2460
1215 AGAATGTTTGGAGACCGAATGATGATGATCTGCACTGGAAGAGTTCGACATCTATGA 1274
2461 AGAATGTTTGGAGACCGAATGATGATGATGATCTGCACTGGAAGAGTTCGACATCTATGA 2520
1275 GAAGCAAAACCAAGGAGAAACCGAATCTGATGCTGATAGAAAACCTGAAGAAAGCTTC 1334
2521 GAAGCAAAACCAAGGAGAAACCGAATCTGATGCTGATAGAAAACCTGAAGAAAGCTTC 2580
1335 TCAGTGAATGAGATTAATTTTATTTTACCTTCACTGTCGACTTGGAGAGA 1383
2581 TCAGTGAATGAGATTAATTTTATTTTACCTTCACTGTCGACTTGGAGAGA 2629

RESULT 10
US-09-825-561A-81
Sequence 81, Application US/09825561A
Patent No. 6777539
GENERAL INFORMATION:
APPLICANT: Sprechter, Cindy A.
APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(966)
US-09-825-561A-81

Query Match 65.1%; Score 901; DB 3; Length 966;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

135 CGGCGCTACGGAATCTGACCACTGTCGACAAATTTGAGTCTCTGTTGAAAACCTGTG 194
15 CGGCGCTACGGAATCTGACCACTGTCGACAAATTTGAGTCTCTGTTGAAAACCTGTG 74
195 CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTGAGTCTATGCTA 254
75 CACAGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTGAGTCTATGCTA 134
255 TTTTAGTCATTTTGGGCAACAACAAGTAAGAAATATGCTCCGGAATCTGCTTCAAT 314
135 TTTTAGTCATTTTGGGCAACAACAAGTAAGAAATATGCTCCGGAATCTGCTTCAAT 194
315 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGTCCTGATGACCAATGA 374
195 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGTCCTGATGACCAATGA 254
375 GAGTGAGAGCCCTGACATTTTGTGTAATAATGATCTCACCCCGAGAGGTGATCTGA 434
255 GAGTGAGAGCCCTGACATTTTGTGTAATAATGATCTCACCCCGAGAGGTGATCTGA 314


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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT FILING DATE: 2002-10-28
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (2352)
US-10-282-162-29
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Query Match 65.1%; Score 901; DB 3; Length 2355;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 195 CACAGTAATATGACATGATGATCCAGCCGAGGAGCCAGCTCAATTTGATGATGATGATG 254
DB 774 CACAGTAATATGACATGATGATCCAGCCGAGGAGCCAGCTCAATTTGATGATGATGATG 833
QY 255 TTTTATGATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 314
DB 834 TTTTATGATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 893
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGTA 374
DB 894 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGTA 953
QY 375 GAGTGAAGAACCTTACATTTTGGTGAATAATGATCTCAACCCGAGAGGTATCTCTGA 434
DB 954 GAGTGAAGAACCTTACATTTTGGTGAATAATGATCTCAACCCGAGAGGTATCTCTGA 1013
QY 435 GTCTGCTGTACATGATTTGATGATTTGGGACCAACCTGAGCTACATGAAAGTGTCTTG 494
DB 1014 GTCTGCTGTACATGATTTGATGATTTGGGACCAACCTGAGCTACATGAAAGTGTCTTG 1073
QY 495 GCTCCCTGGAAGAAATCCAGTCCGACATTAATCTCTCTACTATTTGGGACCAAG 554
DB 1074 GCTCCCTGGAAGAAATCCAGTCCGACATTAATCTCTCTACTATTTGGGACCAAG 1133
QY 555 CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATCTTTGGTGTTC 614
DB 1134 CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATCTTTGGTGTTC 1193
QY 615 CTTTGTATCTGACCAAGATGATTTGCAAGTTTGAACAACAGTGTCCAATATGTGT 674
DB 1194 CTTTGTATCTGACCAAGATGATTTGCAAGTTTGAACAACAGTGTCCAATATGTGT 1253
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QY 975 TTGGAACAGATGAGAAATGAGTCAAAACAAATTAATTTATGATGATGATGATGATGAT 1034
DB 1554 TTGGAACAGATGAGAAATGAGTCAAAACAAATTAATTTATGATGATGATGATGATGAT 1613
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DB 1614 CTGAGTAATTTGAGCCCAAGAAATGAGTATATGATGATGATGATGATGATGATGAT 1665
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RESULT 13

US-09-313-942-31

Sequence 31, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203-A

CURRENT FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 2382

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1) ... (2379)

US-09-313-942-31

Query Match 65.1%; Score 901; DB 3; Length 2382;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 135 CGGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194
DB 78 CGGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 137
QY 195 CACAGTAATATGACATGATGATCCAGCCGAGGAGCCAGCTCAATTTGATGATGATGATG 254
DB 138 CACAGTAATATGACATGATGATCCAGCCGAGGAGCCAGCTCAATTTGATGATGATGATG 197
QY 255 TTTTATGATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 314
DB 198 TTTTATGATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 257
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGTA 374
DB 258 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGTA 317
QY 375 GAGTGAAGAACCTTACATTTTGGTGAATAATGATCTCAACCCGAGAGGTATCTCTGA 434
DB 318 GAGTGAAGAACCTTACATTTTGGTGAATAATGATCTCAACCCGAGAGGTATCTCTGA 377
QY 435 GTCTGCTGTACATGATTTGATGATTTGGGACCAACCTGAGCTACATGAAAGTGTCTTG 494
DB 378 GTCTGCTGTACATGATTTGATGATTTGGGACCAACCTGAGCTACATGAAAGTGTCTTG 437
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Db 438 GCTCCCTGGAAGGAATACCAATGCCACACTAACTTACTCTTACTATTGGAACAGAG 497
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Qy 735 GAAACCTGATCTCCATATTTAAACCTCTCTTCCCAATGATGACCTATATGTGA 794
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Db 858 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTGTATC 917
Qy 975 TTTGAACACAGTCAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACT 1034
Db 918 TTTGAACACAGTCAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACT 977
Qy 1035 CTGAGATAATGGAGCCAAAGAAATGATAGTTAGTAAGAGCGCAATTCACCA 1086
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RESULT 14
US-10-282-162-31
; Sequence 31, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 2382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2379)
US-10-282-162-31

Query Match 65.1%; Score 901; DB 3; Length 2382;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 135 CGCGCTACGAAACTCAGCCACTGTGACAAATTTAGAGTGTCTGTTGAAGAACTCTG 194
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Qy 195 CACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAAAATTTAGTATATGTA 254
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Db 978 CTGAGATAATGGAGCCAAAGAAATGATAGTTAGTAAGAGCGCAATTCACCA 1029

RESULT 15
US-09-949-016-2679
; Sequence 2679, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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GenCore version 5.1.9
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1198	86.6	4009	16 US-11-182-384A-3	Sequence 3, Appl1
3	1198	86.6	4009	16 US-11-183-599A-3	Sequence 3, Appl1
4	1198	86.6	4038	8 US-10-671-697-8	Sequence 8, Appl1
5	1198	86.6	4039	3 US-09-962-832-160	Sequence 16, Appl
6	1198	86.6	4039	3 US-09-880-107-3856	Sequence 3856, App
7	1198	86.6	4039	7 US-10-172-118-633	Sequence 633, App
8	1198	86.6	4039	8 US-10-342-887-633	Sequence 633, App
9	1198	86.6	4039	10 US-10-843-641A-6046	Sequence 6046, App
10	1198	86.6	4468	3 US-09-971-392-58	Sequence 58, Appl1
11	1189	86.0	3880	3 US-09-822-846-109	Sequence 109, App
12	1179	85.2	1383	6 US-10-036-568-3	Sequence 3, Appl1
13	1138	82.3	3906	12 US-10-745-586-32	Sequence 32, Appl1
14	1105	79.9	1284	10 US-10-850-270-3	Sequence 3, Appl1
15	1096	79.2	1572	9 US-10-278-698-6	Sequence 6, Appl1
16	1096	79.2	1572	9 US-10-278-698-520	Sequence 520, App
17	901	65.1	966	3 US-09-825-561A-81	Sequence 81, Appl1

18	901	65.1	966	9 US-10-872-087-81	Sequence 81, Appl1
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20	901	65.1	2343	6 US-10-287-035-33	Sequence 33, Appl1
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22	901	65.1	2355	3 US-09-935-868-29	Sequence 29, Appl1
23	901	65.1	2355	6 US-10-287-035-29	Sequence 29, Appl1
24	901	65.1	2355	7 US-10-282-162-29	Sequence 29, Appl1
25	901	65.1	2355	13 US-11-134-114-29	Sequence 29, Appl1
26	901	65.1	2382	3 US-09-313-942-31	Sequence 31, Appl1
27	901	65.1	2382	3 US-09-935-868-31	Sequence 31, Appl1
28	901	65.1	2382	6 US-10-287-035-31	Sequence 31, Appl1
29	901	65.1	2382	7 US-10-282-162-31	Sequence 31, Appl1
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39	848	61.3	2331	3 US-09-935-868-39	Sequence 39, Appl1
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41	848	61.3	2337	3 US-09-935-868-49	Sequence 49, Appl1
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43	848	61.3	2337	6 US-10-287-035-55	Sequence 55, Appl1
44	840	60.7	2343	3 US-09-935-868-41	Sequence 41, Appl1
45	840	60.7	2343	6 US-10-287-035-41	Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-11-185-230-3
Sequence 3, Application US/11185230
Publication No. US20050282216A1
GENERAL INFORMATION:
APPLICANT: Caprit, Daniel
APPLICANT: Ferrera, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Vitor, Natalio
TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
FILE REFERENCE: IVD924 US CMT 1
CURRENT APPLICATION NUMBER: US/11/185,230
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4009
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-11-185-230-3

Query Match 86.6%; Score 1198; DB 15; Length 4009;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	111	CGGCGCTACGGAACCTGACGACCTGACAAATTTGAGTCTCTGTGAAACCTCTG	170
QY	195	CACAGTAATATGACATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATA	254
DB	171	CACAGTAATATGACATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATA	230
QY	255	TTTATGATATTTTGGGCAACAAAGATTAAGAAATAGCTCCGAAATCTGCTTCAAT	314
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; Sequence 160, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-160
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Query Match      86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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      121  CCGGCTACGGAACCTCAGCCACCTGTGCAAAATTTGAGTGTCTCTGTTGAAAACTCTG 180
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QY      495  GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTTCTTACTATTTGGGACAGAG 554
      481  GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTTCTTACTATTTGGGACAGAG 540
QY      555  CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAAAGGCAATACTTTGGTGTTC 614
      541  CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAAAGGCAATACTTTGGTGTTC 600
QY      615  CTTTGTATGACCAAGATGAGATTCAGTTTGAACAACAAGTGTCCAATTAATGTGT 674
      601  CTTTGTATGACCAAGATGAGATTCAGTTTGAACAACAAGTGTCCAATTAATGTGT 660
QY      675  CAAGATTAATGAGAGAAATTAACCATCTCTCAATATATAGTCCCTTTAACTCCCGTGT 724
      661  CAAGATTAATGAGAGAAATTAACCATCTCTCAATATATAGTCCCTTTAACTCCCGTGT 720
QY      735  GAAACCTGATCTCTCAATATTAACCACTCTCTTCCACAAATGATGACCTATATGTGA 794
      721  GAAACCTGATCTCTCAATATTAACCACTCTCTTCCACAAATGATGACCTATATGTGA 780
QY      795  ATGGAGATTCACAGAAATTTTATATGAGATGAGTCCATTTTATGAAGTGAAGTCAATGA 854
      781  ATGGAGATTCACAGAAATTTTATATGAGATGAGTCCATTTTATGAAGTGAAGTCAATGA 840
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QY      855  CAGCCAAATGAGACATATATGTTTCTACGTCGAAGAGCTTAATGTGAATCCAGA 914
      841  CAGCCAAATGAGACATATATGTTTCTACGTCGAAGAGCTTAATGTGAATCCAGA 900
QY      915  ATTTGAGAAATGTGAGAAATACATTTTGTTCATGTCCTCGTGTCTTCTGTATAC 974
      901  ATTTGAGAAATGTGAGAAATACATTTTGTTCATGTCCTCGTGTCTTCTGTATAC 960
QY      975  TTTGAACACAGTCAGAAATAGAGCAAAACAAATTAAGTATAGATAGAGATCAACT 1034
      961  TTTGAACACAGTCAGAAATAGAGCAAAACAAATTAAGTATAGATAGAGATCAACT 1020
QY      1035  CTGAGATTAATGAGCCAGCAAAATGAGTATAGTAAAGCCGAATTCACACTCTATCAT 1094
      1021  CTGAGATTAATGAGCCAGCAAAATGAGTATAGTAAAGCCGAATTCACACTCTATCAT 1080
QY      1095  AACCATGTTACTATGTTTCTCACTGATCGTCGAGGTGCAATCATATGACTCTGCTTTA 1154
      1081  AACCATGTTACTATGTTTCTCACTGATCGTCGAGGTGCAATCATATGACTCTGCTTTA 1140
QY      1155  CCTAAAAAGCTCAAGATTTATATATCCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1214
      1141  CCTAAAAAGCTCAAGATTTATATATCCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1200
QY      1215  AGAATGTTTGAACCAAGATGATGATCTGCACTGCAAGAGATGACATCTATGA 1274
      1201  AGAATGTTTGAACCAAGATGATGATCTGCACTGCAAGAGATGACATCTATGA 1260
QY      1275  GAAGCAAACTAAGAGAGAAACCGACTCTGTATGCTGATAGAAACCTGAAGAAAGCTTC 1334
      1261  GAAGCAAACTAAGAGAGAAACCGACTCTGTATGCTGATAGAAACCTGAAGAAAGCTTC 1320
QY      1335  TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAAAGA 1383
      1321  TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAAAGA 1369
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RESULT 6

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US-09-880-107-3856
; Sequence 3856, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3856
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y10659
US-09-880-107-3856
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Query Match      86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      135  CCGGCTACGGAACCTCAGCCACCTGTGCAAAATTTGAGTGTCTCTGTTGAAAACTCTG 194
      121  CCGGCTACGGAACCTCAGCCACCTGTGCAAAATTTGAGTGTCTCTGTTGAAAACTCTG 180
QY      195  CACAGTAATATGACATGTGAATCCACCCGAGGAGCCAGCTCAAAATTTGATGTAAGTA 254
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DB 181 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATTTAGTATAGTA 240
QY 255 TTTTATCATTTTGGGACAAACAATAGTAAGTAAGTCCGGAAATCTGTCTCAAT 314
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QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTATGACCAATGA 374
DB 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTATGACCAATGA 360
QY 375 GAGTGAAGGCTTACATTTTGGTGAAGATGATCCACCCGAGAGTATCTCTGA 434
DB 361 GAGTGAAGGCTTACATTTTGGTGAAGATGATCCACCCGAGAGTATCTCTGA 420
QY 435 GTCTGCTGAGCAGATCTCAATGCAATTTGGGCAACCTGAGTACATGAGTCTTG 494
DB 421 GTCTGCTGAGCAGATCTCAATGCAATTTGGGCAACCTGAGTACATGAGTCTTG 480
QY 495 GCTCCCTGAGAGATACAGTCCGACACTAATCTCTGATATTTGGACAGAG 554
DB 481 GCTCCCTGAGAGATACAGTCCGACACTAATCTCTGATATTTGGACAGAG 540
QY 555 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 614
DB 541 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 600
QY 615 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 674
DB 601 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 660
QY 675 CAAGATAATGAGAGAAATTAATCAATCTTCAATATAGTGGCTTAACTCCGCTG 724
DB 661 CAAGATAATGAGAGAAATTAATCAATCTTCAATATAGTGGCTTAACTCCGCTG 720
QY 735 GAAACCTGATCTCCACATATTAATAACCTCTCTCCACATATGATGATGTA 794
DB 721 GAAACCTGATCTCCACATATTAATAACCTCTCTCCACATATGATGATGTA 780
QY 795 ATGGAGAAATCCACAGAAATTTTATGAGAGATGCTTATTAAGAAATGAGCAATGA 854
DB 781 ATGGAGAAATCCACAGAAATTTTATGAGAGATGCTTATTAAGAAATGAGCAATGA 840
QY 855 CAGCCAAATGAGACATATGTTTCTAGCTCCAGAGAGCTAAATGAGATGAGCA 914
DB 841 CAGCCAAATGAGACATATGTTTCTAGCTCCAGAGAGCTAAATGAGATGAGCA 900
QY 915 ATTTGAGAGAAATGAGAGAAATCAATCTTGTCTGAGTCTCTGCTGATAC 974
DB 901 ATTTGAGAGAAATGAGAGAAATCAATCTTGTCTGAGTCTCTGCTGATAC 960
QY 975 TTTGAGACAGTGAAGATGAGCAATCAAAATTAATTTATGATAGAGATGAGCAACT 1034
DB 961 TTTGAGACAGTGAAGATGAGCAATCAAAATTAATTTATGATAGAGATGAGCAACT 1020
QY 1035 CTGAGATTAATTTGAGAGCAAGAAATGAGTATAGTAAAGAGGCAATCCACATCTACAT 1094
DB 1021 CTGAGATTAATTTGAGAGCAAGAAATGAGTATAGTAAAGAGGCAATCCACATCTACAT 1080
QY 1081 AACCATGTTACTCATTTGTCAGTCAATCTGAGAGGCAATCAATGATCTGCTGCTTGA 1140
DB 1155 CCTTAAAGAGGCTCAAGATTTATATTTCTCCCAATCTGATCTGAGCAAGATTTTGA 1214
QY 1141 CCTTAAAGAGGCTCAAGATTTATATTTCTCCCAATCTGATCTGAGCAAGATTTTGA 1200
DB 1215 AGAAGTATTTGAGAGCAGATGATGATCTGCACTGAGAGAGATGAGCAATCTATGA 1274
QY 1201 AGAAGTATTTGAGAGCAGATGATGATCTGCACTGAGAGAGATGAGCAATCTATGA 1260
QY 1275 GAGCAAAACCAAGAGAGAAACGATCTGATGCTGATGAGAAACCTGAGAGAGCTC 1334

DB 1261 GAGCAAAACCAAGAGAGAAACGATCTGATGCTGATGAGAAACCTGAGAGAGCTC 1320
QY 1335 TCAGTATGAGAGATTAATTTATTTTACCTTCACTGAGCTTGAAGA 1383
DB 1321 TCAGTATGAGAGATTAATTTTATTTTACCTTCACTGAGCTTGAAGA 1369
RESULT 7
US-10-172-118-633
; Sequence 633, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172, 118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380, 770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 633
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001560
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-633
Query Match 86.6%; Score 1198; DB 7; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCTTAAGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAACCTCTG 194
DB 121 CGGCTTAAGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAACCTCTG 180
QY 195 CACAGTAATATGAGACATGATCCACCGAGGAGCAGCTCAATTTAGTATAGTA 254
DB 181 CACAGTAATATGAGACATGATCCACCGAGGAGCAGCTCAATTTAGTATAGTA 240
QY 255 TTTTATCATTTTGGGACAAACAATAGTAAGTAAGTCCGGAAATCTGTCTCAAT 314
DB 241 TTTTATCATTTTGGGACAAACAATAGTAAGTAAGTCCGGAAATCTGTCTCAAT 300
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTATGACCAATGA 374
DB 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTATGACCAATGA 360
QY 375 GAGTGAAGGCTTACATTTTGGTGAAGATGATCCACCCGAGAGTATCTCTGA 434
DB 361 GAGTGAAGGCTTACATTTTGGTGAAGATGATCCACCCGAGAGTATCTCTGA 420
QY 435 GTCTGCTGAGCAGATCTCAATGCAATTTGGGCAACCTGAGTACATGAGTCTTG 494
DB 421 GTCTGCTGAGCAGATCTCAATGCAATTTGGGCAACCTGAGTACATGAGTCTTG 480
QY 495 GCTCCCTGAGAGATACAGTCCGACACTAATCTCTGATATTTGGACAGAG 554
DB 481 GCTCCCTGAGAGATACAGTCCGACACTAATCTCTGATATTTGGACAGAG 540
QY 555 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 614
DB 541 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 600
QY 615 CTTGGAATTAATCATCATATGTAAGAAACATCTTTAGAGAGCCCAATATCTTGTGTC 674

Db	601	CTTTGATCGACCAAGTGAAGGATTCACGTTTGAACAACACATGCTCCAAATATAGT	660
Qy	675	CAAGATATATGCAGGAAAAATTAAACATCCTTCAATATAGTGCCTTTAACTTCCCGTGT	734
Db	661	CAAGATATATGCAGGAAAAATTAAACCATCCCTTCAATATAGTGCCTTTAACTTCCCGTGT	720
Qy	735	GAAACCTATCCTCCACATATTTAAAAACCTCCTCTTCCACATATATGACCTTATATGTGA	794
Db	721	GAAACCTATCCTCCACATATTTAAAAACCTCCTCTTCCACATATATGACCTTATATGTGA	780
Qy	795	ATGGAGAAATCCAAGAATTTTATATAGAGATGCTATTTTATGAAATGAGAGCAATTA	854
Db	781	ATGGAGAAATCCAAGAATTTTATATAGAGATGCTATTTTATGAAATGAGAGCAATTA	840
Qy	855	CAGCCAAACTGAGACACATAATGTTTTCTACGTCACAGAGGCTAAATGTGAATCCAGA	914
Db	841	CAGCCAAACTGAGACACATAATGTTTTCTACGTCACAGAGGCTAAATGTGAATCCAGA	900
Qy	915	ATTTGAGAGAAATGTGGAGAAATCACTCTTGTTCATGCTCCCTGCTGTTCTCTGATAC	974
Db	901	ATTTGAGAGAAATGTGGAGAAATCACTCTTGTTCATGCTCCCTGCTGTTCTCTGATAC	960
Qy	975	TTTGAACACACTCCAGAAATTAAGATCAAAACAAATTAATGTTATGCTATGAGATGACAACT	1034
Db	961	TTTGAACACACTCCAGAAATTAAGATCAAAACAAATTAATGTTATGCTATGAGATGACAACT	1020
Qy	1035	CTGGAGTAAATGGAGCCCAAGAAATGAGTATAGTAAAGAGGCAATTCACACTCTAAT	1094
Db	1021	CTGGAGTAAATGGAGCCCAAGAAATGAGTATAGTAAAGAGGCAATTCACACTCTAAT	1080
Qy	1095	AACCATGTTACTCATTTGTTCCAGTCATCGTCGAGAGTCAATTCATAGTACTCTGCTTAA	1154
Db	1081	AACCATGTTACTCATTTGTTCCAGTCATCGTCGAGAGTCAATTCATAGTACTCTGCTTAA	1140
Qy	1155	CCTTAAAAAGGCTCAAGATTTATTAATTCCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA	1214
Db	1141	CCTTAAAAAGGCTCAAGATTTATTAATTCCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA	1200
Qy	1215	AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGACACTGAAAGAAAGTACGACATCTATGA	1274
Db	1201	AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGACACTGAAAGAAAGTACGACATCTATGA	1260
Qy	1275	GAAACCAACCAAGAGGAAACCGACTCTGTAGTGTGATTAAGAAAACCTGAAGAAAGCTC	1334
Db	1261	GAAACCAACCAAGAGGAAACCGACTCTGTAGTGTGATTAAGAAAACCTGAAGAAAGCTC	1320
Qy	1335	TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACTCTTGAGAGA 1383	
Db	1321	TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACTCTTGAGAGA 1369	
RESULT 8			
US-10-342-887-633			
: Sequence 633, Application US/10342887			
: Publication No. US20040058340A1			
: GENERAL INFORMATION:			
: APPLICANT: Dai, Hongyue			
: APPLICANT: He, Jundong			
: APPLICANT: Linsley, Peter S.			
: APPLICANT: Mao, Mao			
: APPLICANT: Roberts, Christopher J.			
: APPLICANT: Van 't Veer, Laura Johanna			
: APPLICANT: Van de Vijver, Marc J.			
: APPLICANT: Bernhards, Rene			
: TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
: FILE REFERENCE: 9301-188-999			
: CURRENT APPLICATION NUMBER: US/10/342,887			
: CURRENT FILING DATE: 2003-01-15			
: PRIOR APPLICATION NUMBER: 60/298,918			
: PRIOR FILING DATE: 2001-06-18			
: PRIOR APPLICATION NUMBER: 60/380,710			
: PRIOR FILING DATE: 2002-05-14			

	PRIOR APPLICATION NUMBER: 10/172,118	
	PRIOR FILING DATE: 2002-06-14	
	NUMBER OF SEQ ID NOS: 2699	
	SEQ ID NO 633	
	LENGTH: 4039	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-342-887-633	
Query Match	86.6%; Score 1198; DB 8; Length 4039;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 1248;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	135 CGCCCTTAGCGAAACTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAACCTCTG	194
DB	121 CGCCCTTAGCGAAACTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAACCTCTG	180
QY	195 CACAGTAATATGACATGGAATCCACCAGGAGCCAGCTCAATTGTAGCTATGTGTA	254
DB	181 CACAGTAATATGACATGGAATCCACCAGGAGCCAGCTCAATTGTAGCTATGTGTA	240
QY	255 TTTTAGTCATTTTGGCGACAAACAGATAGAAATAATAGCTCCGGAACCTGCTCTCAAT	314
DB	241 TTTTAGTCATTTTGGCGACAAACAGATAGAAATAATAGCTCCGGAACCTGCTCTCAAT	300
QY	315 AGAAGTACCCCTGAAATGAGAGATTTTGTCTGCAAGTGGGTCCAGTATGACCAATGA	374
DB	301 AGAAGTACCCCTGAAATGAGAGATTTTGTCTGCAAGTGGGTCCAGTATGACCAATGA	360
QY	375 GAGTGAAGGCTAGCATTTTGTGTGAAAAATGATCTCACCCCGAAGGAGTACTCTGA	434
DB	361 GAGTGAAGGCTAGCATTTTGTGTGAAAAATGATCTCACCCCGAAGGAGTACTCTGA	420
QY	435 GTCTGCTGTGACTGAATCTCAATGATCTTGGCACCACTGAGCTACATGAAGTCTTGG	494
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QY	495 GCTCCCTGGAAGGAATACCAAGTCCCGACACTAATATATCTCTATATTTGGCACAGAG	554
DB	481 GCTCCCTGGAAGGAATACCAAGTCCCGACACTAATATATCTCTATATTTGGCACAGAG	540
QY	555 CTTGGAATAAATTCATCAATGTGAAAAATCTTTAGAGAAAGGCCAATCTTGGTGTTC	614
DB	541 CTTGGAATAAATTCATCAATGTGAAAAATCTTTAGAGAAAGGCCAATCTTGGTGTTC	600
QY	615 CTTTATGCTGACCAAGATGAAGATTCGAGTTTGAACAACACAGTGTCCAAATPAATGT	674
DB	601 CTTTATGCTGACCAAGATGAAGATTCGAGTTTGAACAACACAGTGTCCAAATPAATGT	660
QY	675 CAAGATPAATGCAAGAAAAATTTAAACATCTTCAATATATGTGCTTTAATCTCCGGT	734
DB	661 CAAGATPAATGCAAGAAAAATTTAAACATCTTCAATATATGTGCTTTAATCTCCGGT	720
QY	735 GAAACCTGATCTTCACATATTTAAAAAATCTCTCTTCCACATGATGACCTATATGTGCA	794
DB	721 GAAACCTGATCTTCACATATTTAAAAAATCTCTCTTCCACATGATGACCTATATGTGCA	780
QY	795 ATGGAGAAATCCACAGAAATTTTATTTAGCAATGCTTATTTTATGAAAGTGAATGA	854
DB	781 ATGGAGAAATCCACAGAAATTTTATTTAGCAATGCTTATTTTATGAAAGTGAATGA	840
QY	855 CAGGCAAACTGAGACATATATGTTTCTAGCTCCAGAGGCTTAAATGTGGAATCCAGA	914
DB	841 CAGGCAAACTGAGACATATATGTTTCTAGCTCCAGAGGCTTAAATGTGGAATCCAGA	900
QY	915 ATTGGAAGAAATGTGAGAAATACATTTGTTTATGAGTGTCCCTGCTGTTCTTCTGATAC	974
DB	901 ATTGGAAGAAATGTGAGAAATACATTTGTTTATGAGTGTCCCTGCTGTTCTTCTGATAC	960
QY	975 TTTGGAACACAGTCAGAAATAGAGTCAAAACAAATTAATATATGATAGAGTGAACAAT	1034
DB	961 TTTGGAACACAGTCAGAAATAGAGTCAAAACAAATTAATATGATAGAGTGAACAAT	1020

QY 1035 CTGAGTAATGAGCCAGAAATGACTATAGGTAGAGCCCAATTCACACTCTACAT 1094
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Db 1021 CTGAGTAATGAGCCAGAAATGAGTAAGTAAGAAACGCAATTCACACTCTACAT 1080
QY 1095 AACCATGTTACTGATTTGTCAGTCATCGTCGAGGAGCAATCATGTACTCCGCTTTA 1154
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Db 1081 AACCATGTTACTGATTTGTCAGTCATCGTCGAGGAGCAATCATGTACTCCGCTTTA 1140
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Db 1141 CCTAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1200
QY 1215 AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGCACTGGAAGATGACATCTATGA 1274
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Db 1201 AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGCACTGGAAGATGACATCTATGA 1260
QY 1275 GAAGCAAAACCAAGAGAGAAACCACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334
| | | | |
Db 1261 GAAGCAAAACCAAGAGAGAAACCACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1320
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
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Db 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

RESULT 9

US-10-843-641A-6046
; Sequence 6046, Application US/10843641A
; Publication No. US2005006454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6046
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-6046

Query Match 86.6%; Score 1198; DB 10; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTAGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTGAAAACCTCTG 194
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Db 121 CGGCGCTAGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTGAAAACCTCTG 180

QY 195 CACAGTAATGAGCACTGGAATCCACCCGAGGAGCCAGCTCAATTTGTATGTTATGTA 254
| | | | |
Db 181 CACAGTAATGAGCACTGGAATCCACCCGAGGAGCCAGCTCAATTTGTATGTTATGTA 240
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Db 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 360
QY 375 GAGTGGAAGCCCTAGCAATTTTGTGTGAAAATGCAATCCCGCAAGAGTATCTCTGA 434
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Db 361 GAGTGGAAGCCCTAGCAATTTTGTGTGAAAATGCAATCCCGCAAGAGTATCTCTGA 420
QY 435 GTCTGCTGAGACTGAATCAATGCAATTTTGGCAACCTGAGCTACATGAAAGTCTTCTG 494
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Db 421 GTCTGCTGAGACTGAATCAATGCAATTTTGGCAACCTGAGCTACATGAAAGTCTTCTG 480
QY 495 GCTCCCTGAGAGGAATACAGTCCGACACTAACTACTCTCTACTATTGGCACAAG 554
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Db 481 GCTCCCTGAGAGGAATACAGTCCGACACTAACTACTCTCTACTATTGGCACAAG 540
QY 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAAGCCATCTTGTGTTC 614
| | | | |
Db 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAAGCCATCTTGTGTTC 600
QY 615 CTTGATCTGACCAAGTGAAGATCTCCAGTTTGAACAACAGTGTCCAAATTAATGT 674
| | | | |
Db 601 CTTGATCTGACCAAGTGAAGATCTCCAGTTTGAACAACAGTGTCCAAATTAATGT 660
QY 675 CAAGATAATGACAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGCTG 734
| | | | |
Db 661 CAAGATAATGACAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGCTG 720
QY 735 GAAACCTGATCTCCCATATTTAAAACCTCTCTCCCAATGATGACCTATATGTGCA 794
| | | | |
Db 721 GAAACCTGATCTCCCATATTTAAAACCTCTCTCCCAATGATGACCTATATGTGCA 780
QY 795 ATGGAGAAATCCACAGAAATTTTATGAGATGCTATTTATGAGATGAAATGCAATA 854
| | | | |
Db 781 ATGGAGAAATCCACAGAAATTTTATGAGATGCTATTTATGAGATGAAATGCAATA 840
QY 855 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGCTTAATGTGAGATCCAGA 914
| | | | |
Db 841 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGCTTAATGTGAGATCCAGA 900
QY 915 ATTTGAGAAATGTGAGAAATATCATCTTGTTCATGTCCTGTGTCTTCTGATAC 974
| | | | |
Db 901 ATTTGAGAAATGTGAGAAATATCATCTTGTTCATGTCCTGTGTCTTCTGATAC 960
QY 975 TTTGAAACAGTCAGATTAAGATCAAAACAATAAGTTATGCTATGAGAGTACAACAT 1034
| | | | |
Db 961 TTTGAAACAGTCAGATTAAGATCAAAACAATAAGTTATGCTATGAGAGTACAACAT 1020
QY 1035 CTGAGTAATTTGGAGCCAGAAATGATAGTTAAGAAAGCCGAATTCACACTCTACAT 1094
| | | | |
Db 1021 CTGAGTAATTTGGAGCCAGAAATGATAGTTAAGAAAGCCGAATTCACACTCTACAT 1080
QY 1095 AACCATGTTACTGATTTGTCAGTCATCGTCGAGGAGCAATCATGTACTCCGCTTTA 1154
| | | | |
Db 1081 AACCATGTTACTGATTTGTCAGTCATCGTCGAGGAGCAATCATGTACTCCGCTTTA 1140
QY 1155 CCTAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1214
| | | | |
Db 1141 CCTAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1200
QY 1215 AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGCACTGGAAGATGACATCTATGA 1274
| | | | |
Db 1201 AGAAATGTTTGAGAGCCAGAAATGATGATCTCTGCACTGGAAGATGACATCTATGA 1260
QY 1275 GAAGCAAAACCAAGAGAGAAACCACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334
| | | | |

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Db      1261 GAAGCAACCAAGAGGAGAAACCGACTGTAGTCTGATAGAAAACCTGAAAGAACCTC 1320
Qy      1335 TCAGTGTGAGATTAATTTATTTTACCTTCACGTGTACCTTGAGAGA 1383
Db      1321 TCAGTGTGAGATTAATTTATTTTACCTTCACGTGTACCTTGAGAGA 1369

RESULT 10
US-09-971-392-58
; Sequence 58, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecilia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ. ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Template ID: 331428.2
; LOCATION: 1874-2179, 4212, 4229, 4239, 4254, 4309, 4328, 4335, 4338
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-392-58

Query Match      86.6%; Score 1198; DB 3; Length 4466;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      135 CGGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAAGAAACCTGTG 194
Db      158 CGGCGCTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAAGAAACCTGTG 217
Qy      195 CAGAGTAATATGACATGATGATCCACCCGAGGAGCCAGCTCAATTTGTGTATGTATGTA 254
Db      218 CACAGTAATATGACATGATGATCCACCCGAGGAGCCAGCTCAATTTGTGTATGTATGTA 277
Qy      255 TTTTATGATTTTGGGACAAACAGATAGAAAATAGTCCGGAACCTGTCGTTCAAT 314
Db      278 TTTTATGATTTTGGGACAAACAGATAGAAAATAGTCCGGAACCTGTCGTTCAAT 337
Qy      315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCCAAGTGTAGCAACAAATGA 374
Db      338 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCCAAGTGTAGCAACAAATGA 397
Qy      375 GAGTGTGAGAACCTTATGATTTTGTGTGAAAATGATCTACCCCAAGAGATGATCTCTGA 434
Db      398 GAGTGTGAGAACCTTATGATTTTGTGTGAAAATGATCTACCCCAAGAGATGATCTCTGA 457
Qy      435 GTCTGTGTGACTGAATCTTCAATGATGATTTGGACAAACCTGAGCTACATGAGAGTGTCTTG 494
Db      458 GTCTGTGTGACTGAATCTTCAATGATGATTTGGACAAACCTGAGCTACATGAGAGTGTCTTG 517
Qy      495 GCTTCCTGTGAGAGATTCAGTCTCCGACACTAACTATATCTCTACTATTTGGACAGAGAG 554
Db      518 GCTTCCTGTGAGAGATTCAGTCTCCGACACTAACTATATCTCTACTATTTGGACAGAGAG 577
Qy      555 CCTGGAAGAAATTCATCAATGTGAAAACATCTTTAGGAGAGGCCAATCTTTGGTTGTC 614
Db      578 CCTGGAAGAAATTCATCAATGTGAAAACATCTTTAGGAGAGGCCAATCTTTGGTTGTC 637
Qy      615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGTGAACACAGAGTGTCCAAATATATGT 674
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Db      638 CTTTGATCTGACCAAGATGAGATTCAGTTTGTGAACACAGAGTGTCCAAATATATGT 697
Qy      675 CAAGATATATGACGAGAAAATTTAAACCATCTTCAATATATAGTGTCTTAACTTCCGCTGT 734
Db      698 CAAGATATATGACGAGAAAATTTAAACCATCTTCAATATATAGTGTCTTAACTTCCGCTGT 757
Qy      735 GAAACCTGATCTTCCATATTTAAACCTCTCTCTCCACAAATGATGACCTATATGTGCA 794
Db      758 GAAACCTGATCTTCCATATTTAAACCTCTCTCTCCACAAATGATGACCTATATGTGCA 817
Qy      795 ATGGAGAAATCCACAGAAATTTTATTTAGACAGATGCTATTTATGAGATGAGTCAATAA 854
Db      818 ATGGAGAAATCCACAGAAATTTTATTTAGACAGATGCTATTTATGAGATGAGTCAATAA 877
Qy      855 CAGCCAACTGACACATATATGTTTCTACAGTCCCAAGAGCTTAAATGTAGATCCAGA 914
Db      878 CAGCCAACTGACACATATATGTTTCTACAGTCCCAAGAGCTTAAATGTAGATCCAGA 937
Qy      915 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGAGTCCCTGCTGTCTCTGATAC 974
Db      938 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGAGTCCCTGCTGTCTCTGATAC 997
Qy      975 TTTGAACACAGTACAGATTAAGATCAAAACAAATATGATTAATGATGAGATGACAAACT 1034
Db      998 TTTGAACACAGTACAGATTAAGATCAAAACAAATATGATTAATGATGAGATGACAAACT 1057
Qy      1035 CTGAGATTAATTTGAGACCAAGAAATGATTAAGTAAAGAGCCATTCACACTCTACAT 1094
Db      1058 CTGAGATTAATTTGAGACCAAGAAATGATTAAGTAAAGAGCCATTCACACTCTACAT 1117
Qy      1095 AACCATGTAATCTATGTCATGTCAGTACATGTCGAGGAGCAATCATATACCTCCGCTTAA 1154
Db      1118 AACCATGTAATCTATGTCATGTCAGTACATGTCGAGGAGCAATCATATACCTCCGCTTAA 1177
Qy      1155 CCTAAAAAGGCTCAAGATTTATATATCCCTCCAAATCTGATCCTGCAAGATTTTAA 1214
Db      1178 CCTAAAAAGGCTCAAGATTTATATATCCCTCCAAATCTGATCCTGCAAGATTTTAA 1237
Qy      1215 AGAATGTTTGGAGACCAAGATGATGATCTGACACTGAGAAAGTATGACATCTATGA 1274
Db      1238 AGAATGTTTGGAGACCAAGATGATGATCTGACACTGAGAAAGTATGACATCTATGA 1297
Qy      1275 GAGCAACCAAGAGAGAAACGACCTGTAGTCTGTAGTAAACCTGAAAGAAAGCTC 1334
Db      1298 GAGCAACCAAGAGAGAAACGACCTGTAGTCTGTAGTAAACCTGAAAGAAAGCTC 1357
Qy      1335 TCAGTGTGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db      1358 TCAGTGTGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1406

RESULT 11
US-09-822-846-109
; Sequence 109, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
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; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 3880
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-109
```

Query Match 86.0%; Score 1189; DB 3; Length 3880;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1239; Conservative 0; Indels 0; Gaps 0;

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QY 144 GGAATCTGACGCGACCTGTGACAAATTTGAGTGTCTGTGAAAACCTCTGCACAGTAAT 203
DB 2 GGAATCTGACGCGACCTGTGACAAATTTGAGTGTCTGTGAAAACCTCTGCACAGTAAT 61
QY 204 ATGACATGGAATCCACCCGAGGAGGACCTCAAAATTTGATCTATGTAATTTAGTCA 263
DB 62 ATGACATGGAATCCACCCGAGGAGGACCTCAAAATTTGATCTATGTAATTTAGTCA 121
QY 264 TTTTGGCGACAAACAGATTAAGAAAATAGCTCCGAAAACCTGCTGTTCAATAGAAATCC 323
DB 122 TTTTGGCGACAAACAGATTAAGAAAATAGCTCCGAAAACCTGCTGTTCAATAGAAATCC 181
QY 324 CCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCCAATGTAAGCAACATAGAGTGAAG 383
DB 182 CCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCCAATGTAAGCAACATAGAGTGAAG 241
QY 384 GCTTACATTTTGTGAAAATATGATCTGACCCCGAAGGATGATCTGATCTGCTGT 443
DB 242 GCTTACATTTTGTGAAAATATGATCTGACCCCGAAGGATGATCTGATCTGCTGT 301
QY 444 GATGAACTTCAATGATTTGGCAACCTGAGCTACATGAATGTTCTTGGCTCCCTGG 503
DB 302 GATGAACTTCAATGATTTGGCAACCTGAGCTACATGAATGTTCTTGGCTCCCTGG 361
QY 504 AAGGATACCAAGTCCGACACTACTACTCTCTACTATTTGGCAAGAGCCCTGGAAA 563
DB 362 AAGGATACCAAGTCCGACACTACTACTCTCTACTATTTGGCAAGAGCCCTGGAAA 421
QY 564 AATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTCTTGGATCT 623
DB 422 AATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTCTTGGATCT 481
QY 624 GACCAAGTGAAGGATTTCCAGTTTGAACAACACAGTGTCCAAATATGTTCAAGATTA 683
DB 482 GACCAAGTGAAGGATTTCCAGTTTGAACAACACAGTGTCCAAATATGTTCAAGATTA 541
QY 684 TGCAAGAAAAATTAACCATCTTCAATATATGAGCTTTAATCCCGTGGAAACCTGTA 743
DB 542 TGCAAGAAAAATTAACCATCTTCAATATATGAGCTTTAATCCCGTGGAAACCTGTA 601
QY 744 TCTTCACATATTTAAACCTCTCTTCCAAATGATGACCTATATGTCGCAATGGAGAA 803
DB 602 TCTTCACATATTTAAACCTCTCTTCCCAATGATGACCTATATGTCGCAATGGAGAA 661
QY 804 TCCACGAAATTTATAGCAGATGCTATTTATGAGTGAAGTCAATACAGCCCAAC 863
DB 662 TCCACGAAATTTATAGCAGATGCTATTTATGAGTGAAGTCAATACAGCCCAAC 721
QY 864 TGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGAGAAATCAGAAATTTGAGAG 923
DB 722 TGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGAGAAATCAGAAATTTGAGAG 781
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QY 924 AAATGGAAGATATACATCTTTGTTTCATGTCCTCCGTGTGTTCTTCTGATACCTTTGAAC 983
DB 782 AAATGGAAGATATACATCTTTGTTTCATGTCCTCCGTGTGTTCTTCTGATACCTTTGAAC 841
QY 984 AGTCAAAATTAAGTCAAAACAAATTAAGTCAAAACAAATTAAGTCAAAACCTCGAGTAA 1043
DB 842 AGTCAAAATTAAGTCAAAACAAATTAAGTCAAAACAAATTAAGTCAAAACCTCGAGTAA 901
QY 1044 TTGAGACCAAGAAATGATAGTAAAGAGGCAATTCACACTACATTAACATATGTT 1103
DB 902 TTGAGACCAAGAAATGATAGTAAAGAGGCAATTCACACTACATTAACATATGTT 961
QY 1104 ACTCATTTGTCAGTATGTCGAGGTCGATCATATGATATCTCTCTTAACTTAAAG 1163
DB 962 ACTCATTTGTCAGTATGTCGAGGTCGATCATATGATATCTCTCTTAACTTAAAG 1021
QY 1164 GCTCAAGATTAATATTTCCCTCCATTCCTGATCTCTGCAAGATTTTAAAGAAATGTT 1223
DB 1022 GCTCAAGATTAATATTTCCCTCCATTCCTGATCTCTGCAAGATTTTAAAGAAATGTT 1081
QY 1224 TGAGACCAAGAAATGATATCTGTCATGGAAGAGTACGACATCTATGAGAGCAAC 1283
DB 1082 TGAGACCAAGAAATGATATCTGTCATGGAAGAGTACGACATCTATGAGAGCAAC 1141
QY 1284 CAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTTCAATGATG 1343
DB 1142 CAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTTCAATGATG 1201
QY 1344 GAGATATTTATTTTAACTTCACTGTCGATGAAAGAA 1383
DB 1202 GAGATATTTATTTTAACTTCACTGTCGATGAAAGAA 1241
```

RESULT 12

US-10-036-568-3

; Sequence 3, Application US/10036568

; Publication No. US20020090682A1

; GENERAL INFORMATION:

; APPLICANT: Willson, Tracy

; APPLICANT: Nicola, Nicos A.

; APPLICANT: Hilton, Douglas J.

; APPLICANT: Metcalf, Donald

; TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES

; FILE REFERENCE: ENCODING SAME

; CURRENT APPLICATION NUMBER: US/10/036,568

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US/09/051,843

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1383

; TYPE: DNA

; ORGANISM: Human IL-13 receptor alpha-chain

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (61)..(1338)

US-10-036-568-3

Query Match 85.2%; Score 1179; DB 6; Length 1383;

Best Local Similarity 99.7%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;

Matches 1379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 GAGTCTTAACAACGAGGAGTTTAACACGTCGCGCGGCTTCCAGGCGAGAGCTGC 60
DB 1 GAGTCTTAACAACGAGGAGTTTAACACGTCGCGCGGCTTCCAGGCGAGAGCTGC 60
QY 61 ATGGAATGCGCGCGGCTCTGCGGCGCTGTGGGCGCTGCTGCGCGCGGCGGCGG 120
DB 61 ATGGAATGCGCGCGGCTCTGCGGCGCTGTGGGCGCTGCTGCTGCGCGCGGCGGCGG 120
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QY 121 GCGGGGGGGGGGGGGGGGGCTTACGAACTCAGCCACTGTGCAAAATTTGATGTCTCT 180
DB 121 GCGGGGGGGGGGGGGGGGGCTTACGAACTCAGCCACTGTGCAAAATTTGATGTCTCT 180
QY 181 GTTAAAACTCTGCAAGTAATATGACATGGAATCCACCCGAGGGGCGCAGCTCAAT 240
DB 181 GTTAAAACTCTGCAAGTAATATGACATGGAATCCACCCGAGGGGCGCAGCTCAAT 240
QY 241 TGTAGTCTATGTAATTTTATGCTATTTTGGCGAACAAGATAAGAAATAGCTCCGAAA 300
DB 241 TGTAGTCTATGTAATTTTATGCTATTTTGGCGAACAAGATAAGAAATAGCTCCGAAA 300
QY 301 ACTGCTGCTTCAATAGAAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAG 360
DB 301 ACTGCTGCTTCAATAGAAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAG 360
QY 361 TGTAGCAACATGAGAGTGAAGACCTTACGCTTTTGGTGAATAATGATCTCACCCGCA 420
DB 361 TGTAGCAACATGAGAGTGAAGACCTTACGCTTTTGGTGAATAATGATCTCACCCGCA 420
QY 421 GAAGGTATCTGAGTCTGCTGTGACTGAATCTTCAATGCTTTGGCACAACCTGAGCTAC 480
DB 421 GAAGGTATCTGAGTCTGCTGTGACTGAATCTTCAATGCTTTGGCACAACCTGAGCTAC 480
QY 481 ATGAAGTGTCTTGGCTCCCTGGAAGAAATACAGTCCCGACACTAACTATATCTCTAC 540
DB 481 ATGAAGTGTCTTGGCTCCCTGGAAGAAATACAGTCCCGACACTATATCTCTCTAC 540
QY 541 TATTGGCAAGAAAGCTTGGAAAAATTCATATGTGAAAAATCTTTTAGAAGGCCAA 600
DB 541 TATTGGCAAGAAAGCTTGGAAAAATTCATATGTGAAAAATCTTTTAGAAGGCCAA 600
QY 601 TACTTGTGTGTCTTGTCTTGTCTGACCAAGTGAAGGATTCAGTTTGAACAACAGT 660
DB 601 TACTTGTGTGTCTTGTCTTGTCTGACCAAGTGAAGGATTCAGTTTGAACAACAGT 660
QY 661 GTCCAAATTAATGCTCAAGATATATGACAGAAAAATTAACCATCTTCAATATAGTCT 720
DB 661 GTCCAAATTAATGCTCAAGATATATGACAGAAAAATTAACCATCTTCAATATAGTCT 720
QY 721 TTTAATCTCCGTGTGAAACCTGATCTTCACATTTAAAACTCTCTCCACAAATGAT 780
DB 721 TTTAATCTCCGTGTGAAACCTGATCTTCACATTTAAAACTCTCTCCACAAATGAT 780
QY 781 GACCTATATGCAATGGAAGATCCAGAAATTTTATGAGAGATGCTATTTTATGAA 840
DB 781 GACCTATATGCAATGGAAGATCCAGAAATTTTATGAGAGATGCTATTTTATGAA 840
QY 841 GTAGAACTCAATACAGCCAACTGAGACATATATGTTTCTAGTCCAAAGAGCTAAA 900
DB 841 GTAGAACTCAATACAGCCAACTGAGACATATATGTTTCTAGTCCAAAGAGCTAAA 900
QY 901 TGTGAGAAATCAGAAATTTGAGAGAAATGTGAGAAATCATCTGTTCAATGCTCCGT 960
DB 901 TGTGAGAAATCAGAAATTTGAGAGAAATGTGAGAAATCATCTGTTCAATGCTCCGT 960
QY 961 GTTCTTCCGATCTTGTGAACAAGTGAATGAGAAATTAAGTCAAAATTAAGTATGCTAT 1020
DB 961 GTTCTTCCGATCTTGTGAACAAGTGAATGAGAAATTAAGTCAAAATTAAGTATGCTAT 1020
QY 1021 GAGAGTACAAACTCTGAGATTAATTTGAGCCAAAGAAATGAGTATGTAAGAACGCAAT 1080
DB 1021 GAGAGTACAAACTCTGAGATTAATTTGAGCCAAAGAAATGAGTATGTAAGAACGCAAT 1080
QY 1081 TCCACACTCTACATACATATGTTATGCTATGTTCCAGTCAATGCTGCAAGGTCAATCA 1140
DB 1081 TCCACACTCTACATACATATGTTATGCTATGTTCCAGTCAATGCTGCAAGGTCAATCA 1140
QY 1141 GTACTCTGCTTAACTTAAAGGCTCAAGTATTAATTAATTTCCCTCAATTTCCGATCT 1200
DB 1141 GTACTCTGCTTAACTTAAAGGCTCAAGTATTAATTAATTTCCCTCAATTTCCGATCT 1200
QY 1201 GGCAGAAATTTTAAAGAAATGTTTGAAGACCAAGATGATGATCTGCACTGGAGAG 1260

DB 1201 GGCAGAAATTTTAAAGAAATGTTTGAAGACCAAGATGATGATGATCTGCACTGGAGAG 1260
QY 1261 TAGACATCTATGAGAGCAAAACCAAGAGAAACCACTCTGTATAGCTATGAAAC 1320
DB 1261 TAGACATCTATGAGAGCAAAACCAAGAGAAACCACTCTGTATAGCTATGAAAC 1320
QY 1321 CTGAAGAAAGCCTCTCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACTGAGA 1380
DB 1321 CTGAAGAAAGCCTCTCAGTATGAGATTAATTTTATTTTACCTTCACTGTGAGA 1380
QY 1381 AGA 1383
DB 1381 AGA 1383

RESULT 13
US-10-745-586-32
Sequence 32, Application US/10745586
Publication No. US2006006327A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6011-18X
CURRENT APPLICATION NUMBER: US/10/745,586
PRIOR FILING DATE: 2003-12-29
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 3906
TYPE: DNA
ORGANISM: Homo sapiens
US-10-745-586-32

Query Match 82.3%; Score 1138; DB 12; Length 3906;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 144 GGAATCTGACGACCTGTGCAAAATTTGAGTGTCTCTGTTGAAAACTCTGACAGTAT 203
DB 1 GGAATCTGACGACCTGTGCAAAATTTGAGTGTCTCTGTTGAAAACTCTGACAGTAT 203
QY 204 ATGACATGGAATCCACCCAGGAGCCAGCTCAATTTGATGCTATGATTTATGCA 263
DB 61 ATGACATGGAATCCACCCAGGAGCCAGCTCAATTTGATGCTATGATTTATGCA 120
QY 264 TTTTGGGCAAAACAGATTAAGAAATAGTCTCGGAAATCTGTCGTTCAATAGAGTACC 323
DB 121 TTTTGGGCAAAACAGATTAAGAAATAGTCTCGGAAATCTGTCGTTCAATAGAGTACC 180
QY 324 CTTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCAACCAATGAGAGTGA 383
DB 181 CTTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCAACCAATGAGAGTGA 240
QY 384 GCCTAGCAATTTGTTGAAATATGCAATCTCACCCCAAGAGTGAATCTGAGTCTGCTGT 443
DB 241 GCCTAGCAATTTGTTGAAATATGCAATCTCACCCCAAGAGTGAATCTGAGTCTGCTGT 300
QY 444 GACTGAATCTCAATGCAATTTGGCAAACTGAGCTACATGAAAGTCTTGGCTCCCTGG 503
DB 301 GACTGAATCTCAATGCAATTTGGCAAACTGAGCTACATGAAAGTCTTGGCTCCCTGG 360

QY 504 AAGGAATACCAAGTCCCGACACTAATACTCTCTACTATTGGCACAGAACTGGAAAA 563
| | | | |
Db 361 AAGGAATACCAAGTCCCGACACTAATACTCTCTACTATTGGCACAGAACTGGAAAA 420
| | | | |
QY 564 AATTCATCAATGGAAGAACTCTTTAGAGAGGCCAATACTTTGGTTGCTCTTGTATCT 623
| | | | |
Db 421 AATTCATCAATGGAAGAACTCTTTAGAGAGGCCAATACTTTGGTTGCTCTTGTATCT 480
| | | | |
QY 624 GACCAAGTGAAGAGATTCAGTTTGTGAACAACAGTGTCCAATATATATGCTCAAGATA 683
| | | | |
Db 481 GACCAAGTGAAGAGATTCAGTTTGTGAACAACAGTGTCCAATATATATGCTCAAGATA 540
| | | | |
QY 684 TGCAGGAAAAATTAACCATCTTCAATATATATGCTCTTAATCTCCGCTGAAACCTGA 743
| | | | |
Db 541 TGCAGGAAAAATTAACCATCTTCAATATATATGCTCTTAATCTCCGCTGAAACCTGA 600
| | | | |
QY 744 TCCTCCACATATTAATAAACTCTCTCCCAATGATGACCTATATGTCATATGGAGAA 803
| | | | |
Db 601 TCCTCCACATATTAATAAACTCTCTCCCAATGATGACCTATATGTCATATGGAGAA 660
| | | | |
QY 804 TCCACAGAAATTTATTAGCAGATGCTATTTATGAAAGTCAATACAGCCAAAC 863
| | | | |
Db 661 TCCACAGAAATTTATTAGCAGATGCTATTTATGAAAGTCAATACAGCCAAAC 720
| | | | |
QY 864 TGAACACATATATGTTTCTACGTCGAAGAGCTAAATGAGAAATCCAGAAATTTGAG 923
| | | | |
Db 721 TGAACACATATATGTTTCTACGTCGAAGAGCTAAATGAGAAATCCAGAAATTTGAG 780
| | | | |
QY 924 AAATGAGAGAAATACATCTTTGTTTCAATGATGCTCTGTTCTTCTGATATCTTTGAA 983
| | | | |
Db 781 AAATGAGAGAAATACATCTTTGTTTCAATGATGCTCTGTTCTTCTGATATCTTTGAA 840
| | | | |
QY 984 AGTCAAGATTAAGAGTCAAAACAATATATATGATGATGAGATGACAAATCTGAGATA 1043
| | | | |
Db 841 AGTCAAGATTAAGAGTCAAAACAATATATATGATGATGAGATGACAAATCTGAGATA 900
| | | | |
QY 1044 TTGGAGCCAGAAATGATATAGTAAAGAGCCCAATTCACACTACATAACCAATGTT 1103
| | | | |
Db 901 TTGGAGCCAGAAATGATATAGTAAAGAGCCCAATTCACACTACATAACCAATGTT 960
| | | | |
QY 1104 ACTCATTTGTCGATCATGTCGCGAGTGCAATCATATGATCTCTGTTTACTTAAAG 1163
| | | | |
Db 961 ACTCATTTGTCGATCATGTCGCGAGTGCAATCATATGATCTCTGTTTACTTAAAG 1020
| | | | |
QY 1164 GCTCAAGATTAATATATTCCTCCCAATTCCTGATCCGCGAAGATTTTAAAGAAATGTT 1223
| | | | |
Db 1021 GCTCAAGATTAATATATTCCTCCCAATTCCTGATCCGCGAAGATTTTAAAGAAATGTT 1080
| | | | |
QY 1224 TGGAGACCAAGATGATATCTGCACTGGAAGAAATGACATCTATGAGAGCAAC 1283
| | | | |
Db 1081 TGGAGACCAAGATGATATCTGCACTGGAAGAAATGACATCTATGAGAGCAAC 1140
| | | | |
QY 1284 CAAGAGGAAACCGACTCTGTATGTCGATAGAAAACCTGAAGAACCTCTCATGATG 1343
| | | | |
Db 1141 CAAGAGGAAACCGACTCTGTATGTCGATAGAAAACCTGAAGAACCTCTCATGATG 1200
| | | | |
QY 1344 GAGATATATTTATTTTACCTTCACTGAGACCTTGAGAGAGA 1383
| | | | |
Db 1201 GAGATATATTTATTTTACCTTCACTGAGACCTTGAGAGAGA 1240
| | | | |
RESULT 14
US-10-850-270-3
; Sequence 3, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides

; FILE REFERENCE: 12175890/EU
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
; OTHER INFORMATION:
US-10-850-270-3

Query Match 79.9%; Score 1105; DB 10; Length 1284;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 194
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Db 78 CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 137
| | | | |
QY 195 CACAGTAATATGACATGGAATCCACGAGGGAGCCAGTCAATTTGATGATGATGATG 254
| | | | |
Db 138 CACAGTAATATGACATGGAATCCACGAGGGAGCCAGTCAATTTGATGATGATGATG 197
| | | | |
QY 255 TTTTACTCATTTTGGGACAAACAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 314
| | | | |
Db 198 TTTTACTCATTTTGGGACAAACAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 257
| | | | |
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCCAATGA 374
| | | | |
Db 258 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCCAATGA 317
| | | | |
QY 375 GAGTGAAGAGCCTAGCAATTTGGTGAATAATGATCTCACCCCGAAGAGTATCTGA 434
| | | | |
Db 318 GAGTGAAGAGCCTAGCAATTTGGTGAATAATGATCTCACCCCGAAGAGTATCTGA 377
| | | | |
QY 435 GTCTGCTGATCGAATCTTCAATGCAATTTGGACAACTGAGCTACATGAAGTCTTG 494
| | | | |
Db 378 GTCTGCTGATCGAATCTTCAATGCAATTTGGACAACTGAGCTACATGAAGTCTTG 437
| | | | |
QY 495 GCTCCCTGGAAGAAATCCAGTCCGACACTAATTAATCTTACTTACTATTTGGACAGAG 554
| | | | |
Db 438 GCTCCCTGGAAGAAATCCAGTCCGACACTAATTAATCTTACTTACTATTTGGACAGAG 497
| | | | |
QY 555 CCGGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCCAATPACTTTGGTTGTC 614
| | | | |
Db 498 CCGGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCCAATPACTTTGGTTGTC 557
| | | | |
QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGTGAACAACAGTGTCCAATAATATGTT 674
| | | | |
Db 558 CTTTGATCTGACCAAGTGAAGATTCAGTTTGTGAACAACAGTGTCCAATAATATGTT 617
| | | | |
QY 675 CAAGATTAATGCAAGAAAAATTAACCAATCTTCAATATATATGTCCTTTAACTTCCGTGT 734
| | | | |
Db 618 CAAGATTAATGCAAGAAAAATTAACCAATCTTCAATATATATGTCCTTTAACTTCCGTGT 677
| | | | |
QY 735 GAAACCTGATCCCTCCCATATTAATAAACCTCTCTCCCAATGATGACCTATATGTCGA 794
| | | | |
Db 678 GAAACCTGATCCCTCCCATATTAATAAACCTCTCTCCCAATGATGACCTATATGTCGA 737
| | | | |
QY 795 ATGGAGAAATCCACAGAAATTTATGACAGATGCTATTTATGAGATGAGAACTCAATA 854
| | | | |
Db 738 ATGGAGAAATCCACAGAAATTTATGACAGATGCTATTTATGAGATGAGAACTCAATA 797
| | | | |
QY 855 CAGCCAACTGAGACACATATGTTTCTACGTCAGAGGCTTAATGAGAACTCAGA 914
| | | | |

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Db      798 CAGCCAACTGAGACACATTAATGTTTCTACGTCACAAAGGCTAAATGTGAAATCCAGA 857
Qy      915 ATTTGAGAGAAATGAGAAATACATCTTGTTCATGTCCTGGTGTCTTCTCTGATAC 974
Db      858 ATTTGAGAGAAATGAGAAATACATCTTGTTCATGTCCTGGTGTCTTCTCTGATAC 917
Qy      975 TTTGAAACCACTGACAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1034
Db      918 TTTGAAACCACTGACAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 977
Qy      1035 CTGAGATTAATGAGGACCAAGAAATGAGTAAAGGCAATTCACACTCTACAT 1094
Db      978 CTGAGATTAATGAGGACCAAGAAATGAGTAAAGGCAATTCACACTCTACAT 1037
Qy      1095 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTCAATCATAGTACTCTGCTCTTA 1154
Db      1038 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTCAATCATAGTACTCTGCTCTTA 1097
Qy      1155 CCTTAAAAAGGCTCAAGATTATTTATTTCTCCATTCCTGATCCTGCGCAAGATTCTTAA 1214
Db      1098 CCTTAAAAAGGCTCAAGATTATTTATTTCTCCATTCCTGATCCTGCGCAAGATTCTTAA 1157
Qy      1215 AGAATGTTTGGAGACCAAGATGATGATCTGTCATCTGGAAGAGTACATCTATGA 1274
Db      1158 AGAATGTTTGGAGACCAAGATGATGATCTGTCATCTGGAAGAGTACATCTATGA 1217
Qy      1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCCTC 1334
Db      1218 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCCTC 1277
Qy      1335 TCAGTGA 1341
Db      1278 TCAGTGA 1284

RESULT 15
US-10-278-698-6
; Sequence 6, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Hauptl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-6

Query Match      79.2%; Score 1096; DB 9; Length 1572;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      342 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 401
Qy      375 GAGTGAAGGCTTGACATTTTGTGAAAAATGCACTCACCCAGAGGATCCGGA 434
Db      402 GAGTGAAGGCTTGACATTTTGTGAAAAATGCACTCACCCAGAGGATCCGGA 461
Qy      435 GTCTGCTGTGACTGAATCTTCAATGCAATTTGGACAAACCTGAGCTACATGAAGTGTCTTG 494
Db      462 GTCTGCTGTGATTTAGGCTTGATGATCATTTGGACAAACCTGAGCTACATGAAGTGTCTTG 521
Qy      495 GCTCCCTGGAAGAAATACAGTCCCGACACTAATCTATCTCTGATATTTGGACAGAG 554
Db      522 GCTCCCTGGAAGAAATACAGTCCCGACACTAATCTATCTCTGATATTTGGACAGAG 581
Qy      555 CCTGGAATAAATTCATCAATGTTGAAAACCTTTAGAGAGGCCAATCTTTGGTGTTC 614
Db      582 CCTGGAATAAATTCATCAATGTTGAAAACCTTTAGAGAGGCCAATCTTTGGTGTTC 641
Qy      615 CTTTGATCTGACCAAGAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATPAATGAT 674
Db      642 CTTTGATCTGACCAAGAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATPAATGAT 701
Qy      675 CAAGATATGACAGAAAAATTTAAACCATCTTCAATATAGTGCCTTTACTCCCGTGT 734
Db      702 CAAGATATGACAGAAAAATTTAAACCATCTTCAATATAGTGCCTTTAACTCCCGTGT 761
Qy      735 GAAACCTGATCCTCCACATATTAATAAACCTTCTCTTCCACATATGATGACCTATATGTCGA 794
Db      762 GAAACCTGATCCTCCACATATTAATAAACCTTCTCTTCCACATATGATGACCTATATGTCGA 821
Qy      795 ATGGAGAAATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGAGATCAATPA 854
Db      822 ATGGAGAAATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGAGATCAATPA 881
Qy      855 CAGCCAAACTGAGACACATATATGTTTCTAGCTCCAGAGGCTAAATGTGAAATCCAGA 914
Db      882 CAGCCAAACTGAGACACATATATGTTTCTAGCTCCAGAGGCTAAATGTGAAATCCAGA 941
Qy      915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGTGTCTTCTGATAC 974
Db      942 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGTGTCTTCTGATAC 1001
Qy      975 TTTGAACACAGTCAAGATTAAGAGTCAAAACAAATTAATTTGATAGAGATGCAACT 1034
Db      1002 TTTGAACACAGTCAAGATTAAGAGTCAAAACAAATTAATTTGATAGAGATGCAACT 1061
Qy      1035 CTGAGATTAATTTGAGGACCAAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1094
Db      1062 CTGAGATTAATTTGAGGACCAAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1121
Qy      1095 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGGTGCAATCATAGTACTCTGCTTTA 1154
Db      1122 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGGTGCAATCATAGTACTCTGCTTTA 1181
Qy      1155 CCTTAAAAAGGCTCAAGATTATTTATTTATTCCTCCAAATTCCTGATCCTGCGAAATTTTAA 1214
Db      1182 CCTTAAAAAGGCTCAAGATTATTTATTTATTCCTCCAAATTCCTGATCCTGCGAAATTTTAA 1241
Qy      1215 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAAATGATCTATGA 1274
Db      1242 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAAATGATCTATGA 1301
Qy      1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATGAGAAACCTGAAGAAAGCCTC 1334
Db      1302 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATGAGAAACCTGAAGAAAGCCTC 1361
Qy      1335 TCAGTATGAGATTAATTTATTTTAACTTCACTGACCTGAGAGA 1383
Db      1362 TCAGTATGAGATTAATTTATTTTAACTTCACTGACCTGAGAGA 1410

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Db 168 CACAGTAATATGAGATGGAATCCAGCGAGGAGCCAGCTCAAAATTGATGATAGGTA 227
QY 255 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAACGTGCTCAAT 314
Db 228 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAACGTGCTCAAT 287
QY 315 AGAAGTAACCTGATATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGAACCAATGA 374
Db 288 AGAAGTAACCTGATATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGAACCAATGA 347
QY 375 GAGTGAAGCCCTAGAGATTTGTGTAAGAAAATGATCTACCCCGAAGGATACCTGTA 434
Db 348 GAGTGAAGCCCTAGAGATTTGTGTAAGAAAATGATCTACCCCGAAGGATACCTGTA 407
QY 435 GTCTGCTGTAAGTGAATCTCAATGATGTTGGCAACAACCTGAGTACATGAAGTCTTG 494
Db 408 GTCTGCTGTAAGTGAATCTCAATGATGTTGGCAACAACCTGAGTACATGAAGTCTTG 467
QY 495 GCTCCCTGGAAGAAATACAGTCCCGACACTAACTATCTCTACTATTGGGACAGAAAG 554
Db 468 GCTCCCTGGAAGAAATACAGTCCCGACACTAACTATCTCTACTATTGGGACAGAAAG 527
QY 555 CCTGGAAGAAAATTCATCAATGTAAGAAAACATCTTTAGGAAGGCCAATCTTGGTGTTC 614
Db 528 CTTGGAAGAAAATTCATCAATGTAAGAAAACATCTTTAGGAAGGCCAATCTTGGTGTTC 587
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTCTTTGGAACAACAAGTGTCCAAATATGT 674
Db 588 CTTTGAATCTGACCAAGTGAAGATTCAGTCTTTGGAACAACAAGTGTCCAAATATGT 647
QY 675 CAAAGTAATGACGAAAAATTTAAACCATCTTCAATATATGTGCTTTAACTTCCGTGT 734
Db 648 CAAAGTAATGACGAAAAATTTAAACCATCTTCAATATATGTGCTTTAACTTCCGTGT 707
QY 735 GAAACCTGATCCCTCAATTTAAAAACCTCTCTTCCCAAGATGAGACCTATATGGA 794
Db 708 GAAACCTGATCCCTCAATTTAAAAACCTCTCTTCCCAAGATGAGACCTATATGGA 767
QY 795 ATGGGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAGATAGATCAATTA 854
Db 768 ATGGGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAGATAGATCAATTA 827
QY 855 CAGCCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTTAATGTGAATCCAGA 914
Db 828 CAGCCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTTAATGTGAATCCAGA 887
QY 915 ATTTGAGAAATGTGAGAAATACATCTTCTTCAAGTCCCTGAGTGTCTTCTGATAC 974
Db 888 ATTTGAGAAATGTGAGAAATACATCTTCTTCAAGTCCCTGAGTGTCTTCTGATAC 947
QY 975 TTTGAACACAGTCAGATAGATGTCAAAACAATTAAGTTATGCTATAGAGTACAAT 1034
Db 948 TTTGAACACAGTCAGATAGATGTCAAAACAATTAAGTTATGCTATAGAGTACAAT 1007
QY 1035 CTGAGATATTTGAGCCCAAGAAATGAGTATAGTAAAGCCGAATTCACACTTACAT 1094
Db 1008 CTGAGATATTTGAGCCCAAGAAATGAGTATAGTAAAGCCGAATTCACACTTACAT 1067
QY 1095 AACCATGTTACTGATGTTCCAGTACGTCGCGAGGAGCAATCATAGTACTCTCGCTTA 1154
Db 1068 AACCATGTTACTGATGTTCCAGTACGTCGCGAGGAGCAATCATAGTACTCTCGCTTA 1127
QY 1155 CCTAAAGAGCTCAAGTTATTTATTTCCCTCCAAATCTCGATCTGGCAAGATTTTAA 1214
Db 1128 CCTAAAGAGCTCAAGTTATTTATTTCCCTCCAAATCTCGATCTGGCAAGATTTTAA 1187
QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAAAGTACGACATCTATGA 1274
Db 1188 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAAGAAAGTACGACATCTATGA 1247
QY 1275 GAAAGCAACCAAGAGAAACCGACCTGATAGTGTGATGAAACCTGGAAGAAAGCTC 1334
Db 1248 GAAAGCAACCAAGAGAAACCGACCTGATAGTGTGATGAAACCTGGAAGAAAGCTC 1307

QY 1335 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db 1308 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1356

RESULT 2
US-11-266-748A-56241
; Sequence 56241, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56241
; LENGTH: 4006
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56241

Query Match 86.6%; Score 1198; DB 8; Length 4006;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG 194
Db 121 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG 180
QY 195 CACAGTAATATGAGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGTA 254
Db 181 CACAGTAATATGAGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGTA 240
QY 255 TTTTACTGATTTTGGGACAAACAAGATAGAAAATAGTCCGGAAAACGTGCTCAAT 314
Db 241 TTTTACTGATTTTGGGACAAACAAGATAGAAAATAGTCCGGAAAACGTGCTCAAT 300
QY 315 AGAAGTAACCTGATATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGAACCAATGA 374
Db 301 AGAAGTAACCTGATATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGAACCAATGA 360
QY 375 GAGTGAAGCCCTAGAGATTTTGTGTAAGAAAATGATCTCACCCCGAAGGATGATCTGA 434
Db 361 GAGTGAAGCCCTAGAGATTTTGTGTAAGAAAATGATCTCACCCCGAAGGATGATCTGA 420
QY 435 GTCTGCTGTAAGTGAATCTCAATGATGTTGGCAACAACCTGAGTACATGAAGTCTTG 494
Db 421 GTCTGCTGTAAGTGAATCTCAATGATGTTGGCAACAACCTGAGTACATGAAGTCTTG 480
QY 495 GCTCCCTGGAAGAAATACAGTCCCGACACTAACTATCTTACTATTGGGACAGAAAG 554

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Db 481 GCTCCCTGGAAGAAATACAGTCCCGACACTAATCTCTACTATTGGCAGAG 540
Qy 555 CTTGGAAGAAATTCATCATGTGAAACATCTTTAGAGAGCCAAATCTTGGTGTTC 614
Db 541 CTTGGAAGAAATTCATCATGTGAAACATCTTTAGAGAGCCAAATCTTGGTGTTC 600
Qy 615 CTTTGTATCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATATGT 674
Db 601 CTTTGTATCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATATGT 660
Qy 675 CAAGGATATGCGAGGAAATTAACATCTTCAATATAGTGGCTTAACTCCGCT 734
Db 661 CAAGGATATGCGAGGAAATTAACATCTTCAATATAGTGGCTTAACTCCGCT 720
Qy 735 GAAACCTGATCTCCATATATTAATAACCTCTCCCTCCACATATGACCTATATGCA 794
Db 721 GAAACCTGATCTCCATATATTAATAACCTCTCCCTCCACATATATGACCTATATGCA 780
Qy 795 ATGGAGAAATCCACAGAAATTTATTAAGATGCTTATTTATGAAGTGAATCAATA 854
Db 781 ATGGAGAAATCCACAGAAATTTATTAAGATGCTTATTTATGAAGTGAATCAATA 840
Qy 855 CAGCCAAATCTGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGTGATCCAGA 914
Db 841 CAGCCAAATCTGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGTGATCCAGA 900
Qy 915 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCATGCTCCCTGCTTCTCTGATAC 974
Db 901 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCATGCTCCCTGCTTCTCTGATAC 960
Qy 975 TTTGAAACAGTCAGAAATTAAGAGTCAAAACAAATTAATTAATGCTATGAGATGCAAACT 1034
Db 961 TTTGAAACAGTCAGAAATTAAGAGTCAAAACAAATTAATTAATGCTATGAGATGCAAACT 1020
Qy 1035 CTGAGATTAATTTGAGCCCAAGAAATGATTAATGTTAAAGAGGCAATTCACACTCTATCAT 1094
Db 1021 CTGAGATTAATTTGAGCCCAAGAAATGATTAATGTTAAAGAGGCAATTCACACTCTATCAT 1080
Qy 1095 AACCATGTTAATCTGATGTCATGTCATGTCGAGGAGCAATCAATATGCTCCGCTTAA 1154
Db 1081 AACCATGTTAATCTGATGTCATGTCATGTCGAGGAGCAATCAATATGCTCCGCTTAA 1140
Qy 1155 CCTTAAAGAGGCTCAGATTAATTAATCCCTCCATCTGATCTCTGCAAGATTTTAA 1214
Db 1141 CCTTAAAGAGGCTCAGATTAATTAATCCCTCCATCTGATCTCTGCAAGATTTTAA 1200
Qy 1215 AGAAATGTTTGAAGACCAAGATGATGATCTGCACTGGAAGAGTACGATCTATGA 1274
Db 1201 AGAAATGTTTGAAGACCAAGATGATGATCTGCACTGGAAGAGTACGATCTATGA 1260
Qy 1275 GAAGCAAAACCAAGAGGAAACCGACTCTGTAAGTCTGATAGAAAACCTGAAGAAAGCTC 1334
Db 1261 GAAGCAAAACCAAGAGGAAACCGACTCTGTAAGTCTGATAGAAAACCTGAAGAAAGCTC 1320
Qy 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAGA 1383
Db 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGATGACCTTGAGAGA 1369
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RESULT 3

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US-11-266-748A-185183
; Sequence 185183, Application US/11266748A
; Publication NO. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIORITY APPLICATION NUMBER: EP 04105479.2
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;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105482.6
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105483.4
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105507.0
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105485.9
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105484.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: US 60/662,276
;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700,293
;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 185183
;; LENGTH: 2741
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1520)..(1834)
;; OTHER INFORMATION: n is a, c, g, or t
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2177)..(2186)
;; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-185183
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Query Match 69.3%; Score 958; DB 8; Length 2741;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1008; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 375 GAGTGAGAGACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCGA 434
Db 44 GAGTGAGAGACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCGA 103
Qy 435 GTCTGCTGTGACGTGAATTTCAATGATCTTTGGCACAACCTGAGTCAATGAAGTTCCTG 494
Db 104 GTCTGCTGTGACGTGAGCTTCAATGATCTTTGGCACAACCTGAGTCAATGAAGTTCCTG 163
Qy 495 GCTCCCTGGAAGAAATCCAGTCCCGACCTAATCTCTACTAATTTGGCAGAGAG 554
Db 164 GCTCCCTGGAAGAAATCCAGTCCCGACCTAATCTCTACTAATTTGGCAGAGAG 223
Qy 555 CTTGGAAGAAATTCATCATGTGAAACATCTTTAGAGAGCCAAATCTTGGTGTTC 614
Db 224 CTTGGAAGAAATTCATCATGTGAAACATCTTTAGAGAGCCAAATCTTGGTGTTC 283
Qy 615 CTTTGTATCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATATGT 674
Db 284 CTTTGTATCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATATGT 343
Qy 675 CAAGGATATGCGAGGAAATTAACATCTTCAATATAGTGGCTTAACTCCGCT 734
Db 344 CAAGGATATGCGAGGAAATTAACATCTTCAATATAGTGGCTTAACTCCGCT 403
Qy 735 GAAACCTGATCTCCATATATTAATAACCTCTCCCTCCACATATGACCTATATGCA 794
Db 404 GAAACCTGATCTCCATATATTAATAACCTCTCCCTCCACATATATGACCTATATGCA 463
Qy 795 ATGGAGAAATCCACAGAAATTTATTAAGATGCTTATTTATGAAGTGAATCAATA 854
Db 464 ATGGAGAAATCCACAGAAATTTATTAAGATGCTTATTTATGAAGTGAATCAATA 523
Qy 855 CAGCCAAATCTGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGTGATCCAGA 914
Db 524 CAGCCAAATCTGAGACATATATGTTTCTAGCTCCAGAGGCTAAATGTGATCCAGA 583
Qy 915 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCATGCTCCGCTGTTCTCTGATAC 974
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Db 584 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTGTATAC 643
Qy 975 TTGGAACACAGTCAGATAAGAGTCAAAACAAATTAAGTTATGCTATGAGGATGACAAACT 1034
Db 644 TTGGAACACAGTCAGATAAGAGTCAAAACAAATTAAGTTATGCTATGAGGATGACAAACT 703
Qy 1035 CTGAGTAATTTGAGCCAGAGAAATGAGTATAGTAAAGAGCCAAATTTCCACTCTACAT 1094
Db 704 CTGAGTAATTTGAGCCAGAGAAATGAGTATAGTAAAGAGCCAAATTTCCACTCTACAT 763
Qy 1095 AACCATGTTACTCATTTGTTCTCAGTCATCGTCGAGGAGCAATCATATGTAATCTCCGCTTTA 1154
Db 764 AACCATGTTACTCATTTGTTCTCAGTCATCGTCGAGGAGCAATCATATGTAATCTCCGCTTTA 823
Qy 1155 CCTAAAAGGCTCAAGATTATTAATTTTCCCTCCAAATTTCTGATCTGGCAAGATTTTAA 1214
Db 824 CCTAAAAGGCTCAAGATTATTAATTTTCCCTCCAAATTTCTGATCTGGCAAGATTTTAA 883
Qy 1215 AGAAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAGAGATGACATCTATGA 1274
Db 884 AGAAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAGAGATGACATCTATGA 943
Qy 1275 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1334
Db 944 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1003
Qy 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
Db 1004 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1052

RESULT 4
US-11-266-748A-192679
; Sequence 192679, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 192679
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-192679

Query Match 66.7%; Score 923; DB 8; Length 975;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 135 CGGCCTACGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTGAAAAAAGCTCTG 194

Db 2 CGGCCTACGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTGAAAAAAGCTCTG 61
Qy 195 CACAGTAATATGACATGGAATCCACCCGAGGAGGACAGCTCAAAATTTAGTCTATGTA 254
Db 62 CACAGTAATATGACATGGAATCCACCCGAGGAGGACAGCTCAAAATTTAGTCTATGTA 121
Qy 255 TTTTACTCATTTTGGCGCAACACAGATTAAGAAATAGCTCCGGAATCTGCTTCAAT 314
Db 122 TTTTACTCATTTTGGCGCAACACAGATTAAGAAATAGCTCCGGAATCTGCTTCAAT 181
Qy 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCAAATGA 374
Db 182 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCAAATGA 241
Qy 375 GAGTGAAGAGCCTAGCATTTTGGTTGAAAAATGCAATCCGCCAGAAAGTATCTGA 434
Db 242 GAGTGAAGAGCCTAGCATTTTGGTTGAAAAATGCAATCCGCCAGAAAGTATCTGA 301
Qy 435 GTCTGCTGTGACTGAATCTTCAATGCAATTTGGCAAACTGTAGTACATGAAGTCTTG 494
Db 302 GTCTGCTGTGACTGAATCTTCAATGCAATTTGGCAAACTGTAGTACATGAAGTCTTG 361
Qy 495 GCTCCCTGGAAGGAATACAGTCCGCACTAATCTACTTCTACTATTTGGCAGAGAAG 554
Db 362 GCTCCCTGGAAGGAATACAGTCCGCACTAATCTACTTCTACTATTTGGCAGAGAAG 421
Qy 555 CCTGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAGGCCAATACCTTGGTTTC 614
Db 422 CCTGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAGGCCAATACCTTGGTTTC 481
Qy 615 CTTTGATCTGACCAAGTGAAGANTCCAGTTTGAACAACAGTGTCCAAATTAATGCT 674
Db 482 CTTTGATCTGACCAAGTGAAGANTCCAGTTTGAACAACAGTGTCCAAATTAATGCT 541
Qy 675 CAAGATATGACAGAAAAATTAACATCCTTCAATATATAGTCCCTTAATCCGCTGT 734
Db 542 CAAGATATGACAGAAAAATTAACATCCTTCAATATATAGTCCCTTAATCCGCTGT 601
Qy 735 GAAACCTGATCTCCCATATTTAAACCTCTCTCCCAATGATGACCTATATGTGA 794
Db 602 GAAACCTGATCTCCCATATTTAAACCTCTCTCCCAATGATGACCTATATGTGA 661
Qy 795 ATGGAGAAATCCACAGATTTTATTTAGCAGATGCTATTTTATGAAGTGAAGTCAAT 854
Db 662 ATGGAGAAATCCACAGATTTTATTTAGCAGATGCTATTTTATGAAGTGAAGTCAAT 721
Qy 855 CAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTAAATGAGAAATCCAGA 914
Db 722 CAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTAAATGAGAAATCCAGA 781
Qy 915 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGTTCTCTGTATAC 974
Db 782 ATTTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGTTCTCTGTATAC 841
Qy 975 TTGGAACACAGTCAGATAAGAGTCAAAACAAATTAAGTTATGCTATGAGGATGACAAACT 1034
Db 842 TTGGAACACAGTCAGATAAGAGTCAAAACAAATTAAGTTATGCTATGAGGATGACAAACT 901
Qy 1035 CTGAGTAATTTGAGCCAGAGAAATGAGTATAGTAAAGAGCCAAATTTCCACTCTACAT 1094
Db 902 CTGAGTAATTTGAGCCAGAGAAATGAGTATAGTAAAGAGCCAAATTTCCACTCTACAT 961
Qy 1095 AACCATGTTACTCA 1108
Db 962 AACCATGTTACTCA 975

RESULT 5
US-11-266-748A-226550
; Sequence 226550, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662, 276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700, 293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patent version 3.3
SEQ ID NO 236550
LENGTH: 975
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-226550
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Query Match 56.7%; Score 923; DB 8; Length 975;

Best Local Similarity 99.9%; Pred. No. 0; Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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135 CGCGCCCTACGGAACCTGAGCAGCCTGAGCAAAATTTGAGTCTCTGTGTAACCTCTG 194
2 CGGCCCTACGGAACCTGAGCAGCCTGAGCAAAATTTGAGTCTCTGTGTAACCTCTG 61
195 CACAGTAATATGACATGAGAAATCCAGCCGAGGAGCCAGCTCAATATGATCTATGTA 254
62 CACAGTAATATGACATGAGAAATCCAGCCGAGGAGCCAGCTCAATATGATCTATGTA 121
255 TTTTATGATCTATGAGCAAAATGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 314
122 TTTTATGATCTATGAGCAAAATGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 181
315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCACCAATGA 374
182 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCACCAATGA 241
375 GAGTGAAGCCTTATGATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTGA 434
242 GAGTGAAGCCTTATGATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTGA 301
435 GTCTGCTGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATG 494
302 GTCTGCTGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATG 361
495 GTCTGCTGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATG 554
362 GTCTGCTGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATGATCTATG 421
555 CTTGGAAGAAATTCATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 614
422 CTTGGAAGAAATTCATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 481
615 CTTGGAAGAAATTCATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 674
482 CTTGGAAGAAATTCATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 541
675 CAGGATATGATGAGGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 734
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542 CAAGATATGATGAGGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 601
735 GAAACCTGATCTCTCAATATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 794
602 GAAACCTGATCTCTCAATATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 661
795 ATGGAGAAATCCAGAAATTTATAGAGATGCTATTTATAGAGTAAGTAAGTAAGTAAGTTC 854
662 ATGGAGAAATCCAGAAATTTATAGAGATGCTATTTATAGAGTAAGTAAGTAAGTAAGTTC 721
855 CAGCAAACTGAGACATTAATGTTTCTACGTCAGAGGCTTAATGAGTAAGTAAGTAAGTTC 914
722 CAGCAAACTGAGACATTAATGTTTCTACGTCAGAGGCTTAATGAGTAAGTAAGTAAGTTC 781
915 ATTTGAGAAATTTGAGAAATTAATGATCTGTTTATGATGCTCTGTTTCTCTGATAC 974
782 ATTTGAGAAATTTGAGAAATTAATGATCTGTTTATGATGCTCTGTTTCTCTGATAC 841
975 TTTGACACAGTCAAGTAATTAAGTCAAAACAAATTAAGTATGATGAGTAAGTAAGTTC 1034
842 TTTGACACAGTCAAGTAATTAAGTCAAAACAAATTAAGTATGATGAGTAAGTAAGTTC 901
1035 CTGAGTAATTTGAGCAAGAAATGATATAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 1094
902 CTGAGTAATTTGAGCAAGAAATGATATAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 961
1095 AACCATGTTACTCA 1108
962 AACCATGTTACTCA 975
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RESULT 6

US-11-266-748A-54658

Sequence 54658, Application US/11266748A

Publication No. US2006013463A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcription Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266, 748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662, 276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700, 293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: Patent version 3.3

SEQ ID NO 54658

LENGTH: 1016

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (60)..(60)

OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-54658

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Query Match      61.2%; Score 846; DB 8; Length 1016;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGGAAGTCTGAGCACCCTGAGACAAATTTGAGTGTCTCTGTGAAAAACCTCTG 134
DB 79 CGGCGCTACGGAAGTCTGAGCACCCTGAGACAAATTTGAGTGTCTCTGTGAAAAACCTCTG 138
QY 195 CACAGTAATATGACATGGAATCCACCAGAGGAGCCAGTCAATTTGATGATGTA 254
DB 139 CACAGTAATATGACATGGAATCCACCAGAGGAGCCAGTCAATTTGATGATGTA 198
QY 255 TTTTACTCATTTTGGGACAAACAAGTAAGAAATAGCTCCGGAACCTGTGTTCAAT 314
DB 199 TTTTACTCATTTTGGGACAAACAAGTAAGAAATAGCTCCGGAACCTGTGTTCAAT 258
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACATGA 374
DB 259 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACATGA 318
QY 375 GAGTGAAGACCTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGTATCTCTGA 434
DB 319 GAGTGAAGACCTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGTATCTCTGA 378
QY 435 GTCTGCTGTACTGGAATCTTAATGATCTTGGGACACCTGATGATCACTGAAGTCTTG 494
DB 379 GTCTGCTGTACTGGAATCTTAATGATCTTGGGACACCTGATGATCACTGAAGTCTTG 438
QY 495 GCTCCCTGGAAGGAATCCAGTCCCGACACCTAATCTACTCTACTATTGGGACAGAG 554
DB 439 GCTCCCTGGAAGGAATCCAGTCCCGACACCTAATCTACTCTACTATTGGGACAGAG 498
QY 555 CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 614
DB 499 CCTGGAAGAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 558
QY 615 CTTTGAATCTGACCAAAAGTGAAGATTCAGTTTGAACAAACAAGTCCCAATATGCT 674
DB 559 CTTTGAATCTGACCAAAAGTGAAGATTCAGTTTGAACAAACAAGTCCCAATATGCT 618
QY 675 CAAGATTAATGAGGAAGAAATTTAAACCATCTTCAATATAGTGTCTTAATCTCCGCTG 734
DB 619 CAAGATTAATGAGGAAGAAATTTAAACCATCTTCAATATAGTGTCTTAATCTCCGCTG 678
QY 735 GAAACCTGATCTTCCACATATTTAAACCTCTCTTCCACATATGATGATGATGCA 794
DB 679 GAAACCTGATCTTCCACATATTTAAACCTCTCTTCCACATATGATGATGATGCA 738
QY 795 ATGGGGAATCCACAGATTTTATAGCAGATGCTATTTTATGAGATGAGATCAATTA 854
DB 739 ATGGGGAATCCACAGATTTTATAGCAGATGCTATTTTATGAGATGAGATCAATTA 798
QY 855 CAGCCAAACTGAGACACATATGTTTTCTAGCTCCAAAGAGGCTAAATGTAGAAATCCAGA 914
DB 799 CAGCCAAACTGAGACACATATGTTTTCTAGCTCCAAAGAGGCTAAATGTAGAAATCCAGA 858
QY 915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCCTGTGTCTTCTCTGATAC 974
DB 859 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCCTGTGTCTTCTCTGATAC 918
QY 975 TTTTGAACACAGTCAAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAA 1031
DB 919 TTTTGAACACAGTCAAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAA 975
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RESULT 7

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US-11-266-748A-73628/c
; Sequence 73628; Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
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; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73628
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)-(30)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-73628

Query Match      58.6%; Score 811; DB 8; Length 1294;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 ATGTGAAACATCTTTAGAGAGGCCAATACCTTGTGTCTTCTGATGCAAAAGT 632
DB 1099 ATGTGAAACATCTTTAGAGAGGCCAATACCTTGTGTCTTCTGATGCAAAAGT 1040
QY 633 GAAGATTCAGTTTGAACACACAGTGTCCAAATATAGTATAGATTAATGACAGAAA 692
DB 1039 GAAGATTCAGTTTGAACACACAGTGTCCAAATATAGTATAGATTAATGACAGAAA 690
QY 693 AATTAACCATCTTCAATATAGTGTCTTAACTTCCGCTGGAACCTGATCTCCACA 752
DB 979 AATTAACCATCTTCAATATAGTGTCTTAACTTCCGCTGGAACCTGATCTCCACA 720
QY 753 TATTAACCATCTTCCCTCCACATGATGACCTATATGTGCAATGGAGAAATCCACAGAA 812
DB 919 TATTAACCATCTTCCCTCCACATGATGACCTATATGTGCAATGGAGAAATCCACAGAA 860
QY 813 TTTTATTAGCAGATGCTATTTTATGAGATGAGAGCAATTAACGCCAACTGACACACA 872
DB 859 TTTTATTAGCAGATGCTATTTTATGAGATGAGAGCAATTAACGCCAACTGACACACA 800
QY 873 TAAATGTTTTCTAGCTCCAAAGGCTAAATGTGAGATTCAGAAATTTGAGAGAAATGGA 932
DB 799 TAAATGTTTTCTAGCTCCAAAGGCTAAATGTGAGATTCAGAAATTTGAGAGAAATGGA 740
QY 933 GAATACATCTTGTTCATGAGTCCCTGTGTCTTCTCTGATATCTTTGAACACAGTCAAGAT 992
DB 739 GAATACATCTTGTTCATGAGTCCCTGTGTCTTCTCTGATATCTTTGAACACAGTCAAGAT 680
QY 993 AAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAAACTGTGAGATTAATGGAGCCA 1052
DB 679 AAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAAACTGTGAGATTAATGGAGCCA 620
QY 1053 AGAATGAGATTAATGATGAGAGGCAATTCACACACTCTCATATACCATGTTACTCATTTGT 1112
DB 619 AGAATGAGATTAATGATGAGAGGCAATTCACACACTCTCATATACCATGTTACTCATTTGT 560
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QY 1113 TCAGTCATGTCGACAGTGCATATAGTACTCTGCTTACCTAAAGGCTCAAGAT 1172
DB 559 TCCAGTCATGTCGACAGTGCATATAGTACTCTGCTTACCTAAAGGCTCAAGAT 500
QY 1173 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 1232
DB 499 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 440
QY 1233 GAATGATGATATCTGCACTGCAAGAGTACGATCATATGAGAAGCAACGAGAGAGA 1292
DB 439 GAATGATGATATCTGCACTGCAAGAGTACGATCATATGAGAAGCAACGAGAGAGA 380
QY 1293 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTCAGTGTAGATTAATT 1352
DB 379 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTCAGTGTAGATTAATT 320
QY 1353 TATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB 319 TATTTTACCTTCACTGTGACCTTGAGAGA 289

RESULT 8

US-11-266-748A-107924/C
; Sequence 107924, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107924
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-107924

Query Match 58.6%; Score 811; DB 8; Length 1294;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 ATGTGAAAACATCTTTAGAGAGGCCAATACTTGGTTGTTCTTTGATCTGACCAAGT 632
DB 1099 ATGTGAAAACATCTTTAGAGAGGCCAATACTTGGTTGTTCTTTGATCTGACCAAGT 1040
QY 633 GAAGGATTCAGATTGGTGAACAACAACAGTGTCCCAATATAGTCAAGATTAATGACAGAA 692
DB 1039 GAAGGATTCAGATTGGTGAACAACAACAGTGTCCCAATATAGTCAAGATTAATGACAGAA 980

QY 693 AATTAACCAATCCTTCATATATAGTCCCTTACTTCCGCTGAGAAACCTGATCTCCACA 752
DB 979 AATTAACCAATCCTTCATATATAGTCCCTTACTTCCGCTGAGAAACCTGATCTCCACA 920
QY 753 TATTAAAAACCTCTCCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGA 812
DB 919 TATTAAAAACCTCTCCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGA 860
QY 813 TTTTATAGCAGATGCTTATTTTATGAAATGAGTCAATTAACGCCCAATCTGAGACACA 872
DB 859 TTTTATAGCAGATGCTTATTTTATGAAATGAGTCAATTAACGCCCAATCTGAGACACA 800
QY 873 TATGTTTTCAGTCCCAAGAGGCTAATATGAGATCCAGAAATTTGAGAAATGTGGA 932
DB 799 TATGTTTTCAGTCCCAAGAGGCTAATATGAGATCCAGAAATTTGAGAAATGTGGA 740
QY 933 GAATACATCTTGTTCATGCTCCTGCTGCTTCTGATPACTTTGAAACAGTCAGAT 992
DB 739 GAATACATCTTGTTCATGCTCCTGCTGCTTCTGATPACTTTGAAACAGTCAGAT 680
QY 993 AAGAGTCAAAACCAATATAGTATGCTATGAGATGACAAACTCTGAGTAATTTGAGACCA 1052
DB 679 AAGAGTCAAAACCAATATAGTATGCTATGAGATGACAAACTCTGAGTAATTTGAGACCA 620
QY 1053 AGAAATGATATGATGATGAGAGGCAATTCACACTACATTAACCATGTTACTCATTTG 1112
DB 619 AGAAATGATATGATGATGAGAGGCAATTCACACTACATTAACCATGTTACTCATTTG 560
QY 1113 TCAGTCATGTCGACAGTGCATATAGTACTCTGCTTACCTAAAGGCTCAAGAT 1172
DB 559 TCCAGTCATGTCGACAGTGCATATAGTACTCTGCTTACCTAAAGGCTCAAGAT 500
QY 1173 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 1232
DB 499 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 440
QY 1233 GAATGATGATATCTGCACTGCAAGAGTACGATCATATGAGAAGCAACGAGAGAGA 1292
DB 439 GAATGATGATATCTGCACTGCAAGAGTACGATCATATGAGAAGCAACGAGAGAGA 380
QY 1293 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTCAGTGTAGATTAATT 1352
DB 379 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTCAGTGTAGATTAATT 320
QY 1353 TATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB 319 TATTTTACCTTCACTGTGACCTTGAGAGA 289

RESULT 9

US-11-266-748A-126439
; Sequence 126439, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
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; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03

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1 PRIOR APPLICATION NUMBER: EP 04105484.2
2
3 PRIOR FILING DATE: 2004-11-03
4
5 PRIOR APPLICATION NUMBER: US 60/662,276
6
7 PRIOR FILING DATE: 2005-03-14
8
9 PRIOR APPLICATION NUMBER: US 60/700,293
10
11 PRIOR FILING DATE: 2005-07-18
12
13 NUMBER OF SEQ ID NOS: 483,996
14
15 SOFTWARE: PatentIn version 3.3
16
17 SEQ ID NO 126439
18
19 LENGTH: 1294
20
21 TYPE: DNA
22
23 ORGANISM: Homo Sapiens
24
25 FEATURE:
26
27 NAME/KEY: misc feature
28
29 LOCATION: (1265)..(1265)
30
31 OTHER INFORMATION: n is a, c, g, or t
32
33 US-11-266-748A-126439

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Query Match 58.6%; Score 811; DB 8; Length 1294;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	573	ATGTGAAAACAACCTTTTAGAGAAAGGCCAACTACTTTGGTGTGTTCTCTTGAATCTGACCAAAAGT	632
Db	196	ATGTGAAAACAACCTTTTAGAGAAAGGCCAACTACTTTGGTGTGTTCTCTTGAATCTGACCAAAAGT	255
OY	633	GAGGATTTCCAGTTTGTGAAACAACAAGTGCCTCAAAATAATGGTCAAAGATTAATGACAGAAA	692
Db	256	GAGGATTTCCAGTTTGTGAAACAACAAGTGCCTCAAAATAATGGTCAAAGATTAATGACAGAAA	315
OY	693	AATTAAACCATCTTCAATATATAGTGCCTTTAACTTCCGGTGTGAACCTGATCCTCCACA	752
Db	316	AATTAAACCATCTTCAATATATAGTGCCTTTAACTTCCGGTGTGAACCTGATCCTCCACA	375
OY	753	TATTTAAAAAACCCTCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAGAA	812
Db	376	TATTTAAAAAACCCTCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAGAA	435
OY	813	TTTTATTATGACAGATGCTCATTTTATGAAAGTGAAGTCAATTAACGCCAAACTGAGACACA	872
Db	436	TTTTATTATGACAGATGCTCATTTTATGAAAGTGAAGTCAATTAACGCCAAACTGAGACACA	495
OY	873	TAATGTTTTCTTACGTCGCAAGAGGCTAAATGTGAGATCCAGAAATTTGAGAGAAATGTGGA	932
Db	496	TAATGTTTTCTTACGTCGCAAGAGGCTAAATGTGAGATCCAGAAATTTGAGAGAAATGTGGA	555
OY	933	GAATTCATCTTGTTCATGTGTCCTCGTGTTCTTCTGTATCTTTGAAACAAGTCAGAT	992
Db	556	GAATTCATCTTGTTCATGTGTCCTCGTGTTCTTCTGTATCTTTGAAACAAGTCAGAT	615
OY	993	AAGAGTCAAAACAATTAAGTTATGCTATGAGAGATGACAAACTGTGAGATTAATGGAGCCA	1052
Db	616	AAGAGTCAAAACAATTAAGTTATGCTATGAGAGATGACAAACTGTGAGATTAATGGAGCCA	675
OY	1053	AGAAATGAGTATAGGTGAAGAAAGCGCAATTTCCAACCTTACATTAACATGTTACTCATTTGT	1112
Db	676	AGAAATGAGTATAGGTGAAGAAAGCGCAATTTCCAACCTTACATTAACATGTTACTCATTTGT	735
OY	1113	TCCAGTCATCGTCGCAAGGTGCAATCATATGTAATCTCTGCTTTTAACTTAAAAAGGCTCAAAAT	1172
Db	736	TCCAGTCATCGTCGCAAGGTGCAATCATATGTAATCTCTGCTTTTAACTTAAAAAGGCTCAAAAT	795
OY	1173	TATTAATATCCCTCCCAATCCTCGATCCGTGGCAAGATTTTAAAGAAATGTTTGGAGACCA	1232
Db	796	TATTAATATCCCTCCCAATCCTCGATCCGTGGCAAGATTTTAAAGAAATGTTTGGAGACCA	855
OY	1233	GAATGATGATCTCTGCACTGGAGAAGTACGACATCTATGAGAAAGCAAAACCAAGAGAGA	1292
Db	856	GAATGATGATCTCTGCACTGGAGAAGTACGACATCTATGAGAAAGCAAAACCAAGAGAGA	915
OY	1293	AAACGCACTCTGTAGTGCATGATGAAAACCTGAAAGAAAGCTCTCAGTGTATGAGATTAATT	1352
Db	916	AAACGCACTCTGTAGTGCATGATGAAAACCTGAAAGAAAGCTCTCAGTGTATGAGATTAATT	975

[illegible]

RESULT 10

US-11-266-748A-54614
; Sequence 54614, Application US/11266748A
; Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptional Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03 ;

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105493.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/862,278

PRIOR APPLICATION NUMBER: IIS 60/700-293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: Pate

; SEQ ID NO 546

; LENGTH: 902

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; TYPE: DNA
OCCURANCE: 1 time Confirmed

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ORGANISM: *Homo sapiens*

NAME/KEY: misc feature

LOCATION: (872) .. (872)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

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; NAME/KEY: misc_feature
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LOCATION: (902) .. (902)

OTHER INFORMATION: H IS d, C, g, OR L

US-JL-266/46A-24015-TT-CO

Query Match	42.4%	Score 587	DB 8	Length 902
Best Local Similarity	100.0%	Pred. NC	3.6e-308	
Matches 587; Conservative	0	Mismatches	0	Gaps 0

Qy	797	GGGGAAGATCCACAGAAATTTTATTTGACAATGCTATTTTATGAGTAAGATCAATAACA	856
Db	27	GGGAGATATCCACAGAAATTTTATTTGACAATGCTATTTTATGAGTAAGATCAATAACA	86
Qy	857	GCCAACTGAGACACATATATGTTTTCTACGTCGCAAGAGCTTAAATGTGAAATCCAGAT	916
Db	87	GCCAACTGAGACACATATATGTTTTCTACGTCGCAAGAGCTTAAATGTGAAATCCAGAT	146
Qy	917	TTGAGAGAAATGTGGAGATACATCTTTTCATGTCGCTCGTGTCTTCCTGATCTT	976
Db	147	TTGAGAGAAATGTGGAGATACATCTTTTCATGTCGCTCGTGTCTTCCTGATCTT	206
Qy	977	TGAACACGTCGATATAGATGCAAAACAATTAAGTTATGCTATGAGATGCAAACTT	1036
Db	207	TGAACACGTCGATATAGATGCAAAACAATTAAGTTATGCTATGAGATGCAAACTT	266
Qy	1037	GGAGTATTTGAGCCCAAGAAATGAGTATAGGTAAAGCGCAATTCACACTTACATTA	1096

Db 267 GGAGTAATTGAGCCCAAGAAATGATATAGTAAAGAGCGCAATTCCACTCTACATVA 326
Qy 1097 CCATGTACTCATTTGTTCCAGTCAATCGTCGAGGTGCAATCATAGTACTCTGCTTACC 1156
Db 327 CCATGTACTCATTTGTTCCAGTCAATCGTCGAGGTGCAATCATAGTACTCTGCTTACC 386
Qy 1157 TAAAAAGGCTCAAGATTATTTATTTCCCTCAATTTCTGATCTGGCAAGATTTTAAAG 1216
Db 387 TAAAAAGGCTCAAGATTATTTATTTCCCTCAATTTCTGATCTGGCAAGATTTTAAAG 446
Qy 1217 AAATGTTGGAGACCAAGATATATATCTGCACTGGAAGAAATGACATCTATAGA 1276
Db 447 AAATGTTGGAGACCAAGATATATATCTGCACTGGAAGAAATGACATCTATAGA 506
Qy 1277 AGCAACCAAGAGAAACCGACTCTGATGCTGATGAAACCTGAAAGAGCTCTC 1336
Db 507 AGCAACCAAGAGAAACCGACTCTGATGCTGATGAAACCTGAAAGAGCTCTC 566
Qy 1337 AGTATGAGATATATTTATTTTACCTTCACTGATGACCTTGAGAAGA 1383
Db 567 AGTATGAGATATATTTATTTTACCTTCACTGATGACCTTGAGAAGA 613

RESULT 11
US-11-266-748A-73627
; Sequence 73627, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73627
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60)..(60)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)..(168)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (170)..(171)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (174)..(174)

OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (180)..(180)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1011)..(1121)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1125)..(1125)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1133)..(1133)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1138)..(1140)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1142)..(1187)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-73627

Query Match 20.1%; Score 278; DB 8; Length 1297;
Best Local Similarity 99.7%; Pred. No. 2.6e-140;

Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1055 AAATGATATAGTATGAAAGCGCAATTCACACTCTACATACCATGTTACTATGTTTC 1114
Db 217 AAATGATATAGTATGAAAGCGCAATTCACACTCTACATACCATGTTACTATGTTTC 276
Qy 1115 CAGTCATGTCGAGGTCGATATAGTACTCTGCTTTACTTAAAGAGCTCAAGATTA 1174
Db 277 CAGTCATGTCGAGGTCGATATAGTACTCTGCTTTACTTAAAGAGCTCAAGATTA 336
Qy 1175 TTATATTCCTCCAAATTCCTCGATCCGCAAGATTTTAAAGAAATGTTGGAGACAGA 1234
Db 337 TTATATTCCTCCAAATTCCTCGATCCGCAAGATTTTAAAGAAATGTTGGAGACAGA 396
Qy 1235 ATGATGATACTCTGCACTGGAAGAGTACGACATCTATGAAAGCAACCAAGAGGAAA 1294
Db 397 ATGATGATACTCTGCACTGGAAGAGTACGACATCTATGAAAGCAACCAAGAGGAAA 456
Qy 1295 CCGACTCTGTAGTGTGATGAAAGAGTAAAGAGCTCTCAGTGTGAGATTAATTTA 1354
Db 457 CCGACTCTGTAGTGTGATGAAAGAGTAAAGAGCTCTCAGTGTGAGATTAATTTA 516
Qy 1355 TTTTACCTTCACTGATGACCTTGAGAAGA 1383
Db 517 TTTTACCTTCACTGATGACCTTGAGAAGA 545

RESULT 12
US-11-266-748A-107923
; Sequence 107923, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03


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1 PRIOR APPLICATION NUMBER: EP 04105479
2 PRIOR FILING DATE: 2004-11-03
3 PRIOR APPLICATION NUMBER: EP 04105482.6
4 PRIOR FILING DATE: 2004-11-03
5 PRIOR APPLICATION NUMBER: EP 04105483.4
6 PRIOR FILING DATE: 2004-11-03
7 PRIOR APPLICATION NUMBER: EP 04105507.0
8 PRIOR FILING DATE: 2004-11-03
9 PRIOR APPLICATION NUMBER: EP 04105485.9
10 PRIOR FILING DATE: 2004-11-03
11 PRIOR APPLICATION NUMBER: EP 04105484.2
12 PRIOR FILING DATE: 2004-11-03
13 PRIOR APPLICATION NUMBER: US 60/662,276
14 PRIOR FILING DATE: 2005-03-14
15 PRIOR APPLICATION NUMBER: US 60/700,293
16 PRIOR FILING DATE: 2005-07-18
17 NUMBER OF SEQ ID NOS: 483996
18 SOFTWARE: PatentIn version 3.3
19 SEQ ID NO 107923
20
21 LENGTH: 1297
22
23 TYPE: DNA
24
25 ORGANISM: Homo Sapiens
26 FEATURE:
27 NAME/KEY: misc_feature
28 LOCATION: (60)..(60)
29 OTHER INFORMATION: n is a, c, g, or t
30 FEATURE:
31 NAME/KEY: misc_feature
32 LOCATION: (81)..(168)
33 OTHER INFORMATION: n is a, c, g, or t
34 FEATURE:
35 NAME/KEY: misc_feature
36 LOCATION: (170)..(171)
37 OTHER INFORMATION: n is a, c, g, or t
38 FEATURE:
39 NAME/KEY: misc_feature
40 LOCATION: (180)..(180)
41 OTHER INFORMATION: n is a, c, g, or t
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: (184)..(184)
45 OTHER INFORMATION: n is a, c, g, or t
46 FEATURE:
47 NAME/KEY: misc_feature
48 LOCATION: (1011)..(1121)
49 OTHER INFORMATION: n is a, c, g, or t
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: (1125)..(1125)
53 OTHER INFORMATION: n is a, c, g, or t
54 FEATURE:
55 NAME/KEY: misc_feature
56 LOCATION: (1133)..(1133)
57 OTHER INFORMATION: n is a, c, g, or t
58 FEATURE:
59 NAME/KEY: misc_feature
60 LOCATION: (1138)..(1140)
61 OTHER INFORMATION: n is a, c, g, or t
62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: (1142)..(1187)
65 OTHER INFORMATION: n is a, c, g, or t
66
67 US-11-266-748A-107923

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Query Match	20.1%	Score 278;	DB 8;	Length 1297;
Best Local Similarity	99.7%	Pred. No. 2.6e-140;		
Matches 328; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

1055 AAATGAGTATAGGTAAGAAGCGCAATTCACACTCTACATAACCATGTTACTCATTTGTTTC 1114

Db	217	AAATGAGTATGTTAAGAGGCAATTCACACCTCTACATACCATGTCTCACTTCTC	276
QY	1115	CAGTCATGCTGCAGGTGCATCATAGTACTCTGCTTTACCTTAAAGGCTCAAGTTA	1174
Db	277	CAGTCATGCTGCAGGTGCATCATAGTACTCTGCTTTACCTTAAAGGCTCAAGTTA	336
QY	1175	TTATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTAAAGAAATGTTTGGAGACAGA	1234
Db	337	TTATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTAAAGAAATGTTTGGAGACAGA	396
QY	1235	ATGATGATCTCTGCTCAGTGGAAAGTAGACATCTATGGAAGCAAAACCAAGAGGAAA	1294
Db	397	ATGATGATCTCTGCTCAGTGGAAAGTAGACATCTATGGAAGCAAAACCAAGAGGAAA	456
QY	1295	CCGACTCTGTAGTCTGTATGAAAACTGGAAGAAAGCTCTCACTGATGAGATTAATTTA	1354
Db	457	CCGACTCTGTAGTCTGTATGAAAACTGGAAGAAAGCTCTCACTGATGAGATTAATTTA	516
QY	1355	TTTTTACCTTCACGTGACCTTGGAGGA	1383
Db	517	TTTTTACCTTCACGTGACCTTGGAGGA	545

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RESULT 13
US-11-266-748A-126438/C
/ Sequence 126438, Application US/11266748A
/ Publication No. US2006013463A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ TITLE OF INVENTION: Methods of Using the Same
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 126438
/ LENGTH: 1297
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (111)..(156)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (158)..(160)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (165)..(165)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature

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OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (177)..(287)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (114)..(114)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (118)..(118)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1124)..(1124)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1127)..(1128)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130)..(1217)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1238)..(1238)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-126438
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Query Match 20.1%; Score 278; DB 8; Length 1297;

Best Local Similarity 99.7%; Pred. No. 2.6e-140; Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1055 AATGAGTATAGTAAAGACGCAATTCACACTCTACATACCATCTTCTCATTTTC 1114
DB 1081 AATGAGTATAGTAAAGACGCAATTCACACTCTACATACCATCTTCTCATTTTC 1022
QY 1115 CAGTCATCTGCGAGGTGCAATCTCTCTCTTAACTTAAAGGCTCAAGTAA 1174
DB 1021 CAGTCATCTGCGAGGTGCAATCTCTCTCTTAACTTAAAGGCTCAAGTAA 962
QY 1175 TTATATTCCTCCCAATTCGATCTCGGCAAGATTTTAAAGAAATTTGGAGCCAGA 1234
DB 961 TTATATTCCTCCCAATTCGATCTCGGCAAGATTTTAAAGAAATTTGGAGCCAGA 902
QY 1235 ATGATGATCTGCACTGCACTGCAAGAGTACATCTATGAGAGCAACCAAGAGGAA 1294
DB 901 ATGATGATCTGCACTGCACTGCAAGAGTACATCTATGAGAGCAACCAAGAGGAA 842
QY 1295 CCGACTCTGTAGTGTGATGAGAAACCTGGAAGAGCTTCTAGTGTGAGATTAATTTA 1354
DB 841 CCGACTCTGTAGTGTGATGAGAAACCTGGAAGAGCTTCTAGTGTGAGATTAATTTA 782
QY 1355 TTTTACCTTCACTGAGACCTTGAGAGA 1383
DB 781 TTTTACCTTCACTGAGACCTTGAGAGA 753
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RESULT 14

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US-11-266-748A-51095
Sequence 51095, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51095
LENGTH: 583
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (572)..(572)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-51095
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Query Match 4.6%; Score 63; DB 8; Length 583;

Best Local Similarity 100.0%; Pred. No. 1.5e-23; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1321 CTGAGAAACCTCTCAGTATGAGATTAATTTTACCTTCACTGTGACCTTGAGA 1380
DB 1 CTGAGAAACCTCTCAGTATGAGATTAATTTTACCTTCACTGTGACCTTGAGA 60
QY 1381 AGA 1383
DB 61 AGA 63
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RESULT 15

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US-11-218-305-11789
Sequence 11789, Application US/11218305
Publication No. US20060141495A1
GENERAL INFORMATION:
APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: McIsaid, Paul L.
APPLICANT: Tao, Nengsheng
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53660)B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11789
LENGTH: 1264
TYPE: DNA
ORGANISM: Zea mays
US-11-218-305-11789
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Query Match 1.9%; Score 26; DB 7; Length 1264;

Best Local Similarity 100.0%; Pred. No. 0.002; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 111 CGGCGGCGGGGCGGGGCGGGGCGG 136
DB 315 CGGCGGCGGGGCGGGGCGGGGCGG 340
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Search completed: July 7, 2006, 23:52:18
Job time : 205 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2006, 01:35:08 ; Search time 195 Seconds

(without alignments)
998.842 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320

Sequence: 1 MEWPRLCGHMLLTCAGG.....OTKETDVLVLEIKKASQ 426

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2320	100.0	426	2	AAW09822	AAW09822 Human int
2	2309.5	99.5	427	2	AAW24973	AAW24973 Human int
3	2309.5	99.5	427	4	AAB19807	AAB19807 Human int
4	2309.5	99.5	427	8	ADL17812	ADL17812 Human int
5	2309.5	99.5	427	8	ADL82843	ADL82843 Human PRO
6	2309.5	99.5	427	8	ADN04504	ADN04504 Antipori
7	2309.5	99.5	427	8	ADN62575	ADN62575 Human int
8	2309.5	99.5	427	8	ABM82441	ABM82441 Tumour-as
9	2309.5	99.5	427	9	AEC31473	AEC31473 Human IL-
10	2309.5	99.5	427	10	AEE93788	AEE93788 Human nt
11	2309.5	99.5	427	10	AEEF57817	AEEF57817 Acti-IL-1
12	2303.5	99.3	427	8	ADL17813	ADL17813 Human int
13	2302.5	99.2	427	8	ADP17835	ADP17835 Human IL-
14	2302.5	99.2	427	8	ADL17814	ADL17814 Human int
15	2296.5	99.0	427	4	AAB19808	AAB19808 Human int
16	2230.5	96.1	414	8	ADX97531	ADX97531 Pancreat
17	1878	80.9	405	4	AAU69132	AAU69132 Canine in
18	1875.5	80.8	793	3	AAU92208	AAU92208 IL-13/IL-
19	1875.5	80.8	793	7	ABM02181	ABM02181 Human IL-
20	1784.5	76.9	664	7	ADP17841	ADP17841 Chimeric
21	1779.5	76.7	784	3	AAU92207	AAU92207 IL-13/IL-
22	1779.5	76.7	784	7	ABW02180	ABW02180 Human IL-
23	1769	76.2	322	5	AAE13745	AAE13745 Human sol

24	1741	75.0	776	9	AEC31482	AEC31482 Human IL-
25	1741	75.0	776	9	AEC31484	AEC31484 Human IL-
26	1741	75.0	776	9	AEC31478	AEC31478 Human IL-
27	1741	75.0	776	9	AEC31486	AEC31486 Human IL-
28	1741	75.0	776	9	AEC31480	AEC31480 Human IL-
29	1714	73.9	426	2	AAW09821	AAW09821 Mouse int
30	1696	73.1	424	9	ADX97888	ADX97888 Murine IL
31	1536	66.2	286	4	AAU90678	AAU90678 Human DAL
32	942	40.6	177	2	AAW58987	AAW58987 Homo sapi
33	465	20.0	134	8	ADP84617	ADP84617 Human bre
34	463	20.0	172	8	ADP84616	ADP84616 Human bre
35	463	20.0	226	8	ADQ65618	ADQ65618 Novel hum
36	414.5	17.9	82	8	ADQ26844	ADQ26844 Human rec
37	329	14.2	386	4	AAU69135	AAU69135 Canine in
38	318	13.7	398	2	AAR22212	AAR22212 Sequence
39	318	13.7	415	2	AAR22211	AAR22211 Sequence
40	318	13.7	415	2	AAR22217	AAR22217 Sequence
41	318	13.7	415	5	ADZ58697	ADZ58697 Mouse IL-
42	310	13.4	365	4	AAU69136	AAU69136 Canine in
43	304.5	13.1	561	4	AAU69138	AAU69138 Canine IL
44	303.5	13.1	561	4	AAU69141	AAU69141 Canine IL
45	302	13.0	372	2	AAW36616	AAW36616 Canine IL

ALIGNMENTS

RESULT 1	AAW09822	standard; protein; 426 AA.
ID	AAW09822;	
AC	AAW09822;	
XX	15-JUL-1997	(first entry)
DT	Human interleukin-12 receptor alpha chain NR4.	
XX	NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine;	
KW	allergy; asthma; therapy.	
XX	Homo sapiens.	
OS		
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..27
FT	Protein	/label= Sig_peptide
FT	Domain	28..426
FT	Domain	/label= Mat_protein
FT	Domain	28..118
FT	Domain	/label= Extracellular domain
FT	Domain	/note= "Ig-like domain"
FT	Modified-site	36
FT	Modified-site	/label= N-glycosylation site
FT	Modified-site	104
FT	Domain	/label= N-glycosylation site
FT	Domain	119..342
FT	Domain	/label= Hemoreceptor_receptor-domain
FT	Modified-site	137
FT	Modified-site	/label= N-glycosylation site
FT	Region	326..330
FT	Region	/label= WSDMS_motif
FT	Domain	343..366
FT	Domain	/label= Transmembrane_domain
FT	Domain	367..426
FT	Domain	/label= Cytoplasmic_tail
XX	WO9715663-A1.	
XX	01-MAY-1997.	
XX	23-OCT-1996;	96NO-AUD000668.
XX	23-OCT-1995;	95AU-00006135.
XX	22-DEC-1995;	95AU-00007276.

PR 09-SEP-1996; 96AU-00002208.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX WPI; 1997-259018/23.
XX N-PSDB; AAT6165.
XX
XX DNA encoding animal haemopoietin receptor which interacts with
PT interleukin-13 - useful to treat asthma, allergy or condition exacerbated
PT by IgE production.
XX
XX Claim 5; Page 52-54; 93pp; English.
XX
XX Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),
CC designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
CC The human NR4 amino acid sequence was deduced from a composite DNA
CC sequence (AAT6165) derived from bone marrow cDNA clones. Recombinant
CC NR4, or fusion proteins including NR4, can be produced in transformed
CC host cells. The receptor molecules and their components are useful in the
CC development of a range of agonists, antagonists, therapeutics and
CC diagnostic reagents based on ligand interaction with its receptor. esp.
CC for the development of cpds. capable of modulating the activity of IL-13
CC and related cytokines such as interleukin-4 for the treatment of allergy,
CC asthma and other conditions relating to IgE
XX
XX Sequence 426 AA;
SQ
Query Match 100.0%; Score 2320; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 4, 6e-212;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNTLSVSNLCVITWMPPEGASSN 60
DB 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNTLSVSNLCVITWMPPEGASSN 60
QY 61 CSLMYFSHFGDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
DB 61 CSLMYFSHFGDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
QY 121 EGGPESAVTELOCIMHNLSTYKCSWLPGRNTSPDNTYLLYYHRSLEKIHQCENIFREGQ 180
DB 121 EGGPESAVTELOCIMHNLSTYKCSWLPGRNTSPDNTYLLYYHRSLEKIHQCENIFREGQ 180
QY 181 YFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240
DB 181 YFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240
QY 241 DLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQAKCENPEFERNVENTSCFMPV 300
DB 241 DLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQAKCENPEFERNVENTSCFMPV 300
QY 301 VLPDTLNTVIRIKTKNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
DB 301 VLPDTLNTVIRIKTKNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 361 VLLLYLKRLLKIIFFPIPDGKIFKEMFGDNDTLHMKYDIYEKQTEETSVDLIEN 420
DB 361 VLLLYLKRLLKIIFFPIPDGKIFKEMFGDNDTLHMKYDIYEKQTEETSVDLIEN 420
QY 421 LKKAQSQ 426
DB 421 LKKAQSQ 426
RESULT 2
AAW24973
ID AAW24973 standard; protein; 427 AA.
XX
XX AAW24973;
AC
XX
XX 22-JUN-1998 (first entry)

XX
XX Human interleukin-13 alpha receptor.
DE
XX Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KM
XX Homo sapiens.
OS
XX WO9720926-A1.
PN
XX 12-JUN-1997.
PD
XX
XX
XX 07-NOV-1996; 96WO-FR001756.
PF
XX
XX 06-DEC-1995; 95FR-00014424.
PR
XX (SNFI) SANOFI SA.
PA
XX Caput D, Ferrara P, Vita N;
PI
XX WPI; 1997-319773/29.
DR
XX N-PSDB; AAT85827.
XX
XX
XX Claim 8; Page 46-47; 83pp; French.
PS
XX
XX This sequence represents interleukin-13 (IL-13) alpha receptor. The
CC invention relates to new purified peptides comprising 380 or 427 amino
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC affinity, but acquires high affinity when associated with the IL-4
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC diagnostic probes to identify aberrant synthesis or genetic anomalies
CC such as loss of heterozygosity and rearrangements, or chromosomal
CC anomalies. They are also used for production of recombinant IL-13R beta
CC and alpha which can be used as IL-13 antagonists, specifically to
CC regulate IL-13-induced responses for treatment of inflammation and
CC allergy. IL-13 receptors are also useful as antisense molecules for gene
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC immunoassays) to diagnose diseases associated with abnormal expression of
CC IL-13 receptors; when coupled to a toxin also for treatment of
CC overproduction of IL-13R. Cells that express IL-13R at the surface are
CC used to identify ligands and modulators of IL-13R
XX
XX Sequence 427 AA;
SQ
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 4, 7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNTLSVSNLCVITWMPPEGASS 59
DB 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNTLSVSNLCVITWMPPEGASS 60
QY 60 NCSLWYFSHFGDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 119
DB 61 NCSLWYFSHFGDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
QY 120 PEGDPESAVTELOCIMHNLSTYKCSWLPGRNTSPDNTYLLYYHRSLEKIHQCENIFREG 179
DB 121 PEGDPESAVTELOCIMHNLSTYKCSWLPGRNTSPDNTYLLYYHRSLEKIHQCENIFREG 180
QY 180 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPHIKNLSFHN 239
DB 181 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240
QY 240 DDLVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQAKCENPEFERNVENTSCFMPV 299
DB 241 DDLVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQAKCENPEFERNVENTSCFMPV 300
QY 300 GVLVPLTNTVIRIKTKNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIVPIVAGAI 359

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Db      301 GVLPDITNTVIRIKTKNKLCEYEDDKLWSNMSOEMSIGKRNSTLYITMLLIVPIVAGAI 360
Qy      360 IVLLLYKRLKIIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEETSVDLIE 419
Db      361 IVLLLYKRLKIIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEETSVDLIE 420
Qy      420 NLKASQ 426
Db      421 NLKASQ 427

RESULT 3
AAB19807
ID      AAB19807 standard; protein; 427 AA.
XX
AC      AAB19807;
XX
DT      05-MAR-2001 (first entry)
XX
DE      Human interleukin-13 receptor alpha-1.
XX
KM      Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW      atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX      dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX      Homo sapiens.
XX
FH      Key
FT      Peptide
FT      1. .26
FT      /label= Sig_peptide
FT      27. .347
FT      /label= Extracellular_domain
FT      28. .427
FT      /label= Mature_protein
FT      327. .331
FT      /note= "MSXWS motif conserved in the type-I cytokine
FT      receptor superfamily"
FT      348. .367
FT      /label= Transmembrane_domain
FT      368. .427
FT      /label= Cytoplasmic_domain
FT      405. .408
FT      /note= "YXXQ motif, consensus for STAT binding"
XX
PN      US6143871-A.
XX
PD      07-NOV-2000.
XX
PF      12-NOV-1997; 97US-00969125.
XX
PR      13-DEC-1996; 96GB-00025899.
XX
PA      (GAUC/) GAUCHAT J.
PA      (BONN/) BONNEFOY J.
XX
PI      Gauchat J, Bonnefoy J;
XX
DR      WPI, 2001-006445/01.
XX
DR      N-PSDB; AAA88907.
XX
PT      Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT      useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT      eczema, asthma or AIDS.
XX
PS      Claim 2; Fig 1A; 26pp; English.
XX
CC      The present sequence is that of a protein capable of binding human
CC      interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
CC      of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
CC      from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
CC      polypeptide can be used to inhibit IL-13 or IL-4 induced Ige synthesis in
CC      B cells, useful in the treatment of diseases in which Ige or Th2

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CC      differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
CC      rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC      polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC      them which have been shed from cells as a result of disease, e.g. cancer,
CC      leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC      lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC      psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC      glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC      syndrome and toxoplasmosis
XX
SQ      Sequence 427 AA;
XX
Query Match      99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPVYTNLSVENVLCYIWTWNPPEGASS 59
Db      1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETOPVYTNLSVENVLCYIWTWNPPEGASS 60
Qy      60 NCSLMYSHFGDKODKKIAPETRRSIEVPLNERICLVGSOCSTNESKPSILVEKCTSP 119
Db      61 NCSLMYSHFGDKODKKIAPETRRSIEVPLNERICLVGSOCSTNESKPSILVEKCTSP 120
Qy      120 PEGDPESAATVLELCIMWNLISYMKCSWLPGRNTSPDTYTYWHRSLKIHQCENIPREG 179
Db      121 PEGDPESAATVLELCIMWNLISYMKCSWLPGRNTSPDTYTYWHRSLKIHQCENIPREG 180
Qy      180 QYRGCSFDLTKVXDSFEQHSVQIMVKNAGKIKPSNIVPLTSRVKPDPHIKNLSFHN 239
Db      181 QYRGCSFDLTKVXDSFEQHSVQIMVKNAGKIKPSNIVPLTSRVKPDPHIKNLSFHN 240
Qy      240 DDLVYQWENPONTFSLCLFYEVEVNNSTHNVFYQOEKCENPEERVENNTSCFVP 299
Db      241 DDLVYQWENPONTFSLCLFYEVEVNNSTHNVFYQOEKCENPEERVENNTSCFVP 300
Qy      300 GVLPDITNTVIRIKTKNKLCEYEDDKLWSNMSOEMSIGKRNSTLYITMLLIVPIVAGAI 359
Db      301 GVLPDITNTVIRIKTKNKLCEYEDDKLWSNMSOEMSIGKRNSTLYITMLLIVPIVAGAI 360
Qy      360 IVLLLYKRLKIIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEETSVDLIE 419
Db      361 IVLLLYKRLKIIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEETSVDLIE 420
Qy      420 NLKASQ 426
Db      421 NLKASQ 427

RESULT 4
ADL71812
ID      ADL71812 standard; protein; 427 AA.
XX
AC      ADL71812;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human interleukin-13 receptor alpha (IL-13 R) protein.
XX
DE      Human, IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
XX      eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Peptide
FT      1. .26
FT      /label= Signal_peptide
FT      27. .427
FT      /note= "human mature IL-13 R protein"
FT      27. .347
FT      /note= Extracellular domain
FT      327. .331
FT      /note= MSXWS motif

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FT Domain 368..427
FT /note = Cytoplasmic domain
XX
XX US2004043921-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 29-SEP-2003; 2003US-00671697.
XX
XX PR 13-DEC-1996; 96GB-00025899.
XX PR 12-NOV-1997; 97US-00969125.
XX PR 06-APR-2000; 2000US-00545002.
XX
XX PA (BONN/) BONNEFOY J.
XX PA (GAUC/) GAUCHAT J.
XX
XX PI Bonnefoy J, Gauchat J;
XX
XX DR WPI; 2004-225726/21.
XX DR N-PSDB; ADL71811.
XX
XX PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX PS Claim 1; SEQ ID NO 9; 27pp; English.
XX
XX CC The invention relates to polypeptides capable of binding human
XX CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX CC invention also relates to a method of treatment of a disease in which
XX CC IL13 and IL4 cause adverse effects. The method is useful for treating a
XX CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX CC of the invention are useful in raising antibodies. It is also useful in
XX CC gene therapy. The present sequence is human interleukin-13 receptor alpha
XX CC (IL-13 Ralpha) protein.
XX
XX SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPPGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASS 60
QY 60 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCIAP 119
DB 61 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCIAP 120
QY 120 PRGDPESAATVETLCQIMHNLSTYKMSWLPGRNTSPDNTYTLTYWHRSLKTHQCENTFRG 179
DB 121 PRGDPESAATVETLCQIMHNLSTYKMSWLPGRNTSPDNTYTLTYWHRSLKTHQCENTFRG 180
QY 180 QYFGSGFDLTLYKVDSSFEQHSVQIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKISFHN 239
DB 181 QYFGSGFDLTLYKVDSSFEQHSVQIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKISFHN 240
QY 240 DDLVYQWENPQNFISRLCFYEVAVNNSQETTHNVFYQAEKCNPEFFERNVENTSCFMPV 299
DB 241 DDLVYQWENPQNFISRLCFYEVAVNNSQETTHNVFYQAEKCNPEFFERNVENTSCFMPV 300
QY 300 GVLPTDLNLTVRIRVKTNKLCTYEDDKLMSNKSQEMSGKKNSTLYTMTLLIVPVIYAGAI 359
DB 301 GVLPTDLNLTVRIRVKTNKLCTYEDDKLMSNKSQEMSGKKNSTLYTMTLLIVPVIYAGAI 360
QY 360 IVLLILKRLKLIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLIE 419
DB 361 IVLLILKRLKLIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLIE 420
QY 420 NTKKASQ 426
DB 420 NTKKASQ 426

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DB 421 NTKKASQ 427

RESULT 5
ADL82843
ID ADL82843 standard; protein; 427 AA.
XX
XX ADL82843;
XX
XX AC ADL82843;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE Human PRO2537, SEQ ID 45.
XX
XX KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX KW Antiallergic; Muscular; Neutroprotective; Nephrotoxic; Antiinflammatory;
XX KW Gene Therapy; PRO; B cell related disorder; cancer;
XX KW immune-mediated inflammatory disease; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004024097-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 15-SEP-2003; 2003WO-US029097.
XX
XX PR 16-SEP-2002; 2002US-0411392P.
XX
XX PA (GENTH ) GENENTECH INC.
XX
XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX PI Wu TD;
XX
XX DR WPI; 2004-329389/30.
XX DR N-PSDB; ADL82842.
XX
XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related
XX PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX PS Claim 10; Fig 45; 695pp; English.
XX
XX CC The present invention relates to PRO proteins and their coding sequences.
XX CC The PRO proteins are useful for diagnosing and treating a B cell related
XX CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide
XX CC antigen unresponsiveness, selective IgA deficiency, selective IgM
XX CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
XX CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX CC myasthenia, intermediate lymphoma, rheumatoid arthritis, autoimmune mediated haemolytic
XX CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX CC medicament for treating a condition that is responsive to the PRO
XX CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX CC coding sequences are useful as hybridization probes in chromosome and
XX CC gene mapping, in preparing PRO proteins, or in generating transgenic
XX CC animals or knockout animals, which in turn are useful in the development
XX CC and screening of therapeutically useful reagents.
XX
XX SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPPGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASS 60
QY 60 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCIAP 119
DB 61 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCIAP 120

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QY 120 PEGDPSAVTELOCIIMHNLSTYMKCSWLPGRNTSPDNTVTLTYMHRSLKIHQCENIFREG 179
DB 121 PEGDPSAVTELOCIIMHNLSTYMKCSWLPGRNTSPDNTVTLTYMHRSLKIHQCENIFREG 180
QY 180 QYFCCSFDLTKVKOSSEFQHSVQIMVNDAGKIPSFIVPLTSRVKDPDPHINKLSFHN 239
DB 181 QYFCCSFDLTKVKOSSEFQHSVQIMVNDAGKIPSFIVPLTSRVKDPDPHINKLSFHN 240
QY 240 DDLYVQWENPQNFISRCLEFEVEVNSQTEETHNFYVOEAKCENPEFERVENTSCFMPV 299
DB 241 DDLYVQWENPQNFISRCLEFEVEVNSQTEETHNFYVOEAKCENPEFERVENTSCFMPV 300
QY 300 GVLPTDINTVIRIKYTNKLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIVAGAI 359
DB 301 GVLPTDINTVIRIKYTNKLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 360 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 419
DB 361 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427

RESULT 6

ADN04504 standard; protein; 427 AA.

ADN04504;
01-JUL-2004 (first entry)

Anti-psoriatic protein sequence #445.

antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

W02004028479-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030907.

25-SEP-2002; 2002US-0414006P.

(GENTH) GENENTECH INC.

Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI,

Wu TD,

WPI; 2004-305105/28.

N-PSDB; ADN04503.

New PRO nucleic acid or polypeptide, useful for preparing a

pharmaceutical composition for diagnosing or treating psoriasis in a

mammal.

Claim 9; SEQ ID NO 898; 3069pp; English.

The invention relates to novel polynucleotide and polypeptides for

treating psoriasis or a sequence having at least 80% identity to the

above sequences. The nucleic acid is useful for preparing a composition

for diagnosing or treating psoriasis in a mammal. This sequence

corresponds to one of the polypeptides of the invention.

Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;

Best Local Similarity 99.8%; Pred. No. 4,7e-211; Indels 1; Gaps 1;

Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLGIMALLLCAGGGGGGGG-APTETQPPVTNLISVENLCTVIWMTNPEGASS 59
DB 1 MEMPARLGIMALLLCAGGGGGGGGAAPTEQPPVTNLISVENLCTVIWMTNPEGASS 60
QY 60 NCSLMYFSHFGDKODKKIAPETRSIEVPLNERICLOVGSQCSSTNESKPSILVEKICSP 119
DB 61 NCSLMYFSHFGDKODKKIAPETRSIEVPLNERICLOVGSQCSSTNESKPSILVEKICSP 120
QY 120 PEGDPSAVTELOCIIMHNLSTYMKCSWLPGRNTSPDNTVTLTYMHRSLKIHQCENIFREG 179
DB 121 PEGDPSAVTELOCIIMHNLSTYMKCSWLPGRNTSPDNTVTLTYMHRSLKIHQCENIFREG 180
QY 180 QYFCCSFDLTKVKOSSEFQHSVQIMVNDAGKIPSFIVPLTSRVKDPDPHINKLSFHN 239
DB 181 QYFCCSFDLTKVKOSSEFQHSVQIMVNDAGKIPSFIVPLTSRVKDPDPHINKLSFHN 240
QY 240 DDLYVQWENPQNFISRCLEFEVEVNSQTEETHNFYVOEAKCENPEFERVENTSCFMPV 299
DB 241 DDLYVQWENPQNFISRCLEFEVEVNSQTEETHNFYVOEAKCENPEFERVENTSCFMPV 300
QY 300 GVLPTDINTVIRIKYTNKLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIVAGAI 359
DB 301 GVLPTDINTVIRIKYTNKLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 360 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 419
DB 361 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427

RESULT 7

ADN62575 standard; protein; 427 AA.

ADN62575;

12-AUG-2004 (first entry)

Human interleukin 13 (IL-13) receptor alpha 1 chain.

Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;

IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;

cancer; inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;

lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;

urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;

Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;

Lyme disease; tuberculosis; malaria; leishmaniasis.

Homo sapiens.

Key

Peptide

Protein

US6743604-B1.

01-JUN-2004.

06-APR-2000; 2000US-00545002.

13-DEC-1996; 96GB-00025899.

12-NOV-1997; 97US-00969125.

(SMIK) SMITHKLINE BEECHAM CORP.

Bonney J, Gauchat J;

Bonney J, Gauchat J;

Bonney J, Gauchat J;

DR WPI; 2004-409324/38.
DR N-PSDB; ADN62574.
XX
PT New isolated nucleic acid molecule encoding a polypeptide capable of
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in
PT diagnostics or for producing antibodies.
XX
PS Claim 1; SEQ ID NO 9; 24bp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (ADN62574),
CC which encodes the mature form of a polypeptide capable of binding human
CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
CC IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
CC a vector comprising the nucleic acid molecule and a host cell comprising
CC the vector. The nucleic acids are useful as probes or primers or in the
CC analysis of allelic variation. The polypeptides are useful for binding
CC human IL-13 and/or binding human IL-4 and act as inhibitors by
CC interfering with the interaction between human IL-13 or IL-4 and their
CC natural receptors. They can also be used in medicine, e.g. for treatment
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC used for producing antibodies, which can be used for diagnosing diseases.
CC The present sequence represents IL-13 receptor alpha 1 subunit.
XX
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4,7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPPTNLSVSVENLCVITWNNPREGASS 59
DB 1 MEMPARLCGLMALLCAGGGGGGGGGAAPTETOPPTNLSVSVENLCVITWNNPREGASS 60
QY 60 NCSLWFSHFSGDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 119
DB 61 NCSLWFSHFSGDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120
QY 120 PEGDPESAATELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 179
DB 121 PEGDPESAATELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTKYDSSFEQHSVOIMKDNAGKIKPSNIVPLSRKXPDPPHINKNLSFHN 239
DB 181 QYFGCSFDLTKYDSSFEQHSVOIMKDNAGKIKPSNIVPLSRKXPDPPHINKNLSFHN 240
QY 240 DDLVYOMENPONFISRCLEFYEVEVNNISQETHNVFVYQAEKCNPEFERVENTSCFMP 299
DB 241 DDLVYOMENPONFISRCLEFYEVEVNNISQETHNVFVYQAEKCNPEFERVENTSCFMP 300
QY 300 GVLPTLNTAVRIRVKTNKLCEYEDDKLMSWNSQEMSIGKKRNSLYITMLIIVIVAGAI 359
DB 301 GVLPTLNTAVRIRVKTNKLCEYEDDKLMSWNSQEMSIGKKRNSLYITMLIIVIVAGAI 360
QY 360 IVLLVLRKLTIIIPPIPDGKIFKEMRGDQDDTLHMKKYIVYKQTEERDSVLLIE 419
DB 361 IVLLVLRKLTIIIPPIPDGKIFKEMRGDQDDTLHMKKYIVYKQTEERDSVLLIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427
RESULT 8
ABM82441
ID ABM82441 standard; protein; 427 AA.
XX
AC ABM82441;

XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
DE
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
PN WO2004030615-A2.
PD 15-APR-2004.
XX
XX 29-SEP-2003; 2003MO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA
XX Wu TD, Zhang Z, Zhou Y;
PI
XX
XX WPI; 2004-347921/32.
DR N-PSDB; ACN41073.
DR
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 6271; 7273bp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4,7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPPTNLSVSVENLCVITWNNPREGASS 59
DB 1 MEMPARLCGLMALLCAGGGGGGGGGAAPTETOPPTNLSVSVENLCVITWNNPREGASS 60
QY 60 NCSLWFSHFSGDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 119
DB 61 NCSLWFSHFSGDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120
QY 120 PEGDPESAATELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 179

```

Db      121 PEGDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDNTYLLTYWHRSLKTHQECNIFREG 180
QY      180 QYFGCSFDLTWKVDSSEFGHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db      181 QYFGCSFDLTWKVDSSEFGHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240
QY      240 DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQEAKECENPEFERVENTSCFMPV 299
Db      241 DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQEAKECENPEFERVENTSCFMPV 300
QY      300 GVLPTLNTVIRIKVTKNKLCEYEDDKLMSNNSQEMSIGKKNSTLYTMTLLIVPIYVAGAI 359
Db      301 GVLPTLNTVIRIKVTKNKLCEYEDDKLMSNNSQEMSIGKKNSTLYTMTLLIVPIYVAGAI 360
QY      360 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDTSVLLIE 419
Db      361 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDTSVLLIE 420
QY      420 NLKKAQ 426
Db      421 NLKKAQ 427

```

RESULT 9
AEC31473
ID AEC31473 standard; protein; 427 AA.

AC AEC31473;

DT 03-NOV-2005 (first entry)

DE Human IL-13 receptor alpha-1 SEQ ID NO:3.

XX interleukin-13 receptor; fusion protein; therapeutic; antisthmatic;
XX anti-allergic; dermatological; anti-inflammatory; immunosuppressive;
XX cytotoxic; hepatotropic; anti-HIV; virucide; gastrointestinal-gen;
XX antibacterial; fungicide; antiparasitic; antitumor; antithyroid;
XX nephrotropic.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Domain 27..343
XX /label = extracellular domain

XX US2005191730-A1.

XX 01-SEP-2005.

XX 25-FEB-2005; 2005US-00067251.

XX 27-FEB-2004; 2004US-0548541P.

XX 17-AUG-2004; 2004US-0602139P.

XX 16-NOV-2004; 2004US-0628343P.

XX (REG-) REGENERON PHARM INC.

XX Karow M, Fairhurst J;

XX WPI; 2005-590777/60.

XX New nucleic acid molecules encoding polypeptides capable of binding
XX interleukin-4 and interleukin-13, useful for diagnosing and/or treating
XX asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer
XX and infections.

XX Claim 1; SEQ ID NO 3; 35pp; English.

XX The invention relates to a novel nucleic acid molecule encoding a fusion
XX polypeptide. The fusion polypeptide consists (R1)-(R2)-Y-F, where R1 is 1
XX -231 and 24-231 of a fully defined sequence of 231 amino acids
XX (AEC31472), which sequences may comprise 1-10 modifications, R2 is a

CC fully defined sequence of 427 or 380 bp (AEC31473+AEC31474), which
CC sequences may comprise one to three modifications. F is a fusion
CC component, and x and y are each independently a positive integer 1. The F
CC is a multimerizing component, a serum protein, or a molecule capable of
CC binding a serum protein, where the multimerizing component is an
CC immunoglobulin-derived domain, a cleavable region (C-region), an amino
CC acid sequence between 1-500 amino acids in length, optionally comprising
CC at least one cysteine residue, a leucine zipper, a helix loop motif, or a
CC coil-coil motif. The immunoglobulin-derived domain is the Fc domain of
CC IgG or the heavy chain of IgG. A fusion protein of the invention has
CC antiasthmatic, anti-allergic, dermatological, anti-inflammatory,
CC immunosuppressive, cytostatic, hepatotropic, anti-HIV, virucide,
CC gastrointestinal-gen, antibacterial, fungicide, antiparasitic, antitumor,
CC antithyroid, and nephrotropic activity. The protein has a use in gene
CC therapy, and acts as an interleukin-antagonist. The methods and
CC compositions of the invention are useful for the diagnosis, prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of IL-4 and/or IL-13, such as asthma, atopic
CC dermatitis, lupus, nephritis, Grave's disease, hepatic fibrosis, HIV
CC infection, ulcerative colitis, cancer, and viral, parasitic, bacterial
CC and fungal infections. The present sequence represents human IL-13
CC receptor alpha-1.

XX SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 9; Length 427;

Best Local Similarity 99.8%; Pred. No. 4.7e-211; Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLACAGGGGGGGG-APTETOPVNTLSVSVENLCVITWNPPEGASS 59
Db 1 MEMPARLCGLMALLLACAGGGGGGGGAAPTETOPVNTLSVSVENLCVITWNPPEGASS 60

QY 60 NCSLWTFSHFGDKQDKKIAETRRSIFVPLNERICLOVSGQCSNSESKEKSLVEKICISP 119
Db 61 NCSLWTFSHFGDKQDKKIAETRRSIEVPLNERICLOVSGQCSNSESKEKSLVEKICISP 120

QY 120 PEGDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDNTYLLTYWHRSLKTHQECNIFREG 179
Db 121 PEGDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDNTYLLTYWHRSLKTHQECNIFREG 180

QY 180 QYFGCSFDLTWKVDSSEFGHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFGHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQEAKECENPEFERVENTSCFMPV 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQEAKECENPEFERVENTSCFMPV 300

QY 300 GVLPTLNTVIRIKVTKNKLCEYEDDKLMSNNSQEMSIGKKNSTLYTMTLLIVPIYVAGAI 359
Db 301 GVLPTLNTVIRIKVTKNKLCEYEDDKLMSNNSQEMSIGKKNSTLYTMTLLIVPIYVAGAI 360

QY 360 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDTSVLLIE 419
Db 361 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDTSVLLIE 420

QY 420 NLKKAQ 426
Db 421 NLKKAQ 427

RESULT 10
AEE93788
ID AEE93788 standard; protein; 427 AA.

AC AEE93788;

DT 23-FEB-2006 (first entry)

DE Human interleukin-13 alpha receptor.

XX Monoclonal antibody; IL-13 alpha receptor; cytokine;

KW		protein-co-ordinate data; protein structure; crystallography;
KM		Anitahematic; Antiallergic; Cytostatic; Respiratory-Gen.;
KX		Antiinflammatory; Immunosuppressive; Dermatological;
KW		Gastrointestinal-Gen.; Vasotropic; CNS-Gen.; Hepatotropic; asthma;
KW		cancer; eosinophilia; fibrosis; inflammation; autoimmune disease;
KW		chronic obstructive pulmonary disease; cystic fibrosis;
KW		pulmonary fibrosis; allergic rhinitis; atopic dermatitis;
KM		inflammatory bowel disease; Crohn's disease; cirrhosis; scleroderma;
KX		Hodgkins disease.
XK		
OS		Homo sapiens.
XX		
FH		Key Location/Qualifiers
FT		76 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		77 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		78 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		79 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		254 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		255 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		256 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		318 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		320 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		321 /note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		/note= "Residue interacting with IL-13, specifically claimed in claim 61"
FT		
PV		WO2005121177-A2.
PD		22-DEC-2005.
PF		09-JUN-2005; 2005WO-US020334.
PR		09-JUN-2004; 2004US-0578473P. 09-JUN-2004; 2004US-0578736P.
PR		22-JUN-2004; 2004US-0581375P.
PA	(AMHP) WYETH.	
PI	Llin LL, Parris KD, Tam ASP, Tan X, Shane T, Wilhelm JW,	
PI	Stahl M, Mosyak L, Hu Z;	
DR	WPI; 2006-067089/07.	
XX	SWISSPROT; P78552.	
XX		
PT		Crystalline antibody useful for designing agent that interacts with IL-13 polypeptide, comprises anti-IL-13 antibody capable of binding site of IL-13 polypeptide to which IL-4R polypeptide binds in vivo.
PS		Claim 58; SEQ ID NO 12; 31bp; English.
CC		The invention relates to a crystalline antibody (I), where the antibody comprises an anti-interleukin (IL)-13 antibody or its Fab fragment, and is capable of binding a site of an IL-13 polypeptide to which an IL-4R (interleukin-4 receptor) polypeptide binds in vivo. Also included are a crystalline composition/complexes that comprises an antibody (where the
CC		

CC		antibody comprises an anti-IL-13 antibody or a Fab fragment of an anti-IL-
CC	-13 antibody in complex with IL-13 or IL-13 alpha receptor), use of a	
CC	three-dimensional model of an antibody to design an agent that interacts	
CC	with an IL-13, a software system/computer for storing/analyzing	
CC	information relating to a structure of an IL-13 polypeptide bound to an	
CC	antibody, modulating IL-13 activity in a subject, treating a subject	
CC	having a condition associated with IL-13 activity, a method of	
CC	prophylactically treating a subject susceptible to a condition associated	
CC	with IL-13 activity, and the use of an agent (AI) designed or selected by	
CC	the methods above in the manufacture of a medicament for the prophylaxis	
CC	or treatment of a condition associated with IL-13 activity. The antibody	
CC	crystal and methods are useful for designing an agent that interacts with	
CC	an IL-13 polypeptide. The agent is useful for treating an IL-13 condition	
CC	chosen from allergic asthma or nonallergic asthma, cancer, airway	
CC	inflammation, eosinophilia, fibrosis, excess mucus production,	
CC	vessels or connective tissue, and an autoimmune condition of the skin,	
CC	obstructive pulmonary disorder, cystic fibrosis, pulmonary fibrosis, chronic	
CC	disease, cirrhosis, scleroderma, or Hodgkin's lymphoma. The present	
CC	sequence is the human IL-13 alpha receptor protein.	
XX		
SQ	Sequence 427 AA:	
Query Match	99.5%, Score 2309.5; DB 10; Length 427;	
Best Local Similarity	99.8%; Pred. No. 4.7e-211;	
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
QY	1 MEMPARLCGMALLLCAAGGGGGGGG-APTENOPVTNLVSVENLCTVITMTNPEGASS 59	
DB	1 MEMPARLCGMALLLCAAGGGGGGGGAAPTEPPTNLVSVENLCTVITMTNPEGASS 60	
QY	60 NCSLMYFSHFEDKDKKIAPETRRSIEVPLNERICLVQSOCSTNESKEPSILVEKCISP 119	
DB	61 NCSLMYFSHFEDKDKKIAPETRRSIEVPLNERICLVQSOCSTNESKEPSILVEKCISP 120	
QY	120 PEGDPESAVTELQCIMHNL SYMKCSWLPGRNTSPDVTNYLLYHRSLEKIHQCENIPREG 179	
DB	121 PEGDPESAVTELQCIMHNL SYMKCSWLPGRNTSPDVTNYLLYHRSLEKIHQCENIPREG 180	
QY	180 QYFGCSPLTIVKVCSSFEHQSVOLMVDKNACKIRPSFNIIVLTSRVKRDPPIIKNLSRHN 239	
DB	181 QYFGCSPLTIVKVCSSFEHQSVOLMVDKNACKIRPSFNIIVLTSRVKRDPPIIKNLSRHN 240	
QY	240 DDLVYOMENPNFIISRCLEFYEVEVNNSOTETHANFYVOEACENDEPERANTENTSCEFVP 299	
DB	241 DDLVYOMENPNFIISRCLEFYEVEVNNSOTETHANFYVOEACENDEPERANTENTSCEFVP 300	
QY	300 GVLPDTINTVAIRVKTINKLCYEDDKLMSNMWSQEMSIGKRNSTLYITMLLIIVPIVAGAI 359	
DB	301 GVLPDTINTVAIRVKTINKLCYEDDKLMSNMWSQEMSIGKRNSTLYITMLLIIVPIVAGAI 360	
QY	360 IVALLIYLKRLKIITPPPIPDGKIFKMEFGQNDTLHMKKYDIYEKTKKETDSVLIE 419	
DB	361 IVALLIYLKRLKIITPPPIPDGKIFKMEFGQNDTLHMKKYDIYEKTKKETDSVLIE 420	
QY	420 NLKKASQ 426	
DB	421 NLKKASQ 427	
RESULT 11		
AEEF57817		
ID AEF57817	standard; proteoin. 427 AA.	
XX AEF57817;		
XX AC		
XX DT 23-MAR-2006	(first entry)	
XX Anti-IL-13	antibody associated polypeptide SEQ ID NO 37.	
XX antiasthmatic; dermatological; respiratory-gen.; immunosuppressive;		

KM antiinflammatory; cytostatic; virucide; antiallergic;
 KM gastrointestinal-gen.; vaccine; antibody; diagnosis; therapeutic; asthma;
 KM antidiabetic; chronic obstructive pulmonary disease; respiratory-gen.;
 KM infection; viral infection; virucide; autoimmune disorder;
 KM immunosuppressive; immune disorder; inflammatory bowel disease;
 KM antiinflammatory; gastrointestinal-gen.; gastrointestinal disease;
 KM inflammation; allergic rhinitis; antiallergic; ear, nose, throat disease;
 KM immune disorder; respiratory disease.
 XX Homo sapiens.
 OS
 XX
 PN W02005123126-A2.
 PD
 PD 29-DEC-2005.
 XX
 XX
 PF 09-JUN-2005; 2005WO-US020160.
 XX
 XX
 PR 09-JUN-2004; 2004US-0578473P.
 PR 09-JUN-2004; 2004US-0578736P.
 PR 22-JUN-2004; 2004US-0581375P.
 XX
 XX (AMHP) WYETH.
 XX
 PI Kasajan MT, Tchistiakova L, Veldman GM, Marquette KA, Tan X;
 PI Donaldson DP, Lin LL, Shane T, Tam AS, Feyfant E, Wood NL, Fitz LJ;
 PI Widom AM, Parris KD, Goldman SJ;
 XX
 XX WPI; 2006-172770/18.
 XX
 PT New antibody against human interleukin-13, useful for diagnosing,
 PT preventing, and/or treating a disorder, e.g. asthma, tumors, allergic
 PT rhinitis, or inflammatory bowel disease.
 XX
 PS Disclosure; SEQ ID NO 37; 169pp; English.
 XX
 CC The invention describes an antibody, or its antigen-binding, that binds
 CC to interleukin (IL)-13. Also described are: a pharmaceutical composition
 CC comprising the antibody, or its antigen-binding fragment above and a
 CC pharmaceutical carrier; a nucleic acid that comprises a sequence that
 CC encodes a polypeptide that comprises a heavy chain immunoglobulin
 CC variable region or a light chain immunoglobulin variable region described
 CC above; a host cell comprising a nucleic acid sequence that encodes the
 CC antibody, or its antigen-binding fragment, above; providing a recombinant
 CC antibody; treating an IL-13-associated disorder; and detecting the
 CC presence of IL-13 in a sample. The antibody, composition, and method are
 CC useful for diagnosing, preventing, and/or treating IL-13 associated
 CC disorder, e.g. asthmatic disorders, atopic disorders, chronic obstructive
 CC pulmonary disease (COPD), conditions involving airway inflammation,
 CC eosinophilia, fibrosis and excess mucus production, inflammatory
 CC conditions, autoimmune conditions, tumors or cancers, viral infection,
 CC suppression of expression of protective type 1 immune responses, allergic
 CC rhinitis, or inflammatory bowel disease. This is the amino acid sequence
 CC of a polypeptide associated with anti-IL-13-antibodies of the invention.
 XX
 SQ Sequence 427 AA:
 Query Match 99.5%; Score 2309.5; DB 10; Length 427;
 Best Local Similarity 99.8%; Pred. No. 4,7e-211;
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MEMPARLCGLMALLCAGGGGGGGG-APETOPPVNTLSVSVENLCTVITWMPPEGASS 59
 Db 1 MEMPARLCGLMALLCAGGGGGGGGAPETOPPVNTLSVSVENLCTVITWMPPEGASS 60
 QY 60 NCSLWTFSHFGYQDKKIAPETRRSIVPINERICLOVSGQCSSTNESEKPSIIIVEKCI 119
 Db 61 NCSLWTFSHFGYQDKKIAPETRRSIVPINERICLOVSGQCSSTNESEKPSIIIVEKCI 120
 QY 120 PEGDPESAVTELCICIMHNTLSYMKCSWLPGRNTSPDNTVYTYWHRSLKTHCCENTPRG 179
 Db 121 PEGDPESAVTELCICIMHNTLSYMKCSWLPGRNTSPDNTVYTYWHRSLKTHCCENTPRG 180
 QY 180 QYFGCSFDLTIKVDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 239

Db 181 QYFGCSFDLTIKVDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
 QY 240 DDLYVQWENQONFSLCLFVEVNNQOTETHNVFYQVQKCCNPEPERNVENSCFVNP 299
 Db 241 DDLYVQWENQONFSLCLFVEVNNQOTETHNVFYQVQKCCNPEPERNVENSCFVNP 300
 QY 300 GVLPTDINTVIRIKTKTKLCEYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIVAGAI 359
 Db 301 GVLPTDINTVIRIKTKTKLCEYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIVAGAI 360
 QY 360 IVLLLYKRLKIIFPPIPDPGKIFKEMFGDQNDTLHWKXYDIYEKQNEETDSVLIIE 419
 Db 361 IVLLLYKRLKIIFPPIPDPGKIFKEMFGDQNDTLHWKXYDIYEKQNEETDSVLIIE 420
 QY 420 NLKKASQ 426
 Db 421 NLKKASQ 427
 RESULT 12
 ADL71813
 ID ADL71813 standard; protein; 427 AA.
 AC
 AC ADL71813;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, T130I.
 XX
 KW Human, IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
 KW mouse; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
 KW mutcin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 130 /note="Wild-type Thr is substituted with Ile"
 FT
 XX US2004043921-A1.
 PN
 XX 04-MAR-2004.
 PD
 PF 29-SEP-2003; 2003US-00671697.
 XX
 XX 13-DEC-1996; 96GB-00025899.
 PR 12-NOV-1997; 97US-00969125.
 PR 06-APR-2000; 2000US-00545002.
 XX
 XX (BONN/) BONNEFOY J.
 PA (GAUC/) GAUCHAT J.
 PA
 XX
 PI Bonnefoy J, Gauchat J;
 XX
 DR WPI; 2004-225726/21.
 XX
 PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
 PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
 PT or AIDS, comprising administering a polypeptide or soluble polypeptide.
 PT
 PS Claim 14; Page; 27pp; English.
 XX
 CC The invention relates to polypeptides capable of binding human
 CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
 CC invention also relates to a method of treatment of a disease in which
 CC IL13 and IL4 cause adverse effects. The method is useful for treating a
 CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
 CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
 CC of the invention are useful in raising antibodies. It is also useful in
 CC gene therapy. The present sequence is human interleukin-13 receptor alpha
 CC (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the

CC specification, however it is constructed based on human IL-13 Ralph
CC protein shown as SEQ ID NO:9 in the specification.

XX
SQ Sequence 427 AA;

Query Match 99.3%; Score 2303.5; DB 8; Length 427;
Best Local Similarity 99.5%; Pred. No. 1,7e-210;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPVTNLSVSVNLCVITWMPBGCASS 59
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Db 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETOPVTNLSVSVNLCVITWMPBGCASS 60
   |||||
QY 60 NCSLWYFSHFGDKODKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 119
   |||||
Db 61 NCSLWYFSHFGDKODKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 120
   |||||
QY 120 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYMHRSLKTHOCENIFREG 179
   |||||
Db 121 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYMHRSLKTHOCENIFREG 180
   |||||
QY 180 QYFGCSFDLTKVDSSEFEOHSVOIMVKDNAGKIKPSFNIVPLTSRYKPPDPHIXNLSFHN 239
   |||||
Db 181 QYFGCSFDLTKVDSSEFEOHSVOIMVKDNAGKIKPSFNIVPLTSRYKPPDPHIXNLSFHN 240
   |||||
QY 240 DDLVYQWENPQNIFSRCLFYEVENVNSQETETHNVFYQEAKECNPEFERNVENTSCFMPV 239
   |||||
Db 241 DDLVYQWENPQNIFSRCLFYEVENVNSQETETHNVFYQEAKECNPEFERNVENTSCFMPV 300
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QY 300 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYTMTLIVPIVAGAI 359
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Db 301 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYTMTLIVPIVAGAI 360
   |||||
QY 360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDNDDTLHMKKYDIYEKQTEETDSVLLIE 419
   |||||
Db 361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDNDDTLHMKKYDIYEKQTEETDSVLLIE 420
   |||||
QY 420 NLKKAQ 426
   |||||
Db 421 NLKKAQ 427
```

RESULT 13
ADL17835
ID . ADL17835 standard; protein; 427 AA.

XX
AC ADL17835;

DT 12-FEB-2004 (first entry)

DE Human IL-13 alpha 1 receptor (IL-13R) protein.

XX
KW IL-13R; human; receptor; anaphylaxis; hay fever; asthma;
KW antiinflammatory; cytoskeletal; antitumor; dermatological; antiasthma;
KW antiasthma; fibrosis; Hodgkin's disease; ulcerative colitis;
KW scleroderma; allergic rhinitis; oncological;
KW chronic obstructive pulmonary disease.

OS Homo sapiens.

PN WO2003080675-A2.

PD 02-OCT-2003.

PF 21-MAR-2003; 2003WO-AU000352.

PR 22-MAR-2002; 2002AU-00001301.

PR 03-FEB-2003; 2003AU-00900437.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Dunlop FM, Baca M, Nash AD, Fabri LJ;

XX

DR WPI; 2003-876912/81.
DR N-PSDB; ADL17834.

XX

PT New monoclonal antibodies against interleukin-13 receptor alpha, useful
PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
PT inflammatory disorder.

PS Disclosure; SEQ ID NO 4; 99pp; English.

CC This invention relates to a novel antibodies that function as interleukin
CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
CC for treating certain conditions induced by IL-13. Specifically, it refers
CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
CC and IL-4 induced signaling. IL-13 is a mediator in the immunostimulatory
CC system, such that it is involved in the induction of IgE, IgG4 and T-
CC helper cells and accordingly is implicated in conditions from anaphylaxis
CC to hay fever and asthma. As such, the present invention describes these
CC novel antibodies as antiinflammatory, cytoskeletal, antitumor,
CC dermatological, antiasthma and antiasthma. The methods and
CC compositions are useful for treating various disorders including
CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
CC rhinitis, oncological conditions and chronic obstructive pulmonary
CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
CC protein of the invention.

XX
SQ Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 7; Length 427;
Best Local Similarity 99.5%; Pred. No. 2,2e-210;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPVTNLSVSVNLCVITWMPBGCASS 59
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Db 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETOPVTNLSVSVNLCVITWMPBGCASS 60
   |||||
QY 60 NCSLWYFSHFGDKODKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 119
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Db 61 NCSLWYFSHFGDKODKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 120
   |||||
QY 120 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYMHRSLKTHOCENIFREG 179
   |||||
Db 121 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYMHRSLKTHOCENIFREG 180
   |||||
QY 180 QYFGCSFDLTKVDSSEFEOHSVOIMVKDNAGKIKPSFNIVPLTSRYKPPDPHIXNLSFHN 239
   |||||
Db 181 QYFGCSFDLTKVDSSEFEOHSVOIMVKDNAGKIKPSFNIVPLTSRYKPPDPHIXNLSFHN 240
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QY 240 DDLVYQWENPQNIFSRCLFYEVENVNSQETETHNVFYQEAKECNPEFERNVENTSCFMPV 239
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Db 241 DDLVYQWENPQNIFSRCLFYEVENVNSQETETHNVFYQEAKECNPEFERNVENTSCFMPV 300
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QY 300 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYTMTLIVPIVAGAI 359
   |||||
Db 301 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYTMTLIVPIVAGAI 360
   |||||
QY 360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDNDDTLHMKKYDIYEKQTEETDSVLLIE 419
   |||||
Db 361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDNDDTLHMKKYDIYEKQTEETDSVLLIE 420
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QY 420 NLKKAQ 426
   |||||
Db 421 NLKKAQ 427
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RESULT 14
ADL17814
ID ADL17814 standard; protein; 427 AA.

XX ADL17814;

DT 20-MAY-2004 (first entry)

XX

DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.
 XX
 KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
 KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
 KW mutant.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 358 /note= "Wild-type Gly is substituted with Asp"
 XX
 XX US2004043921-A1.
 XX
 XX 04-MAR-2004.
 XX
 XX 29-SEP-2003; 2003US-00671697.
 XX
 XX 13-DEC-1996; 96GB-00025899.
 PR 12-NOV-1997; 97US-00969125.
 PR 06-APR-2000; 2000US-00545002.
 XX
 PA (BONN/) BONNEFOY J.
 PA (GAUC/) GAUCHAT J.
 PI Bonnefoy J, Gauchat J;
 XX
 DR WPI; 2004-225726/21.
 XX
 PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
 PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
 PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
 XX
 PS Claim 14; Page; 27pp; English.
 CC The invention relates to polypeptides capable of binding human
 CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
 CC invention also relates to a method of treatment of a disease in which
 CC IL13 and IL4 cause adverse effects. The method is useful for treating a
 CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
 CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
 CC of the invention are useful in raising antibodies. It is also useful in
 CC gene therapy. The present sequence is human interleukin-13 receptor alpha
 CC (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
 CC specification, however it is constructed based on human IL-13 Ralpha
 CC protein shown as SEQ ID NO:9 in the specification.
 CC
 SQ Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 8; Length 427;
 Best Local Similarity 99.5%; Pred. No. 2.2e-210;
 Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MEMPARLCGIMALLLCAGGGGGGGG-APTETOPVTNLVSVENLCTVITWNPPEGASS 59
 DB 1 MEMPARLCGIMALLLCAGGGGGGGAAPTETOPVTNLVSVENLCTVITWNPPEGASS 60
 QY 60 NCSLMWFSHFGDQDKKIAPETRSIEVPLNERICLOVSGQSTNESEKPSIIVEKCI 119
 DB 61 NCSLMWFSHFGDQDKKIAPETRSIEVPLNERICLOVSGQSTNESEKPSIIVEKCI 120
 QY 120 PEGDPESAATELOCIMHNLISYKCSMLPGRNTSPDNTLYYHRSLEKIHOCENIFREG 179
 DB 121 PEGDPESAATELOCIMHNLISYKCSMLPGRNTSPDNTLYYHRSLEKIHOCENIFREG 180
 QY 180 QYFGCSFDLTKVDSFEGHSVQIMYKDNAGKIKPSFNIVPLTSRYKPDPEPHIKNLSFHN 239
 DB 181 QYFGCSFDLTKVDSFEGHSVQIMYKDNAGKIKPSFNIVPLTSRYKPDPEPHIKNLSFHN 240
 QY 240 DDLIYQWENPONTISCLFYEVEVNSQRTTHNVFYVQAKCENPEPERVENTSCFMPV 299
 DB 241 DDLIYQWENPONTISCLFYEVEVNSQRTTHNVFYVQAKCENPEPERVENTSCFMPV 300

QY 300 GVLPDITNTVRIKYNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLIIVPIYAGAI 359
 DB 301 GVLPDITNTVRIKYNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLIIVPIYADAI 360
 QY 360 IVLLLYLRLKIIIFPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEKETSVDLIE 419
 DB 361 IVLLLYLRLKIIIFPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEKETSVDLIE 420
 QY 420 NLKRSQ 426
 DB 421 NLKRSQ 427
 RESULT 15
 AAB19808
 ID AAB19808 standard; protein; 427 AA.
 XX
 AC AAB19808;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 XX Human interleukin-13 receptor alpha-1 variant.
 DE
 KW Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
 KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
 KW dermatological; antiasthmatic; anti-allergic; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Sig_peptide
 FT Domain 27..347
 FT /label= Extracellular_domain
 FT Protein 28..427
 FT /label= Mature_protein
 FT Misc-difference 130
 FT /note= "Gly in "
 FT Peptide 327..331
 FT /note= "MSXWS motif conserved in the type-I cytokine
 FT receptor superfamily"
 FT Domain 348..367
 FT /label= Transmembrane_domain
 FT Domain 368..427
 FT /label= Cytoplasmic_domain
 FT Binding-site 405..408
 FT /note= "YXXQ motif, consensus for STAT binding"
 XX
 PN US6143871-A.
 XX
 PD 07-NOV-2000.
 XX
 PF 12-NOV-1997; 97US-00969125.
 XX
 PR 13-DEC-1996; 96GB-00025899.
 XX
 PA (GAUC/) GAUCHAT J.
 PA (BONN/) BONNEFOY J.
 PI Bonnefoy J, Gauchat J;
 XX
 DR WPI; 2001-006445/01.
 XX
 XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
 PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
 PT eczema, asthma or AIDS.
 XX
 PS Claim 4; -: 26pp; English.
 XX
 CC The present sequence is that of a claimed isolated polypeptide which is
 CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
 CC 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:38:58 ; Search time 41 Seconds
(without alignments)
999.716 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320
Sequence: 1 MEMPARLCGLMALLCAGG.....QTKRETDVVLINLKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1653	71.2	426	JC7773	IL-13Ralpha 1 prot
2	318	13.7	415	S12357	interleukin-5 rece
3	294.5	12.7	420	S21052	interleukin-5 rece
4	269.5	11.6	348	JC7907	common cytokine re
5	229	9.9	335	A40267	interleukin-5 rece
6	228	9.8	400	S06945	granulocyte-macrop
7	207	8.9	373	A55718	interleukin-2 rece
8	205.5	8.9	369	I49280	interleukin-2 rece
9	202	8.7	369	A42565	interleukin-2 rece
10	197.5	8.5	831	JQ1655	prolactin receptor
11	190	8.2	610	A34631	lactogen receptor
12	189	8.1	310	A29884	prolactin receptor
13	189	8.1	412	A41070	prolactin receptor
14	189	8.1	412	A36116	prolactin receptor
15	186	8.0	561	I45971	prolactin receptor
16	185	8.0	616	A30304	prolactin receptor
17	183	7.9	262	I77525	prolactin receptor
18	180	7.8	303	I77524	prolactin receptor
19	180	7.8	608	I53269	prolactin receptor
20	176	7.6	630	I51086	prolactin receptor
21	173	7.5	918	A36337	membrane glycoprot
22	172.5	7.4	288	B59405	prolactin receptor
23	172.5	7.4	376	A40144	prolactin receptor
24	172.5	7.4	622	A40144	prolactin receptor
25	170	7.3	897	A39255	cytokine receptor
26	165	7.1	396	S22909	interleukin-3 rece
27	163	7.0	830	I50455	prolactin receptor
28	162.5	7.0	333	S13684	granulocyte-macrop
29	161.5	7.0	1092	JX0312	differentiation-st

30	157	6.8	378	2	A40266	interleukin-3 rece
31	157	6.8	896	1	A35782	cytokine receptor
32	156.5	6.7	378	2	S50040	granulocyte-macrop
33	154.5	6.7	896	2	I56563	interleukin-3 rece
34	149	6.4	878	1	A40091	interleukin-3 rece
35	146.5	6.3	608	2	S32823	somatotropin recep
36	145	6.2	638	2	A33991	somatotropin recep
37	144.5	6.2	1097	2	S17308	leukemia inhibitor
38	144	6.2	918	2	A44257	interleukin-6 sign
39	142.5	6.1	917	2	I49699	glycoprotein 130 -
40	141	6.1	638	2	S12136	somatotropin recep
41	140	6.0	638	2	B28176	somatotropin recep
42	139	6.0	508	1	ZUHUR	erythropoietin rec
43	139	6.0	634	2	S33339	somatotropin recep
44	135.5	5.8	286	2	S50039	granulocyte-macrop
45	134.5	5.8	557	2	A32654	interferon alpha/b

ALIGNMENTS

RESULT 1
JC7773
IL-13Ralpha 1 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: JC7773
R/Protein: C.; Benigne, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A/Title: Expression of a functional IL-13Ralpha by rat B cells.
A/Reference number: JC7773; PMID:11573960
A/Accession: JC7773
A/Molecule type: mRNA
A/Residues: 1-426 <PIR>
A/Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251
C/Comment: This protein is an functionally binding protein involved in B cell prolifera
C/Genetics:
A/Gene: IL-13Ralpha1

Query Match	71.2%	Score 1653	DB 2	Length 426
Best Local Similarity	73.3%	Pred. No. 3e-121		
Matches 313	Conservative 43	Mismatches 67	Indels 4	Gaps 3
QY	1	MEMPARLCGLMALLCAGGSGGAGPTENQPTVNLVSVENCTVIMTNPEGASNN	60	
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DB	60	CSLMYFSHFQDKODKKIAPETRRKKEPLNEKICLQVSGCSTNSESKEPSILVEKCTSP	119	
QY	121	EGDPESAVTELQCTMHNLSYMKCSWLPGRNTSPDNTYLYWHSLEKIHOCENIFREQ	180	
DB	120	RGSSESATVELQCTMHNLSYMKCSWLPGRNTSPDNTYLYWHSLEKIHOCENIFREQ	179	
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DB	180	HIGCSFPLTV-ESNVEHNIQIMVKNAKIRSYIVFTSVKGPPIKHLPLKNG	238	
QY	241	DLVYWMENPQNTSRCLFEVEVNSQTEH--NVFVQAKCENPEFEHVENTSCFMV	298	
DB	239	ALFVQWKNPQNTSRCLFEVEVNSQTEH--NVFVQAKCENPEFEHVENTSCFMV	298	
QY	299	PGVLPDLTAVTRVAVTKNKLCEYDDKLSWMSQSMGIGKGRNSTLYTMLIYVYAGA	358	
DB	299	PGVLPDLTAVTRVAVTKNKLCEYDDKLSWMSQSMGIGKGRNSTLYTMLIYVYAGA	358	
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QY	419	ENLKAS 425		

DB 419 ENLKKA 425

RESULT 2
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S12357
R:Takaki, S.; Tomimaga, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.
EMBO J. 9, 4367-4374, 1990
A>Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; PMID:91092260; PMID:2265612
A:Accession: S12357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: UNIPROT:P21183; UNIPARC:UPI0000028472; GB:D90205; NID:g220465; PIDD:
C:Keywords: cytokine receptor, transmembrane protein

Query Match 13.7%; Score 318; DB 2; Length 415;
Best Local Similarity 23.9%; Pred. No. 4.2e-17;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 32 PPVTNLVSVENICTVIWYNP-PEGASSNCSLMTFSHF-GDKOKIAPEFRRSIEVPL 89
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Db 29 PPV-NETIKATGLAOVLHMDPNPDQEOHRHDLFHVKINAPQEEDYTRKTESKCVPPL 87
90 NERICLGVOGSGCTNSESEKSILVEKCSPEGPDESAVTELOCIWHNL----- 138
HGCFASVRTILKSSHTTLASSSWVAELKADPPSGISVTNLTCTHTTVSSHTLRPYQ 147
QY 139 SYMKSCWLPGRNTPSDNTNYLLYWHRSLLEKIHCENIFRE--GOYFGSFDTLYKDSGF 196
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Db 148 VSLRCWLVWGKDAPEDQFLYRFGLVLE--KOEYSRDALNRYTACFPPTFINSKEF 205
197 EGHSVOIMWKDNGAKIKPSFNIVPLTSRKVDPRPHIKLSFHNDLLVYOEWNPQN-FISR 255
||| :
Db 206 EOLAHHINGSSKRRAIKRPDLFSPLAIDQVNPRTNVJIESNSLYIQWEKPLSAFDPH 265
256 CLEFEUVANNSSQETHNFVFVQGEAKCENPFERNAVENTSCEVNPBGVLPDLTNVARIKYT 315
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Db 266 CFNEYELKITVTKNG---HIQEKLIANKFKISKIDVSTY-----SIGVRAAV 309
316 INKLGYDDDKLMWSMSQEMSIGKKNSTLYITMLIPIVAGAILVLLYLKRLKI--- 372
QY 310 SSPCRMRGR-WGMMSQPIYVGKERKS-LVENHLIVLP---TRACVLLIFSLICRVCHLM 364
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.
U. Med. Med. 175, 341-351, 1992
A>Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; PMID:92121815; PMID:1732409
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: UNIPROT:Q14633; UNIPARC:UPI00000729EE; EMBL:X61176; NID:g33843; PIDD:
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395,'T' <MU2>
A:Cross-references: UNIPARC:UPI0000179A7F; EMBL:X61177; NID:g33839; PIDD:CNA43484.1; PID:
A:Experimental source: clone lambda h5R.27

A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332, 'K' <MU3>
A:Cross-references: UNIPARC:UPI0000179A80; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PI
A:Experimental source: clone lambda hSR.25
R:Tavernier, J.; Typens, T.; Pleatnick, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A>Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A:Reference number: A46175; MUID:9235767; PMID:1149599
A:Accession: A46175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Cross-references: UNIPARC:UPI0000179A81
A:Experimental source: HL-60 cells and eosinophils
A>Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIPI:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA
A:Residues: 1-128, 'I', '130-395, 'I' <MDM>
A:Cross-references: UNIPARC:UPI000006EDIC; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PH
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128, 'I', '130-332, 'K' <MU4>
A:Cross-references: UNIPARC:UPI000006DIE; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PI
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F:345-365/Domain: transmembrane #status predicted <TMS>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 294.5; DB 2; Length 420;
Best Local Similarity 24.8%; Pred. No. 2,9e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

Gy 32 PVTTLASVENVLCITYITWNP--PEGASSNCSIMYFEHFGDKODKIAPETRRSIEVPLN 90
 ||| ::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 32 PFV-NFTIKVTGLAOVLQWKPNPDORVNLEY-----QVKINAFK-EDDYETRIT 82

Gy 91 ERICHQV-----GSQCSTNESEKPSILVEKCIS---PRGGDPESAATVLOCIMHNLT--- 138
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 83 ESKCTILAHKGFSASVRTLLQNDSHLASSMAAEALHAPGSPGTSVNLCTTNTEBDN 142

Gy 139 ----SY--MKCSWLGRNTSPDINTYTYWHRSLEKHOCENIFRE--GOYFGCSFDL 188
 ::::~::~:~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::
Db 143 YSRLSYGVSLHCMTMLVGTDAPEDTOYFLYYRYGSWTE--ECOEYSKDTLGRNIACWPPR 200

Gy 189 TKVKDSSPFGHSVOIQMVKNAGKIKPSFNIVPLTSRKPKDRPHKINLSFHNDLYOVOMEN 248
 ::::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::
Db 201 TFIISKGRMWLAIVLVGSSKSHAIRPDDLFALHAIDQINPPLNVTAIEIGTRUSTSQWEK 260

Gy 249 PON-FISRCLPFYEVENNSQTETHNFVVYOEAACKENPEFRNVENTSCFWPGVLPDTLN 307
 ::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 261 FVSAPFHPHFDEVKIHNRNG-----YLQIEKLMTNAFISIIDDLSKY----- 304

Gy 308 TVRIKVTNKLCYEDDKLMSNWQEMSIGKRNSTLYTMLLVPAIVVAGAIIVLLLYLK 367
 |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 305 DVQVRAAAVSMCREAG-LTMSWSQPIYGVGNDEHKPLREWFVIAMATICFILILSLICK 363

Gy 368 --RLKIIIFPPIPDGKITFKEMGDQNDTLHKKKDIIYEKQTEEFDSVVL 417
 ::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 364 ICHMIKLKFPPIPAPKSNIKDLFVTTN-----YKAGSGSTEIEEVI 404

RESULT 4
ICT907
common cytokine receptor gamma chain, isoform a - chicken
[Species: Gallus gallus (chicken)]

GenCore version 5.1.9
Copyright (c) 1993 - 2006. Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2006, 01:35:33 ; Search time 299 Seconds

(without alignments)
1317.915 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 2320

Sequence: 1 MEWPARLCGLWALLCAGAG.....QTKETDSVLIENIKTASQ 426

Scoring table: BIOSUM62

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	1 I13R1_HUMAN	P78552 homo sapien
2	2309.5	99.5	427	05JSL4_HUMAN	O5JSL4 homo sapien
3	2296.5	99.0	427	096BB4_HUMAN	O96BB4 homo sapien
4	2291.5	98.8	426	059EG2_HUMAN	O59EG2 homo sapien
5	2140	92.2	409	07YRV5_MACFA	O7YRV5 macaca fasc
6	1939.5	83.6	423	0863Z6_PIG	O863Z6 sus scrofa
7	1927	83.1	401	06U6T1_SHEEP	O6U6T1 ovis aries
8	1878	80.9	405	095LFL_CANFA	O95LFL canis famli
9	1696	73.1	424	1 I13R1_MOUSE	O09030 mus musculu
10	1690	72.8	424	08C1Z3_MOUSE	O8C1Z3 mus musculu
11	1687	72.4	426	0561K3_RAT	O561K3 rattus norv
12	1680	72.4	424	08BNM4_MOUSE	O8BNM4 mus musculu
13	1654	71.3	426	08VHC2_RAT	O8VHC2 rattus norv
14	1610	69.4	349	097597_BOVIN	O97597 bos taurus
15	1533	66.1	399	03UPQ9_MOUSE	O3UPQ9 mus musculu
16	1524.5	65.7	279	09UDJ5_HUMAN	O9UDJ5 homo sapien
17	977.5	42.1	252	08VDU7_MOUSE	O8VDU7 mus musculu
18	463	20.0	226	06ZMW0_HUMAN	O6ZMW0 homo sapien
19	329	14.2	386	1 I13R2_CANFA	O951F0 canis famli
20	329	14.2	386	03HTU7_CANFA	O3HTU7 canis famli
21	318	13.7	415	1 I15RA_MOUSE	P21189 mus musculu
22	296.5	12.8	420	1 I15RA_HUMAN	Q01344 homo sapien
23	294.5	12.7	380	1 I13R2_HUMAN	Q14627 homo sapien
24	287.5	12.4	383	088786_MOUSE	O14633 homo sapien
25	285.5	12.3	383	03VZV5_MOUSE	O3VZV5 mus musculu
26	282.5	12.2	396	014631_HUMAN	O3VZV5 mus musculu
27	279.5	12.0	415	0920K4_CAVPO	O14631 homo sapien
28	277	11.9	385	08VHK6_RAT	O20K04 cavia porce
29	273.5	11.8	414	0920B8_RAT	O8VHK6 rattus norv
30	272.5	11.7	414	0920B8_RAT	O920B8 rattus norv
31			2	099P53_RAT	O99P53 rattus norv

32	269.5	11.6	348	2 O8AUP2_CHICK	O8AUP2 gallus gall
33	263	11.3	391	2 O6UAN8_TETNG	O6UAN8 tetradon n
34	262.5	11.3	374	2 O8AV07_CHICK	O8AV07 gallus gall
35	242.5	10.5	393	2 O5U516_XENLA	O5U516 xenopus lae
36	241.5	10.4	404	2 O90XP8_ONCMY	O90XP8 oncorhynch
37	229	9.9	333	2 O15469_HUMAN	O15469 homo sapien
38	228	9.8	400	1 CSF2R_HUMAN	P15509 homo sapien
39	228	9.8	400	2 O4V311_HUMAN	O4V311 homo sapien
40	225	9.7	335	2 O8NHV7_HUMAN	O8NHV7 homo sapien
41	221.5	9.5	410	2 O4V312_HUMAN	O4V312 homo sapien
42	216.5	9.3	415	2 O661N1_XENLA	O661N1 xenopus lae
43	215	9.3	368	2 O76KD0_PIG	O76KD0 sus scrofa
44	215	9.3	368	2 O8S071_PIG	O8S071 sus scrofa
45	211	9.1	368	2 O68F06_RAT	O68F06 rattus norv

ALIGNMENTS

RESULT 1

ID I13R1_HUMAN STANDARD, PRT, 427 AA.

AC P78552; 095646; 099656;

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-MAY-1997, sequence version 1.

DT 07-MAR-2006, entry version 50.

DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).

GN Name=IL13RA1; Synonyms=IL13R, IL13RA;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

OX [1]

RN NCBIOTIDE SEQUENCE [MRNA].

RC TISSUE=Carcinoma;

RX MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7; Milioux B., Laurent P., Bonnin O., Luppker J., Caput D., Vltz N., Ferrata P.;

RA "Cloning of the human IL-13R alpha chain and reconstruction with the IL13R alpha of a functional IL-4/IL-13 receptor complex.";

RL FEBS Lett. 401:163-166(1997).

[2]

RN NCBIOTIDE SEQUENCE [MRNA].

RC TISSUE=B-cell;

RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M., Jeanin P., Aouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonney J.Y.;

RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

[3]

RN NCBIOTIDE SEQUENCE [MRNA].

RC TISSUE=T-cell;

RX MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265; Amen M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;

RA "cDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";

RL J. Biol. Chem. 271:29265-29270(1996).

[4]

RN NCBIOTIDE SEQUENCE [MRNA].

RC TISSUE=Pancereas;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Dackiwko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshitsuki S., Carninci P., Prange C.;

RA	Raha S.S.,	Logunov N.A.,	Peters G.J.,	Abrahamson R.D.,	Mullaly S.J.,
RA	Boak S.S.,	McEwan P.J.,	McEwan K.U.,	Malek J.A.,	Ginnatone P.H.S.,
RA	Richards S.,	Motley K.C.,	Hale S.,	Garcia A.M.,	Gay L.J.,
RA	Villalón D.K.,	Muzny D.M.,	Sodegen E.U.,	Lu X.,	Gibbs R.A.,
RA	Faney J.,	Helton E.,	Keteman M.,	Madan A.,	Rodriguez S.,
RA	Whiting M.,	Madan A.,	Young A.C.,	Shevchenko Y.,	Bouffard G.G.,
RA	Blakeley R.W.,	Touchman J.W.,	Green E.D.,	Dickson M.C.,	
RA	Rodriguez A.C.,	Grimwood J.,	Schmutz J.,	Myers R.M.,	
RA	Butterfield Y.S.N.,	Krzywinski M.I.,	Skalska U.,	Smalins D.E.,	
RA	Schmerch A.,	Schein U.E.,	Jones S.J.M.,	Marra M.A.,	
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
CC	-I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha				
CC	can form a functional receptor for IL13. Also serves as an				
CC	alternate accessory protein to the common cytokine receptor gamma				
CC	chain for IL4 signaling, but cannot replace the function of gamma				
CC	C in allowing enhanced IL2 binding activity.				
CC	-I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,				
CC	and possibly other components.				
CC	-I- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane				
CC	protein.				
CC	-I- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,				
CC	skeletal muscle and ovary; lowest levels in brain, lung and				
CC	kidney. Also found in B-cells, T-cells and endothelial cells.				
CC	-I- DOMAIN: The WSXWS motif appears to be necessary for proper protein				
CC	folding and thereby efficient intracellular transport and cell-				
CC	surface receptor binding.				
CC	-I- DOMAIN: The box 1 motif is required for JAK interaction and/or				
CC	activation.				
CC	-I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5				
CC	subfamily.				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/item				
CC	Distributed under the Creative Commons Attribution-NonDerivs license				
CC	-----				
DR	EMBL, Y10659, CAA71669.1, -, mRNA.				
DR	EMBL, Y09328, CAA70508.1, -, mRNA.				
DR	EMBL, U62858, AAB37127.1, -, mRNA.				
DR	EMBL, U81379, AAD00510.3, -, mRNA.				
DR	EMBL, BC009960, AA099960.1, -, mRNA.				
DR	Ensembl, ENSG00000131724; Homo sapiens.				
DR	H-invDB, HIX0017008; -				
DR	HGNC, HGNC:5974; IL13RA1.				
DR	DR	MIW, 300119; gene.			
DR	DR	GO, GO:0005898; C:interleukin-13 receptor complex; TAS.			
DR	DR	GO, GO:0005886; C:plasma membrane; TAS.			
DR	DR	GO, GO:0007166; P:cell surface receptor linked signal transdu. . . ; TA			
DR	DR	InterPro, IPR002996; Cytkn_rcptc_B/G.			
DR	DR	InterPro, IPR003533; Hempt_rcptc_S_F2.			
DR	DR	PROSITE, PS01356; HEMA700 REC S F2; 1.			
DR	DR	GlycoProtein, Membrane; Receptor; Signal; Transmembrane.			
KW	GLYCOPROTEIN, Membrane; Receptor; Signal; Transmembrane.				
FT	SIGNAL	1	21		
FT	CHAIN	22	427		
FT					
FT	TOPO_DOM	22	343		
FT	TRANSMEM	344	367		
FT	TOPO_DOM	368	427		
FT	MOTIF	327	331		
FT	MOTIF	374	382		
FT	CARBOHYD	37	37		
FT	CARBOHYD	61	61		
FT	CARBOHYD	105	105		
FT	CARBOHYD	138	138		
FT	CARBOHYD	157	157		
FT	CARBOHYD	235	235		
FT	CARBOHYD	265	265		
FT	CARBOHYD	293	293		
FT	CARBOHYD	329	329		
FT	CARBOHYD	341	341		
FT	DISULFID	46	95		
FT	DISULFID	134	144		
FT	DISULFID	173	185		

FT	CONFLICT	130	130	T -> I (in Ref. 3):
SO	CONFLICT	358	358	G -> D (in Ref. 3).
SEQ	SEQUENCE	427 AA; 48760 MW; 598353EBF554107B CRC64;		
Query Match 99.5%; Score 2309.5; DB 1; Length 427;				
Best Local Similarity 99.8%; Pred. No. 6.5e-167;				
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
QY	1	MEMPARLCGLMALLLCAGGGGGGGG-APTETOPVYTNLSVENVLCIVITWNPBEGASS	59	
DB	1	MEMPARLCGLMALLLCAGGGGGGGGAPTETQPVYTNLSVENVLCIVITWNPBEGASS	60	
QY	60	NCSLMYSHFEDKODKKIAPETRSIEVPLNERICLVGSOCCSNSEKESILVEKICSP	119	
DB	61	NCSLMYSHFEDKODKKIAPETRSIEVPLNERICLVGSOCCSNSEKESILVEKICSP	120	
QY	120	PEGDPESAATVELQCIWMNLSTYKMSMLPGHNTSPDTYTYLYMHRSLKIHOCENIPREG	179	
DB	121	PEGDPESAATVELQCIWMNLSTYKMSMLPGHNTSPDTYTYLYMHRSLKIHOCENIPREG	180	
QY	180	QYFCGSFDLTLYKVDSEFQHSVQIMVKDNGAKIKPSFNIPLTSRYKDPDPIIKNLSFHN	239	
DB	181	QYFCGSFDLTLYKVDSEFQHSVQIMVKDNGAKIKPSFNIPLTSRYKDPDPIIKNLSFHN	240	
QY	240	DDLIVYQENPQNFISRLCFYEVVNNSTETHNVFYQEAKECENPEPERVENTSCMPV	299	
DB	241	DDLIVYQENPQNFISRLCFYEVVNNSTETHNVFYQEAKECENPEPERVENTSCMPV	300	
QY	300	GVLPDPTLNTVYIRKYNKTKLCYEDDKLMSNNSQEKSKNSTLYITMLIVPIYVAGAI	359	
DB	301	GVLPDPTLNTVYIRKYNKTKLCYEDDKLMSNNSQEKSKNSTLYITMLIVPIYVAGAI	360	
QY	360	IVLLVLYKRLKIIIFPPIPDPGKIFKEMFQDNDLTHMKKYDIYEKQTEETDSVVLIE	419	
DB	361	IVLLVLYKRLKIIIFPPIPDPGKIFKEMFQDNDLTHMKKYDIYEKQTEETDSVVLIE	420	
QY	420	NLKRAAQ 426		
DB	421	NLKRAAQ 427		
RESULT 2				
Q5JSL4 HUMAN PRELIMINARY; PRT; 427 AA.				
ID	Q5JSL4 HUMAN	PRELIMINARY;	PRT;	427 AA.
AC	Q5JSL4;			
DT	10-MAY-2005,	integrated into UniProtKB/TrEMBL.		
DT	10-MAY-2005,	sequence version 1.		
DT	21-FEB-2006,	entry version 6.		
DE	Interleukin 13 receptor, alpha 1.			
GN	Name=IL13RA1; ORFNames=Rp13-12804.2-001;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RA	Lawlor S;			
RA	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RL	-1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane			
CC	protein (By similarity).			
CC	-1- DOMAIN: The WSXWS motif appears to be necessary for proper protein			
CC	folding and thereby efficient intracellular transport and cell-			
CC	surface receptor binding (By similarity)			
CC	-1- DOMAIN: The box 1 motif is required for JAK interaction and/or			
CC	activation (By similarity).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonCommercial license			
DR	EMBL, AL391280; CA141410.1; -; Genomic DNA.			
DR	Ensembl, ENSG00000131724; Homo sapiens.			
DR	GO, GO:0016021; C:integral to membrane; IEA.			

DR GO: 0016020; C:membrane; IEA.
 DR GO: 0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO: 0004872; F:receptor activity; IEA.
 DR InterPro: IPR002996; Cyt_kn_rcpt_B/G.
 DR InterPro: IPR003532; Hempt_rcpt_S_F2.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
 DR KEGG: Transmembrane.
 SQ SEQUENCE 427 AA; 48760 MW; 598383B8F54107B CRC64;
 Query Match 99.5%; Score 2309.5; DB 2; Length 427;
 Best Local Similarity 99.8%; Pred. No. 6.5e-167;
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPPVNTLSVENVLCVITWNPPEGASS 59
 DB 1 MEMPARLCGLMALLLCAGGGGGGGGAPTEPPTVNTLSVENVLCVITWNPPEGASS 60
 QY 60 NCSLWTFSHRGDKQDKKIAPETRRSIEVPLNERICLOVSGCSTNESEKPSILVEKCTSP 119
 DB 61 NCSLWTFSHRGDKQDKKIAPETRRSIEVPLNERICLOVSGCSTNESEKPSILVEKCTSP 120
 QY 120 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQCENTIFREG 179
 DB 121 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQCENTIFREG 180
 QY 180 QYFGCSFDLTKVSDSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
 DB 181 QYFGCSFDLTKVSDSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
 QY 240 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEPERVENTSCMPV 299
 DB 241 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEPERVENTSCMPV 300
 QY 300 GVLPTLNTVIRIVKTNKLCYEDDKLMSNWSQMSIGKKNSTLYITMLLIVPIVAGAI 359
 DB 301 GVLPTLNTVIRIVKTNKLCYEDDKLMSNWSQMSIGKKNSTLYITMLLIVPIVAGAI 360
 QY 360 IVLLVLYKRLKIIIPPIPDPGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 419
 DB 361 IVLLVLYKRLKIIIPPIPDPGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 420
 QY 420 NLKKAQ 426
 DB 421 NLKKAQ 427
 RESULT 3
 Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.
 AC Q96BB4; O8MK08;
 DT 01-DEC-2001. Integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001. sequence version 1.
 DE 21-FEB-2006. entry version 23.
 GN Interleukin 13 receptor, alpha 1.
 GN Name=IL13RA1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow R.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Mausius K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Vallation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RA Klausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -----
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 CC
 DR EMBL, BC015768; AAH15768.1; -; mRNA.
 DR Ensembl; ENSG00000131724; Homo sapiens.
 DR GO: 0016021; C:integral to membrane; IEA.
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO: 0004872; F:receptor activity; IEA.
 DR InterPro: IPR002996; Cyt_kn_rcpt_B/G.
 DR InterPro: IPR003532; Hempt_rcpt_S_F2.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
 DR KEGG: Transmembrane.
 SQ SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC64;
 Query Match 99.0%; Score 2296.5; DB 2; Length 427;
 Best Local Similarity 99.5%; Pred. No. 6.3e-166;
 Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPPVNTLSVENVLCVITWNPPEGASS 59
 DB 1 MEMPARLCGLMALLLCAGGGGGGGGAPTEPPTVNTLSVENVLCVITWNPPEGASS 60
 QY 60 NCSLWTFSHRGDKQDKKIAPETRRSIEVPLNERICLOVSGCSTNESEKPSILVEKCTSP 119
 DB 61 NCSLWTFSHRGDKQDKKIAPETRRSIEVPLNERICLOVSGCSTNESEKPSILVEKCTSP 120
 QY 120 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQCENTIFREG 179
 DB 121 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQCENTIFREG 180
 QY 180 QYFGCSFDLTKVSDSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
 DB 181 QYFGCSFDLTKVSDSFEQHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
 QY 240 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEPERVENTSCMPV 299
 DB 241 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEPERVENTSCMPV 300
 QY 300 GVLPTLNTVIRIVKTNKLCYEDDKLMSNWSQMSIGKKNSTLYITMLLIVPIVAGAI 359
 DB 301 GVLPTLNTVIRIVKTNKLCYEDDKLMSNWSQMSIGKKNSTLYITMLLIVPIVAGAI 360
 QY 360 IVLLVLYKRLKIIIPPIPDPGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 419
 DB 361 IVLLVLYKRLKIIIPPIPDPGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 420
 QY 420 NLKKAQ 426
 DB 421 NLKKAQ 427

Db 421 LKKAQ 427

RESULT 4
O59EG2_HUMAN PRELIMINARY; PRT; 426 AA.
AC O59EG2;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=orta endothelial cell;
RA Totsuki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB209849; BAD93086.1; -; mRNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytok rcpt B/G.
DR InterPro; IPR003532; Hempt rcpt S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KM Receptor.
FT NON_TER
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;

Query Match 98.8%; Score 2291.5; DB 2; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.5e-165;
Matches 444; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 EMPARLCGLMALLLCAGGGGGGGG-APTETQPPVNLVSVENLCTVIWTPNPEGASNN 60
DB 1 EMPARLCGLMALLLCAGGGGGGGGAPTEIQPPVNLVSVENLCTVIWTPNPEGASNN 60
QY 61 CSLWYSHFGDKODKLIAPETRSLVPLNERICLOVGSQCSNSESKESSLVEKCI 120
DB 61 CSLWYSHFGDKODKLIAPETRSLVPLNERICLOVGSQCSNSESKESSLVEKCI 120
QY 121 EGPDESAVTELOCIMHNLSTYKCSMLPGRTSPDTNTLYYHRSLEKIHQCENIRREG 180
DB 121 EGPDESAVTELOCIMHNLSTYKCSMLPGRTSPDTNTLYYHRSLEKIHQCENIRREG 180
QY 181 YFGCSFDLTKVDSFEQHSVOIMVNDAGKIKPSFNIVPLTSRVKPDPHIKNLSFND 240
DB 181 YFGCSFDLTKVDSFEQHSVOIMVNDAGKIKPSFNIVPLTSRVKPDPHIKNLSFND 240
QY 241 DLYVQWENQNFISRLTFYEVVNSQTEHNVFYQEAACENPEFRNVENTSCFVWG 300
DB 241 DLYVQWENQNFISRLTFYEVVNSQTEHNVFYQEAACENPEFRNVENTSCFVWG 300
QY 301 VLPDITNTYRIKTKLCYEDDKLMSNSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
DB 301 VLPDITNTYRIKTKLCYEDDKLMSNSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGDNDTLHMKKYDIYEKQTEETDSVVLIN 420
DB 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGDNDTLHMKKYDIYEKQTEETDSVVLIN 420
QY 421 LKKAQ 426
|||||

Db 421 LKKAQ 426

RESULT 5
Q7YRV5_MACFA PRELIMINARY; PRT; 409 AA.
AC Q7YRV5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13R1;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheinae; Macaca.
OX NCBI_TaxId=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RA "Cynomolgus monkey interleukin 13 receptor alpha 1."
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY312267; AAP78901.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytok rcpt B/G.
DR InterPro; IPR003532; Hempt rcpt S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KM Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON_TER
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 92.2%; Score 2140; DB 2; Length 409;
Best Local Similarity 96.6%; Pred. No. 4.7e-154;
Matches 394; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 19 GGGGGGGAAPTETQPPVNLVSVENLCTVIWTPNPEGASNNCSLWYFSHFGDKODKXIA 78
DB 2 GGGGGGGAAPTETQPPVNLVSVENLCTVIWTPNPEGASNNCSLWYFSHFGDKODKXIA 61
QY 79 PETRSLVPLNERICLOVGSQCSNSESKESSLVEKCSPEGPDESAVTELOCIMHNL 138
DB 79 PETRSLVPLNERICLOVGSQCSNSESKESSLVEKCSPEGPDESAVTELOCIMHNL 121
QY 139 SYMKCSMLPGRTSPDTNTLYYHRSLEKIHQCENIPREGQYFGCSFDLTKVDSFEQ 198
DB 139 SYMKCSMLPGRTSPDTNTLYYHRSLEKIHQCENIPREGQYFGCSFDLTKVDSFEQ 181
QY 181 YFGCSFDLTKVDSFEQHSVOIMVNDAGKIKPSFNIVPLTSRVKPDPHIKNLSFND 240
DB 181 YFGCSFDLTKVDSFEQHSVOIMVNDAGKIKPSFNIVPLTSRVKPDPHIKNLSFND 241
QY 241 DLYVQWENQNFISRLTFYEVVNSQTEHNVFYQEAACENPEFRNVENTSCFVWG 300
DB 241 DLYVQWENQNFISRLTFYEVVNSQTEHNVFYQEAACENPEFRNVENTSCFVWG 301
QY 301 VLPDITNTYRIKTKLCYEDDKLMSNSQEMSIGKRNSTLYITMLLIVPIVAGAI 360
DB 301 VLPDITNTYRIKTKLCYEDDKLMSNSQEMSIGKRNSTLYITMLLIVPIVAGAI 361
QY 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGDNDTLHMKKYDIYEKQTEETDSVVLIN 420
DB 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGDNDTLHMKKYDIYEKQTEETDSVVLIN 409
QY 421 LKKAQ 426
|||||

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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:44:03 ; Search time 50 Seconds
(without alignments)
745.761 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320
Sequence: 1 MEMPARLCGMALLICAGGCGGGGGGAGTETQPPPTNLSVSVENLCITVITWNPPEGASNN 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patente_AA:*

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3: /EMC_Celexra_SIDS3/prodata/2/iaa/6.COMB.pep:*

4: /EMC_Celexra_SIDS3/prodata/2/iaa/7.COMB.pep:*

5: /EMC_Celexra_SIDS3/prodata/2/iaa/H.COMB.pep:*

6: /EMC_Celexra_SIDS3/prodata/2/iaa/PCTUS.COMB.pep:*

7: /EMC_Celexra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2320	100.0	426	2 US-09-688-286D-4	Sequence 4, Appli
2	2309.5	99.5	427	2 US-08-969-125-9	Sequence 9, Appli
3	2309.5	99.5	427	2 US-09-545-002-9	Sequence 9, Appli
4	2309.5	99.5	427	2 US-09-949-016-6094	Sequence 6094, Ap
5	1878	80.9	405	2 US-08-828-995B-50	Sequence 50, Appli
6	1875.5	80.8	793	2 US-09-313-942-32	Sequence 32, Appli
7	1875.5	80.8	793	2 US-10-282-162-32	Sequence 32, Appli
8	1779.5	76.7	784	2 US-09-313-942-30	Sequence 30, Appli
9	1779.5	76.7	784	2 US-10-282-162-30	Sequence 30, Appli
10	1769	76.2	322	2 US-09-825-561A-82	Sequence 82, Appli
11	1696	73.1	424	2 US-08-688-286D-2	Sequence 2, Appli
12	1265	54.5	223	2 US-09-949-016-8550	Sequence 8550, Ap
13	329	14.2	386	2 US-09-828-995B-61	Sequence 61, Appli
14	318	13.7	398	1 US-07-757-390-6	Sequence 6, Appli
15	318	13.7	398	1 US-08-442-282-6	Sequence 6, Appli
16	318	13.7	398	1 US-08-442-281-6	Sequence 6, Appli
17	318	13.7	398	1 US-08-939-727-6	Sequence 6, Appli
18	318	13.7	415	1 US-07-757-390-5	Sequence 5, Appli
19	318	13.7	415	1 US-08-442-282-5	Sequence 5, Appli
20	318	13.7	415	1 US-08-442-281-5	Sequence 5, Appli
21	318	13.7	415	1 US-08-939-727-5	Sequence 5, Appli
22	318	13.7	415	2 US-09-886-319A-23	Sequence 23, Appli
23	310	13.4	365	2 US-09-828-995B-66	Sequence 66, Appli
24	304.5	13.1	561	2 US-08-828-995B-72	Sequence 72, Appli
25	303.5	13.1	561	2 US-08-828-995B-81	Sequence 81, Appli
26	297	12.8	565	2 US-09-828-995B-75	Sequence 75, Appli

27	296.5	12.8	420	2 US-09-886-319A-24	Sequence 24, Appli
28	296.5	12.8	420	2 US-09-949-016-5958	Sequence 5958, Ap
29	296	12.8	318	2 US-09-828-995B-69	Sequence 69, Appli
30	296	12.8	563	2 US-09-828-995B-78	Sequence 78, Appli
31	294.5	12.7	380	1 US-08-609-572-4	Sequence 4, Appli
32	294.5	12.7	380	2 US-08-841-751-4	Sequence 4, Appli
33	294.5	12.7	380	2 US-08-846-340-4	Sequence 4, Appli
34	294.5	12.7	380	2 US-08-846-344-4	Sequence 4, Appli
35	294.5	12.7	420	2 US-09-301-808-4	Sequence 4, Appli
36	294.5	12.7	420	1 US-07-757-380-13	Sequence 13, Appli
37	294.5	12.7	420	1 US-08-442-282-13	Sequence 13, Appli
38	294.5	12.7	420	1 US-08-442-281-13	Sequence 13, Appli
39	294.5	12.7	420	1 US-08-939-727-13	Sequence 13, Appli
40	293.5	12.7	427	2 US-09-949-016-8614	Sequence 8614, Ap
41	293.5	12.7	427	2 US-09-949-016-8620	Sequence 8620, Ap
42	287.5	12.4	383	1 US-08-609-572-2	Sequence 2, Appli
43	287.5	12.4	383	2 US-08-841-751-2	Sequence 2, Appli
44	287.5	12.4	383	2 US-08-846-340-2	Sequence 2, Appli
45	287.5	12.4	383	2 US-08-846-344-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-688-286D-4
Sequence 4, Application US/09688286D
Patent No. 691530
GENERAL INFORMATION:
APPLICANT: Willson, Tracey
APPLICANT: Nicola, Nicos
APPLICANT: Hilton, Douglas
APPLICANT: Metcalf, Donald
APPLICANT: Zhang, Jian
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
FILE REFERENCE: 23199-215
CURRENT APPLICATION NUMBER: US/09/688, 286D
CURRENT FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: AU P66135
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: AU P67276
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: AU P62208
PRIOR FILING DATE: 1996-09-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 426
TYPE: PRT
ORGANISM: human
US-09-688-286D-4
Query Match 100.0%; Score 2320; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.7e-220;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
MEMPARLCGMALLICAGGCGGGGGAGTETQPPPTNLSVSVENLCITVITWNPPEGASNN 60
1 MEMPARLCGMALLICAGGCGGGGGAGTETQPPPTNLSVSVENLCITVITWNPPEGASNN 60
1 MEMPARLCGMALLICAGGCGGGGGAGTETQPPPTNLSVSVENLCITVITWNPPEGASNN 60
CSLMYFHPGDKODKTAIPETRRSIEVPLNERICTLOVGSOCSTSEKSPSLVEKCTSP 120
61 CSLMYFHPGDKODKTAIPETRRSIEVPLNERICTLOVGSOCSTSEKSPSLVEKCTSP 120
61 CSLMYFHPGDKODKTAIPETRRSIEVPLNERICTLOVGSOCSTSEKSPSLVEKCTSP 120
EGDPSAVTELCIWNHLSYMKCSWLPGRNTSPDTNVTLYWHRSLKIHOCENI FREGQ 180
121 EGDPSAVTELCIWNHLSYMKCSWLPGRNTSPDTNVTLYWHRSLKIHOCENI FREGQ 180
EGDPSAVTELCIWNHLSYMKCSWLPGRNTSPDTNVTLYWHRSLKIHOCENI FREGQ 180
121 EGDPSAVTELCIWNHLSYMKCSWLPGRNTSPDTNVTLYWHRSLKIHOCENI FREGQ 180
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181 YFGSFPDLTVKXKSPFQSHVOIMVKNAGIKRSENVIPLTSPVKDPPIIKLSFRRND 240
YFGSFPDLTVKXKSPFQSHVOIMVKNAGIKRSENVIPLTSPVKDPPIIKLSFRRND 240
181 YFGSFPDLTVKXKSPFQSHVOIMVKNAGIKRSENVIPLTSPVKDPPIIKLSFRRND 240
DLVYQWENPONFISRLCFYEVEVNNSTETHNVFYQEAACENDEPERNVENTSCFMVPG 300
241 DLVYQWENPONFISRLCFYEVEVNNSTETHNVFYQEAACENDEPERNVENTSCFMVPG 300

DB 241 DLVQWENPQNFISRLCFYEVEVNNSTQETHNVFYQEAACENPEFERNVENTSCFMPV 300
QY 301 VLPDPLNTVRIRKTKKLCYEDDKLMSNWSQEMSIGKRSSTLYITMLLIVPIVAGAI 360
DB 301 VLPDPLNTVRIRKTKKLCYEDDKLMSNWSQEMSIGKRSSTLYITMLLIVPIVAGAI 360
QY 361 VLLLYKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIEN 420
DB 361 VLLLYKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIEN 420
QY 421 LKKSQ 426
DB 421 LKKSQ 426
RESULT 2
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-NO. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.2e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
DB 1 MEMPARLCGLMALLLACAGGGGGGGG--APETPTPTVNTLSVENLCTVITNTPPGAS 59
DB 1 MEMPARLCGLMALLLACAGGGGGGGGAAPIPTQPPVTNLSVENLCTVITNTPPGAS 60
QY 60 NCSLWFSHFGDKQDKKIAPETRSIEVPLNERICLVQVSGCSTNSEKPSILVEKCI 119
DB 61 NCSLWFSHFGDKQDKKIAPETRSIEVPLNERICLVQVSGCSTNSEKPSILVEKCI 120
QY 120 PGSDPSAVTEIQCIIHNLSYMKCSWLPGRNTSPDTNTYILYYHRSLEKIHQCENTFR 179

DB 121 PGSDPSAVTEIQCIIHNLSYMKCSWLPGRNTSPDTNTYILYYHRSLEKIHQCENTFR 180
QY 180 QYFGCSFDLTLYKXDSFEGHSVQIWKVDNAGIKESFNIVPLTSRKVPDPPIKXLSFN 239
DB 181 QYFGCSFDLTLYKXDSFEGHSVQIWKVDNAGIKESFNIVPLTSRKVPDPPIKXLSFN 240
QY 240 DDLVQWENPQNFISRLCFYEVEVNNSTQETHNVFYQEAACENPEFERNVENTSCFMPV 299
DB 241 DDLVQWENPQNFISRLCFYEVEVNNSTQETHNVFYQEAACENPEFERNVENTSCFMPV 300
QY 300 GVLPTPLNTVRIRKTKKLCYEDDKLMSNWSQEMSIGKRSSTLYITMLLIVPIVAGAI 359
DB 301 GVLPTPLNTVRIRKTKKLCYEDDKLMSNWSQEMSIGKRSSTLYITMLLIVPIVAGAI 360
QY 360 IVLLLYKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLI 419
DB 361 IVLLLYKRLKIIIFPPIPDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLI 420
QY 420 NLKKSQ 426
DB 421 NLKKSQ 427
RESULT 3
US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-NO. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-NO. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.2e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG -AETETOPPTNLSVSVENLCTVIWTMNPPEGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAETETOPPTNLSVSVENLCTVIWTMNPPEGASS 60
QY 60 NCSLMYFHSFEDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSP 119
DB 61 NCSLMYFHSFEDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSP 120
QY 120 PEGDPESAATLQOCIMHNLSTYKCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREG 179
DB 121 PEGDPESAATLQOCIMHNLSTYKCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREG 180
QY 180 QYFGCSFDLTRKVDKSSFEQHSVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 239
DB 181 QYFGCSFDLTRKVDKSSFEQHSVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240
QY 240 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 299
DB 241 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 300
QY 300 GVLPTDNTVIRIKVTKNLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAI 359
DB 301 GVLPTDNTVIRIKVTKNLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAI 360
QY 360 IVLLLYKRLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 419
DB 361 IVLLLYKRLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427

RESULT 4
US-09-949-016-6094
Sequence 6094, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6094
LENGTH: 427
TYPE: PRF
ORGANISM: Human
US-09-949-016-6094

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.2e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEMPARLCGLMALLLCAGGGGGGGG -AETETOPPTNLSVSVENLCTVIWTMNPPEGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAETETOPPTNLSVSVENLCTVIWTMNPPEGASS 60
QY 60 NCSLMYFHSFEDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSP 119
DB 61 NCSLMYFHSFEDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSP 120
QY 120 PEGDPESAATLQOCIMHNLSTYKCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREG 179
DB 121 PEGDPESAATLQOCIMHNLSTYKCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREG 180

DB 121 PEGDPESAATLQOCIMHNLSTYKCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREG 180
QY 180 QYFGCSFDLTRKVDKSSFEQHSVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 239
DB 181 QYFGCSFDLTRKVDKSSFEQHSVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240
QY 240 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 299
DB 241 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 300
QY 300 GVLPTDNTVIRIKVTKNLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAI 359
DB 301 GVLPTDNTVIRIKVTKNLCYEDDKLWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAI 360
QY 360 IVLLLYKRLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 419
DB 361 IVLLLYKRLKIIIFPPIPDGKIFKEMFGQNDTLHMKKYDIYEKOTKEETDSVLAIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427

RESULT 5
US-09-828-995B-50
Sequence 50, Application US/09828995B
Patent No. 6703360
GENERAL INFORMATION:
APPLICANT: Heeska Corporation
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
FILE REFERENCE: A1-7
CURRENT APPLICATION NUMBER: US/09/828, 995B
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 405
TYPE: PRF
ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 2; Length 405;
Best Local Similarity 85.2%; Pred. No. 2e-176;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
QY 22 GGGGAPTETPTPTNLSVSVENLCTVIWTMNPPEGASSNCSLMYFHSFEDKODKXIAPET 81
DB 1 GGGGAPTETPTPTNLSVSVENLCTVIWTMNPPEGASSNCSLMYFHSFEDKODKXIAPET 60
QY 82 RRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSPPEGDPESAATLQOCIMHNLSTY 141
DB 61 HRSIEVPLNERICLOVGSOCSTNESEKPSILVEKICSPPEGDPESAATLQOCIMHNLSTY 120
QY 142 KCSWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREGQYFGCSFDLTRKVDKSSFEQHSV 201
DB 121 KCTWLPGRNTSPDNTLYTWMHRSLEKIHQECENIFREGQYFGCSFDLTRKVDKSSFEQHSV 180
QY 202 QIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHNDDLVYQWENPQNFISRCLEFEV 261
DB 181 QIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHNDDLVYQWENPQNFISRCLEFEV 240
QY 262 EVNNSQOTETHNVFYQEAACENPEFRNVENTSCFMPVGVLPDNTVIRIKVTKNLCY 321
DB 241 EVNNSQOTETHNVFYQEAACENPEFRNVENTSCFMPVGVLPDNTVIRIKVTKNLCY 300
QY 322 DDLKWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAIIVLLLYKRLKIIIFPPIPDG 381
DB 322 DDLKWSNMSQEMSIGKRNSTLYITMLLIVPIYVAGAIIVLLLYKRLKIIIFPPIPDG 361


```

Db      301 DDKLSMNSQASIGENTDPFYITMLLATQYIVACAIILLLLYKRLKILITPPPIPDG 360
QY      382 KIFKMPFGQNDTLHMKKYDIYEKQTKRETSVVLINLKKASQ 426
        |||||:|||||
Db      361 KIFKMPFGQNDTLHMRYDIYEKQTKRETSVVLINLKKASQ 405

```

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RESULT 6
US-09-313-942-32
: Sequence 32, Application US/09313942
: Patent No. 6472179
: GENERAL INFORMATION:
: APPLICANT: REGENERON PHARMACEUTICALS, INC.
: TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
: TITLE OF INVENTION: AND USING
: FILE REFERENCE: REG 203-A
: CURRENT APPLICATION NUMBER: US/09/313,942
: CURRENT FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 09/313,942
: PRIOR FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 60/101,858
: PRIOR FILING DATE: 1998-09-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 793
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-313-942-32

```

Query Match	80.8%;	Score 1875.5;	DB 2;	Length 793;
Best Local Similarity	99.4%;	Pred. No. 1e-175;		
Matches 341;	Conservative	0;	Mismatches 1;	Indels 1;
				Gaps 1;

QY	1	MEMPARLCEIMALLILCAGGGGGGGG-APEETQCPPTNLISVSVENLCVITWMPPEASS	59
Db	1	MWMPARLCEIMALLILCAGGGGGGGAAPETQCPPTNLISVSVENLCVITWMPPEASS	60
QY	60	NCSLWYFHFSGDKODKKIAPETRRSIEVPLNEIKCQVQSGCSTNBEKKSILVEKCI	119
Db	61	NCSLWYFHFSGDKODKKIAPETRRSIEVPLNEIKCQVQSGCSTNBEKKSILVEKCI	120
QY	120	PEGDESAVTELOCIIMHNSYMKCSMLPGNTSPDNTYTLTYWHRSLSEKHOCENIFREG	179
Db	121	PEGDESAVTELOCIIMHNSYMKCSMLPGNTSPDNTYTLTYWHRSLSEKHOCENIFREG	180
QY	180	OYFGGSPDLTKYKXDSFEQHSVQIMYKDNAGKIKPSENIYPLTSRYKDPDPHINKNSFHN	239
Db	181	OYFGGSPDLTKYKXDSFEQHSVQIMYKDNAGKIKPSENIYPLTSRYKDPDPHINKNSFHN	240
QY	240	DDLZYQWENPQNFISRCLEFYEVEVNNSSQETETHAVFYQEAKECENPEFERVENTSCMPV	299
Db	241	DDLZYQWENPQNFISRCLEFYEVEVNNSSQETETHAVFYQEAKECENPEFERVENTSCMPV	300
QY	300	GVLPTLTLVTRIRVKTNKCIEBDDKLSMWSQEMSGGKKNST	342
Db	301	GVLPTLTLVTRIRVKTNKCIEBDDKLSMWSQEMSGGKKNST	343

```

RESULT 7
US-10-282-162-32
; Sequence 32, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045

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; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

```

Query Match	80.8%;	Score 1875.5;	DB 2;	Length 793;
Best Local Similarity	99.4%;	Pred. No. 1e-175;		
Matches 341;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;

QY	1	MEMPRILGIMALLILCAGGGGGGGG-APRTEIOPRPTNLISVSEJENICTVIMTWMPREGASS	59
Db	1	MWMPRLGIMALLILCAGGGGGGGAAPTETOPRPTNLISVSEJENICTVIMTWMPREGASS	60
QY	60	NCSLMTEFHFGDKOKKTAIAPETRBSIEVPLNRICLQVSGCOSTNESEKPSILIVEKCI	119
Db	61	NCSLMTEFHFGDKOKKTAIAPETRBSIEVPLNRICLQVSGCOSTNESEKPSILIVEKCI	120
QY	120	PEGDESAVTELOCIMHNLVYMKCGMILPGRINTSPDNTYLLYWHRSLEKIHQECNIFREG	179
Db	121	PEGDESAVTELOCIMHNLVYMKCGMILPGRINTSPDNTYLLYWHRSLEKIHQECNIFREG	180
QY	180	QYFGGSPDLTKKXKSSFEQSHVQIIMWKONAGIKIKSFNIVPLTSRYKPPRPHIKNISFHN	239
Db	181	QYFGGSPDLTKKXKSSFEQSHVQIIMWKONAGIKIKSFNIVPLTSRYKPPRPHIKNISFHN	240
QY	240	DDLZYQWENPQIFIRCLFEYEVENVNNSQETETNAVFEVQAEKCNPEFERVENTSCFMP	299
Db	241	DDLZYQWENPQIFIRCLFEYEVENVNNSQETETNAVFEVQAEKCNPEFERVENTSCFMP	300
QY	300	GVLPTLNTVRIRVKTINKLCYEDDKLMSWSQEMSIGKKRNST	342
Db	301	GVLPTLNTVRIRVKTINKLCYEDDKLMSWSQEMSIGKKRNST	343

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RESULT 8
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-313-942-30

```

Query Match	76.7%;	Score 1779.5;	DB 2;	Length 784;
Best Local Similarity	90.4%;	Pred. No. 2.9e-166;		
Matches 328;	Conservative 5;	Mismatches 15;	Indels 15;	Gaps 2;

QY	20	GGGGGGAATETLP	PATNINLSVSVENICTVATWNNP	PAGASNSCLWFSHGGDQDKKIAP	79
Db	233	GGGGGAAPETETQ	PATNINLSVSVENICTVATWNNP	PAGASNSCLWFSHGGDQDKKIAP	232
QY	80	ETRRRIEVLPLNRICL	QVGSOSTNSEKPSILVEKCI	PPRGGDPSAATLQCIWNHLS	139
Db	233	ETRRRIEVLPLNRICL	QVGSOSTNSEKPSILVEKCI	PPRGGDPSAATLQCIWNHLS	352


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Db 61 NCSLWFSHFHGDQDKKIAIPETRRSIEVPLNERICLQVGSQCSTNSEKPSIIIEKCI6P 120
Qy 120 PGDPSAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTIHQCENTFRFG 179
Db 121 PGDPSAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTIHQCENTFRFG 180
Qy 180 QYFGCSFDLTLYKXDSFEGHSVOIMWKDAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
Db 181 QYFGCSFDLTLYKXDSFEGHSVOIMWKDAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
Qy 240 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVFYVQAKCENPFERNVENTSCFMP 299
Db 241 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVFYVQAKCENPFERNVENTSCFMP 300
Qy 300 GVLPTLNTVIRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLIIVPIVAGAI 359
Db 301 GVLPTLNTVIRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLIIVPIVAGAI 360
Qy 360 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQDDTLHWKXYDIYEKQTEETDSVLLIE 419
Db 361 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQDDTLHWKXYDIYEKQTEETDSVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 2
US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3

Query Match 99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2,9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

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Qy 240 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVFYVQAKCENPFERNVENTSCFMP 299
Db 241 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVFYVQAKCENPFERNVENTSCFMP 300
Qy 300 GVLPTLNTVIRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLIIVPIVAGAI 359
Db 301 GVLPTLNTVIRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLIIVPIVAGAI 360
Qy 360 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQDDTLHWKXYDIYEKQTEETDSVLLIE 419
Db 361 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQDDTLHWKXYDIYEKQTEETDSVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 3
US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferreira, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vitor, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match 99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2,9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 420 NLKASQ 426
 Db 421 NLKASQ 427

RESULT 4 US-11-182-384A-4

Sequence 4, Application US/11182384A
 Publication No. US20060035855A1
 GENERAL INFORMATION:
 APPLICANT: Caput, Daniel
 APPLICANT: Ferrata, Pascual
 APPLICANT: Laurent, Patrick
 APPLICANT: Valta, Natalio
 TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
 FILE REFERENCE: IVD924 US Div 2
 CURRENT APPLICATION NUMBER: US/11/182,384A
 PRIOR FILING DATE: 2005-07-15
 PRIOR APPLICATION NUMBER: 09/077,817
 PRIOR FILING DATE: 1998-09-14
 PRIOR APPLICATION NUMBER: PCT/FR96/01756
 PRIOR FILING DATE: 1996-11-07
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-182-384A-4

Query Match 99.5%; Score 2309.5; DB 6; Length 427;
 Best Local Similarity 99.8%; Pred. No. 2.9e-188;
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPEGASS 59
 Db 1 MEMPARLCGLMALLLCAGGGGGGGGAPTETQPPVTNLVSVENLCTVIWTPNPEGASS 60
 QY 60 NCSLMYSHFGDKODKKIAETRSIEVPLNERICLVGSGCSTNSESKEPSILVEKCI 119
 Db 61 NCSLMYSHFGDKODKKIAETRSIEVPLNERICLVGSGCSTNSESKEPSILVEKCI 120
 QY 120 PEGDPESAVTELQCIWNLISYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 179
 Db 121 PEGDPESAVTELQCIWNLISYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 180
 QY 180 QYFGCSFDLTKVSDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 239
 Db 181 QYFGCSFDLTKVSDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 240
 QY 240 DDLVQWENQNFISRLCFYEVENVNSQTEHNVFYQEAKECENPEERVENVENTSCFMP 299
 Db 241 DDLVQWENQNFISRLCFYEVENVNSQTEHNVFYQEAKECENPEERVENVENTSCFMP 300
 QY 300 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIYVAGAI 359
 Db 301 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIYVAGAI 360
 QY 360 IVLLLYLKRLLKIIIFPIPDPGKIFKEMFGDQNDTLHMKKYDIYERQTEETDSVLLIE 419
 Db 361 IVLLLYLKRLLKIIIFPIPDPGKIFKEMFGDQNDTLHMKKYDIYERQTEETDSVLLIE 420
 QY 420 NLKASQ 426
 Db 421 NLKASQ 427

RESULT 5
 US-11-183-599A-4
 Sequence 4, Application US/11183599A
 Publication No. US20060035855A1
 GENERAL INFORMATION:
 APPLICANT: Caput, Daniel

APPLICANT: Ferrata, Pascual
 APPLICANT: Laurent, Patrick
 APPLICANT: Valta, Natalio
 TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
 FILE REFERENCE: IVD924 US Div 1
 CURRENT APPLICATION NUMBER: US/11/183,599A
 PRIOR FILING DATE: 2005-07-15
 PRIOR APPLICATION NUMBER: 09/077,817
 PRIOR FILING DATE: 1998-09-14
 PRIOR APPLICATION NUMBER: PCT/FR96/01756
 PRIOR FILING DATE: 1996-11-07
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-183-599A-4

Query Match 99.5%; Score 2309.5; DB 6; Length 427;
 Best Local Similarity 99.8%; Pred. No. 2.9e-188;
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPEGASS 59
 Db 1 MEMPARLCGLMALLLCAGGGGGGGGAPTETQPPVTNLVSVENLCTVIWTPNPEGASS 60
 QY 60 NCSLMYSHFGDKODKKIAETRSIEVPLNERICLVGSGCSTNSESKEPSILVEKCI 119
 Db 61 NCSLMYSHFGDKODKKIAETRSIEVPLNERICLVGSGCSTNSESKEPSILVEKCI 120
 QY 120 PEGDPESAVTELQCIWNLISYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 179
 Db 121 PEGDPESAVTELQCIWNLISYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 180
 QY 180 QYFGCSFDLTKVSDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 239
 Db 181 QYFGCSFDLTKVSDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 240
 QY 240 DDLVQWENQNFISRLCFYEVENVNSQTEHNVFYQEAKECENPEERVENVENTSCFMP 299
 Db 241 DDLVQWENQNFISRLCFYEVENVNSQTEHNVFYQEAKECENPEERVENVENTSCFMP 300
 QY 300 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIYVAGAI 359
 Db 301 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSQEMSIKKNSTLYITMLLIVPIYVAGAI 360
 QY 360 IVLLLYLKRLLKIIIFPIPDPGKIFKEMFGDQNDTLHMKKYDIYERQTEETDSVLLIE 419
 Db 361 IVLLLYLKRLLKIIIFPIPDPGKIFKEMFGDQNDTLHMKKYDIYERQTEETDSVLLIE 420
 QY 420 NLKASQ 426
 Db 421 NLKASQ 427

RESULT 6
 US-11-149-309-37
 Sequence 37, Application US/11149309
 Publication No. US20060063228A1
 GENERAL INFORMATION:
 APPLICANT: Kasarian, Marion T.
 APPLICANT: Tchistiakova, Lioudmila
 APPLICANT: Veldman, Geetruida M.
 APPLICANT: Marquette, Kimberly Ann
 APPLICANT: Tan, Xiang-Yang
 APPLICANT: Donaldson, Debora D.
 APPLICANT: Lin, Laura Long
 APPLICANT: Shane, Tanja
 APPLICANT: Tam, Amy Szepuni
 APPLICANT: Feyfiant, Eric
 APPLICANT: Wood, Nancy L.
 APPLICANT: Fitz, Lori J.

```
/ APPLICANT: widom, Angela M.
/ APPLICANT: Parits, Kevin D.
/ APPLICANT: Goldman, Samuel J.
/ TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
/ FILE REFERENCE: 16158-048001 / AM01493
/ CURRENT APPLICATION NUMBER: US/11/149,309
/ PRIOR FILING DATE: 2005-06-09
/ PRIOR APPLICATION NUMBER: US 60/578,473
/ PRIOR FILING DATE: 2004-06-09
/ PRIOR APPLICATION NUMBER: US 60/581,375
/ PRIOR FILING DATE: 2004-06-22
/ PRIOR APPLICATION NUMBER: US 60/578,736
/ PRIOR FILING DATE: 2004-06-09
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-149-309-37
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Query Match          99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY      1 MEMPARLCGIMALLLCAAGGGGGGGG-APETOPPVNTLSVSVNLCVITWNPPEGASS 59
DB      1 MEMPARLCGIMALLLCAAGGGGGGGGAAPTETOPPVNTLSVSVNLCVITWNPPEGASS 60
QY      60 NCSLWYFHSFGDKQDKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCISP 119
DB      61 NCSLWYFHSFGDKQDKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCISP 120
QY      120 PEGDPSAATTELOCIMHNLSTYKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 179
DB      121 PEGDPSAATTELOCIMHNLSTYKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 180
QY      180 QYFGCSFDLTKVDSFEGHSVOIMVKNAGIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
DB      181 QYFGCSFDLTKVDSFEGHSVOIMVKNAGIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
QY      240 DDLYVQWENPQNTISRCLEFEVEVNNNSQETETNHFVVOEAKCENPEFERVENTSCFMPV 299
DB      241 DDLYVQWENPQNTISRCLEFEVEVNNNSQETETNHFVVOEAKCENPEFERVENTSCFMPV 300
QY      300 GVLPTLNTVRLRVKTNKLCYEDDKLMSNWSQEMSGKKRNSLTLYTMLIIVPIVADAI 359
DB      301 GVLPTLNTVRLRVKTNKLCYEDDKLMSNWSQEMSGKKRNSLTLYTMLIIVPIVADAI 360
QY      360 IVLLVLYLKRLLKIIIPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIE 419
DB      361 IVLLVLYLKRLLKIIIPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIE 420
QY      420 NLKKAQ 426
DB      421 NLKKAQ 427
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RESULT 7
US-10-850-270-4
/ Sequence 4, Application US/10850270
/ Publication No. US20050058645A1
/ GENERAL INFORMATION:
/ APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
/ APPLICANT: Dunlop, Felicity (US only)
/ APPLICANT: Baca, Manuel (US only)
/ APPLICANT: Nash, Andrew (US only)
/ APPLICANT: Fabri, Louis (US only)
/ TITLE OF INVENTION: Novel peptides
/ FILE REFERENCE: 12175890/BJH
/ CURRENT APPLICATION NUMBER: US/10/850,270
/ CURRENT FILING DATE: 2004-05-20
/ PRIOR APPLICATION NUMBER: AU PS1301
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/ PRIOR FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: AU 2003900437
/ PRIOR FILING DATE: 2003-02-03
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: human
US-10-850-270-4
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Query Match          99.2%; Score 2302.5; DB 5; Length 427;
Best Local Similarity 99.5%; Pred. No. 1.2e-187;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY      1 MEMPARLCGIMALLLCAAGGGGGGGG-APETOPPVNTLSVSVNLCVITWNPPEGASS 59
DB      1 MEMPARLCGIMALLLCAAGGGGGGGGAAPTETOPPVNTLSVSVNLCVITWNPPEGASS 60
QY      60 NCSLWYFHSFGDKQDKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCISP 119
DB      61 NCSLWYFHSFGDKQDKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCISP 120
QY      120 PEGDPSAATTELOCIMHNLSTYKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 179
DB      121 PEGDPSAATTELOCIMHNLSTYKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 180
QY      180 QYFGCSFDLTKVDSFEGHSVOIMVKNAGIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
DB      181 QYFGCSFDLTKVDSFEGHSVOIMVKNAGIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
QY      240 DDLYVQWENPQNTISRCLEFEVEVNNNSQETETNHFVVOEAKCENPEFERVENTSCFMPV 299
DB      241 DDLYVQWENPQNTISRCLEFEVEVNNNSQETETNHFVVOEAKCENPEFERVENTSCFMPV 300
QY      300 GVLPTLNTVRLRVKTNKLCYEDDKLMSNWSQEMSGKKRNSLTLYTMLIIVPIVADAI 359
DB      301 GVLPTLNTVRLRVKTNKLCYEDDKLMSNWSQEMSGKKRNSLTLYTMLIIVPIVADAI 360
QY      360 IVLLVLYLKRLLKIIIPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIE 419
DB      361 IVLLVLYLKRLLKIIIPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIE 420
QY      420 NLKKAQ 426
DB      421 NLKKAQ 427
```

```
RESULT 8
US-10-036-568-4
/ Sequence 4, Application US/10036568
/ Publication No. US20020090682A1
/ GENERAL INFORMATION:
/ APPLICANT: Willson, Tracy
/ APPLICANT: Nicols, Nicos A.
/ APPLICANT: Hilton, Douglas J.
/ APPLICANT: Metcalf, Donald
/ APPLICANT: Zhang, Jian G.
/ TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
/ FILE REFERENCE: ENCODING SAME
/ CURRENT APPLICATION NUMBER: US/10/036,568
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US/09/051,843
/ PRIOR FILING DATE: 1998-06-29
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 426
/ TYPE: PRT
/ ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4
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Query Match 99.2%; Score 2302; DB 4; Length 426;
Best Local Similarity 99.3%; Pred. No. 1,3e-187;
Matches 423; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLVSVENLCTVIWTPNPEGASSN 60
DB 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLVSVENLCTVIWTPNPEGASSN 60
QY 61 CSLMYFHFSGDKODKKIAPETRRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PP 120
DB 61 CSLMYFHFSGDKODKKIAPETRRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PP 120
QY 121 EGPESAVTELOCIMHNLSTYKCSWMLPGRNTSPDTNTLYYHRSLEKIHOCENIFREGQ 180
DB 121 EGPESAVTELOCIMHNLSTYKCSWMLPGRNTSPDTNTLYYHRSLEKIHOCENIFREGQ 180
QY 181 YFGCSFDLTGVKOSSEFQHSVOIMVKNACKIKPSFNIIVPLTSRVKDPPIHKNLSFHN 240
DB 181 YFGCSFDLTGVKOSSEFQHSVOIMVKNACKIKPSFNIIVPLTSRVKDPPIHKNLSFHN 240
QY 241 DLVYOMENPONFISRCLEFEVEVNNQOTETHNVFYOEACENPEFERNVENTSCFVWP 300
DB 241 DLVYOMENPONFISRCLEFEVEVNNQOTETHNVFYOEACENPEFERNVENTSCFVWP 300
QY 301 VLBDTLNTVIRIRKTNKLCYEDDKLMSNMSQEMSIGKKNSTLYITMLLIVPIVAGAI 360
DB 301 VLBDTLNTVIRIRKTNKLCYEDDKLMSNMSQEMSIGKKNSTLYITMLLIVPIVAGAI 360
QY 361 VLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLIEN 420
DB 361 VLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLIEN 420
QY 421 LKKASQ 426
DB 421 LKKASQ 426
```

RESULT 9

US-11-155-843-125
Sequence 125, Application US/11155843
Publication No. US20060073148A1
GENERAL INFORMATION:
APPLICANT: Tchiastakova, Lioudmila
APPLICANT: Kasalan, Marion T.
APPLICANT: Donaldson, Debra D.
APPLICANT: Tan, Xiang-Yang
APPLICANT: Gill, Davinder
APPLICANT: Jin, Macy X.
APPLICANT: Jacobson, Bruce
APPLICANT: Goldman, Samuel J.
APPLICANT: Knopf, John
APPLICANT: Widom, Angela M.
TITLE OF INVENTION: IL-13 BINDING AGENTS
FILE REFERENCE: 16158-020001
CURRENT APPLICATION NUMBER: US/11/155,843
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/581,078
PRIOR FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 11/149,025
PRIOR FILING DATE: 2005-06-09
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 125
LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
US-11-155-843-125

Query Match 99.0%; Score 2296.5; DB 6; Length 427;
Best Local Similarity 99.3%; Pred. No. 3.8e-187;
Matches 424; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MEMPARLCGIMALLLCAGGGGGGAG--APTEPTOPPTVNLVSVENLCTVIWTPNPEGASS 59

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DB 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLVSVENLCTVIWTPNPEGASS 60
QY 60 NCSLMYFHFSGDKODKKIAPETRRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3P 119
DB 61 NCSLMYFHFSGDKODKKIAPETRRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3P 120
QY 120 EGPESAVTELOCIMHNLSTYKCSWMLPGRNTSPDTNTLYYHRSLEKIHOCENIFREG 179
DB 121 EGPESAVTELOCIMHNLSTYKCSWMLPGRNTSPDTNTLYYHRSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTGVKOSSEFQHSVOIMVKNACKIKPSFNIIVPLTSRVKDPPIHKNLSFHN 239
DB 181 QYFGCSFDLTGVKOSSEFQHSVOIMVKNACKIKPSFNIIVPLTSRVKDPPIHKNLSFHN 240
QY 240 DDLVYOMENPONFISRCLEFEVEVNNQOTETHNVFYOEACENPEFERNVENTSCFVWP 299
DB 241 DDLVYOMENPONFISRCLEFEVEVNNQOTETHNVFYOEACENPEFERNVENTSCFVWP 300
QY 300 GVLBDTLNTVIRIRKTNKLCYEDDKLMSNMSQEMSIGKKNSTLYITMLLIVPIVAGAI 359
DB 301 GVLBDTLNTVIRIRKTNKLCYEDDKLMSNMSQEMSIGKKNSTLYITMLLIVPIVAGAI 360
QY 360 IYLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLI 419
DB 361 IYLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLI 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427
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RESULT 10

US-09-828-995B-50
Sequence 50, Application US/09828995B
Patent No. US20020165135A1
GENERAL INFORMATION:
APPLICANT: Heeka Corporation
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 405
TYPE: PRT
ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 3; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.9e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

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QY 22 GGGGAPTEPTOPPTVNLVSVENLCTVIWTPNPEGASSNCSLMYFHFSGDKODKKIAPET 81
DB 1 GGYAAPTETPTPTVNLVSVENLCTVIWTPNPEGASPNCCLRYFHFNDKQDKIAPET 60
QY 82 RRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PPGDPESAVTELOCIMHNLSTY 141
DB 61 HRSKEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PPGDPESAVTELOCIMHNLSTY 120
QY 142 KCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFREGQYFGCSFDLTGVKOSSEFQHSV 201
DB 121 KCTWLPGRNTSPDTNTLYYHRSLEKIHOCENIFREGQYFGCSFDLTGVKOSSEFQHSV 180
QY 202 QIMVKNACKIKPSFNIIVPLTSRVKDPPIHKNLSFHNDDL VYOMENPONFISRCLEFEV 261
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Db      181 QIMVKDNARKIRSFNIVPLTSHVKPDPPIKRLFPQNGMLYQWKNPQNFYSRCLSYQV 240
Qy      262 EVNNSOTETHNAVYVOEAKCENPEFERNAVNTSCFMWPGVLPPTLTNTRIRVTKNLCYE 321
Db      241 EVNNSOTETHNDIFYVEEAKCQNSEFEGNLEGTICFMWPGVLPPTLTNTRIRVTKNLCYE 300
Qy      322 DDKLMSNWSQEMSIGKRNSLTITMLLIVPVIAGAIIVLLYLKRLKIIFPPIDPG 381
Db      301 DDKLMSNWSQAMSIGENTDPTFYITMLLATQVIVAGAIITLLYLKRLKIIFPPIDPG 360
Qy      382 KIFKEMFGQNDDTLHMKKYDIYEKQTKETSDSVLIENLKASQ 426
Db      361 KIFKEMFGQNDDTLHMKKYDIYEKQTKETSDSVLIENLKASQ 405

RESULT 11
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heeska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-753-159-50

Query Match      80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.9e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
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RESULT 12
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203d
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-935-868-34
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Query Match      80.8%; Score 1875.5; DB 3; Length 780;
Best Local Similarity 99.4%; Pred. No. 7.5e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Qy      1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPPTVNTLSVSENLCTVIWTNPPREGASS 59
Db      1 MWMPARLCGLMALLCAGGGGGGGGAAPTETOPPTVNTLSVSENLCTVIWTNPPREGASS 60
Qy      60 NCSLWFSHFGDKODKKIAPETRRSIEVPLNERICLOVSGOSTNESEKPSILVEKICSP 119
Db      61 NCSLWFSHFGDKODKKIAPETRRSIEVPLNERICLOVSGOSTNESEKPSILVEKICSP 120
Qy      120 PEGDPESAATELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKIHQENIFREG 179
Db      121 PEGDPESAATELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKIHQENIFREG 180
Qy      180 QYFGCSFDLTKYKDSSEFQHSQVQIMVKDNAGKIKPSFNIVPLTSRKVPPPHIKNLSFHN 239
Db      181 QYFGCSFDLTKYKDSSEFQHSQVQIMVKDNAGKIKPSFNIVPLTSRKVPPPHIKNLSFHN 240
Qy      240 DDLYQWENPQNFISRCLEFEVEVNNSSOTETHNAVYVOEAKCENPEFERNAVNTSCFMW 299
Db      241 DDLYQWENPQNFISRCLEFEVEVNNSSOTETHNAVYVOEAKCENPEFERNAVNTSCFMW 300
Qy      300 GVLPTLTNTRIRVTKNLCYEDDDKLMSNWSQEMSIGKRNST 342
Db      301 GVLPTLTNTRIRVTKNLCYEDDDKLMSNWSQEMSIGKRNST 343
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RESULT 13
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-32

Query Match      80.8%; Score 1875.5; DB 3; Length 793;
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:45:43 ; Search time 21 Seconds
(without alignments)
544,307 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 2320
Sequence: 1 MEMPARLCGMALILCAGCG.....QTKETDSVLIENIKTKASQ 426

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	13.0	372	US-11-331-993-7	Sequence 7, Appli
2	294.5	12.7	380	US-11-220-888-4	Sequence 4, Appli
3	294.5	12.7	380	US-11-331-993-2	Sequence 2, Appli
4	293.5	12.7	380	US-11-331-993-4	Sequence 4, Appli
5	284	12.2	310	US-11-220-888-1	Sequence 1, Appli
6	202	8.7	369	US-10-511-937-2966	Sequence 2966, Ap
7	167.5	7.2	422	US-11-296-092-32	Sequence 32, Appli
8	167.5	7.2	422	US-11-296-155-32	Sequence 32, Appli
9	162.5	7.0	371	US-11-297-957-4	Sequence 4, Appli
10	142.5	6.1	662	US-11-301-764-5	Sequence 5, Appli
11	142.5	6.1	764	US-11-301-764-39	Sequence 39, Appli
12	139	6.0	508	US-10-511-937-2426	Sequence 2426, Ap
13	137	5.9	519	US-11-301-764-71	Sequence 71, Appli
14	125	5.4	825	US-10-505-928-650	Sequence 650, App
15	125	5.4	825	US-10-511-937-3001	Sequence 3001, App
16	123.5	5.3	547	US-11-301-764-114	Sequence 114, App
17	123.5	5.3	662	US-11-301-764-112	Sequence 112, App
18	112	4.8	336	US-10-953-349-18546	Sequence 18546, A
19	112	4.8	372	US-10-953-349-18545	Sequence 18545, A
20	111.5	4.8	979	US-11-301-764-7	Sequence 7, Appli
21	106	4.6	635	US-10-511-937-2424	Sequence 2424, Ap
22	104.5	4.5	530	US-10-449-902-36140	Sequence 36140, A
23	104	4.5	970	US-11-301-764-120	Sequence 120, App
24	103.5	4.5	459	US-10-511-937-2465	Sequence 2465, Ap
25	102.5	4.4	459	US-11-297-957-2	Sequence 2, Appli

26	102	4.4	17	US-11-134-871-727	Sequence 727, App
27	98.5	4.2	731	US-11-155-444-6	Sequence 6, Appli
28	98.5	4.2	731	US-11-155-109-6	Sequence 6, Appli
29	98.5	4.2	735	US-11-155-444-10	Sequence 10, Appli
30	98.5	4.2	735	US-11-156-109-10	Sequence 10, Appli
31	97.5	4.2	984	US-11-259-133-22	Sequence 22, Appli
32	96	4.1	384	US-11-293-697-2595	Sequence 2595, Ap
33	96	4.1	996	US-11-285-738-2	Sequence 2, Appli
34	94.5	4.1	1259	US-10-561-015-5	Sequence 5, Appli
35	93.5	4.0	836	US-10-511-937-2988	Sequence 2988, Ap
36	93	4.0	531	US-10-449-902-43013	Sequence 43013, A
37	92.5	4.0	287	US-10-953-349-18547	Sequence 18547, A
38	92.5	4.0	983	US-11-302-678-2	Sequence 2, Appli
39	92.5	4.0	983	US-11-259-133-6	Sequence 6, Appli
40	92	4.0	353	US-10-953-349-32271	Sequence 32271, A
41	90.5	3.9	739	US-11-301-764-69	Sequence 69, Appli
42	89.5	3.9	337	US-11-274-375-2	Sequence 2, Appli
43	89.5	3.9	428	US-11-274-375-4	Sequence 4, Appli
44	89.5	3.9	629	US-11-274-375-6	Sequence 6, Appli
45	89.5	3.9	1204	US-11-289-102-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-11-331-993-7
Sequence 7, Application US/11331993
Publication No. US20060110800A1
GENERAL INFORMATION:
APPLICANT: Baumgartner, James W.
Farragh, Theresa M.
Foster, Donald C.
Grant, Frank J.
O'Hara, Patrick J.
TITLE OF INVENTION: Testis-Specific Receptor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/331,993
FILING DATE: 04-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/090,867
FILING DATE: 04-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E.
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-331-993-7
Query Match 13.0%; Score 302; DB 7; Length 372;

[illegible]

```

RESULT 2
US-11-220-888-4
Sequence 4, Application US/11220888
Publication No. US2006009652a1
GENERAL INFORMATION:
APPLICANT: GATELY, Stephen C.
APPLICANT: MANASKI, Stephen P.
TITLE OF INVENTION: IL 13 RECEPTOR ALPHA 2 ANTIBODY AND METHODS OF USE
FILE REFERENCE: 238603
CURRENT APPLICATION NUMBER: US/11/220, 888
CURRENT FILING DATE: 2005-09-07
PRIOR APPLICATION NUMBER: PCT/US2004/009354
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US 60/457, 898
PRIOR FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 380
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Interleukin 13 receptor, alpha 2
US-11-220-888-4

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	Query Match	12.7%	Score 294.5	DB 7	Length 380
	Best Local Similarity	27.0%	Pred. No. 14e-17		
	Matches	100	Conservative	59	Mismatches 138, Indels 73, Gaps 20
Qy	51	WNPEGAS-SNCSLMYFHFHGDKDKKIAIETRRSI-----EVLNERICLQVGS	99		
	53	WQPLSLDHFKECTVEY-----ELKYRIGSESTWKTITIKNLHYKDFGLNKIGIAEKIHT	107		
Db	100	-----QCSNSESEKPSILVEKC--ISPRGDPESATLELCIMHNLNYSKKCSMLPGRNISP	153		
Qy	108	LIPMOC-TNGSEVOSSMAETTYWIS-PCGPIETKQDDMCVYNNQYLLCSKPSGIGVLL	165		
Db	154	DTNNTLLYMHRSLEKIHOC-ENIFREGQYFGCSFDLTFRKDSFPOHSQVQIMWKNACKI	212		
Qy	166	DTNNTLLFYWEGDLHALQCVDIYKADGQNIIGRFRPLYEASD--YDFIYICVNGSSENNPI	223		
Db	213	KPSRNIVLTSRKVRDPPIHKLKLSHND---DLVQEMENPQNT-SRCLFVEVEVNNQSQT	268		
Qy	224	RSSYFTFQLOQIVKPLRP--VLLTTRSSCEIKLKWBIPLGPIPARCFDEVEIEREDTT	281		
Db					

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QY      269  ETHANFVYQKACKECPPEPERNVENTS---CFNVPGLPDLTNTVTRLRVTNNKCYEDDKL 325
Db      282  T-----LVATATVENETTLTKTNNETRLQCFVV-----RSKVNIVC-SDDGI 321
QY      326  MSNWGQEM-----SIGKRNSTLYITMLLIVPVIAGAIIVLLYLKRLKIIIFPPIPD 380
Db      322  MSWMSDKOCWESGEDLSKTLNRFWLP-----GPIILIVIVTGL--LIRKENTYP 370
QY      381  GKIFKEMFGD 390
Db      371  -KMIDFEFCD 379

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1      RESULT 3
2      US-11-331-993-2
3      Sequence 2, Application US/11331993
4      Publication No. US20060110800A1
5      GENERAL INFORMATION:
6      APPLICANT: Baumgartner, James W.
7      Faarrah, Theresa M.
8      Foster, Donald C.
9      Grant, Frank J.
10     O'Hara, Patrick J.
11     TITLE OF INVENTION: Testis-Specific Receptor
12     NUMBER OF SEQUENCES: 33
13     CORRESPONDENCE ADDRESSES:
14     ADDRESSEE: Zymogenetics, Inc.
15     STREET: 1201 Eastlake Avenue East
16     CITY: Seattle
17     STATE: WA
18     COUNTRY: USA
19     ZIP: 98102
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patent in Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/11/331,993
27     FILING DATE: 04-Jun-1998
28     CLASSIFICATION: <Unknown>
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US/09/090,867
31     FILING DATE: 04-Jun-1998
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Parker, Gary E.
34     REGISTRATION NUMBER: 31,648
35     REFERENCE/DOCKET NUMBER: 95-33
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 206-442-6673
38     TELEFAX: 206-442-6678
39     INFORMATION FOR SEQ ID NO: 2:
40     SEQUENCE CHARACTERISTICS:
41     LENGTH: 380 amino acids
42     TYPE: amino acid
43     TOPOLOGY: linear
44     MOLECULE TYPE: protein
45     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
46     US-11-331-993-2

```

	Query Match	Similarity	Best Local Matches Match 100; Conservative	Score 294.5;	DB 7;	Length 380;
		27.0%; Pred.No.	1.4e-17; Mismatches 138;		Indels 73;	Gaps 20;
Cy	51	MNPEGAS--SNGSLWYFHSHGDKODKIAIPETRSI-----EVLPLNERICLOVGS	99			
D6	53	WQPLSLDHFKEFEKV---ELKYRNIGSEITKTIIYNKLHYKDGFDLKKGIKAIKHT	107			
Oy	100	----QCSTNESEKSILVEKC--ISPEGDESAVTLECIWHNLSYWKCSWLPGRNTSP	153			
D6	108	LTPWC--TNSGEVOSSNAETTWTIS-DGLADPTLVVDMDCCYYMMQTLLSCSKRGDIGVL	165			

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:21:03 ; Search time 195 Seconds
(without alignments)
998.842 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426
Sequence: 1 MEMPARLCGMALLCAGGG.....QTKETDSVVLIENTKKASQ 426

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Geneseqp_8:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	426	100.0	426	AAW09822	AAW09822 Human int
2	401	94.1	414	ADX97531	ADX97531 Pandreati
3	401	94.1	427	AAW24973	AAW24973 Human int
4	401	94.1	427	AAB19807	AAB19807 Human int
5	401	94.1	427	ADL17812	ADL17812 Human int
6	401	94.1	427	ADL82843	ADL82843 Human PRO
7	401	94.1	427	ADN04504	ADN04504 Antipocri
8	401	94.1	427	ADN62575	ADN62575 Human int
9	401	94.1	427	ABM82441	ABM82441 Tumour-as
10	401	94.1	427	AEC31473	AEC31473 Human IL-
11	401	94.1	427	AEEB3788	AEEB3788 Human IL-
12	401	94.1	427	AEP57817	AEP57817 Anti-IL-1
13	401	94.1	427	ADP17835	ADP17835 Human IL-
14	331	77.7	427	ADL17814	ADL17814 Human int
15	331	77.7	427	ADL17814	ADL17814 Human int
16	317	74.4	664	AAE13745	AAE13745 Human sol
17	317	74.4	664	ADL17841	ADL17841 ChimERIC
18	317	74.4	784	AAV92207	AAV92207 IL-13/IL-
19	317	74.4	793	ABW02180	ABW02180 Human IL-
20	317	74.4	793	AAV92208	AAV92208 IL-13/IL-
21	300	70.4	427	ADL17813	ADL17813 Human int
22	297	69.7	776	AEC31482	AEC31482 Human IL-
23	297	69.7	776	AEC31484	AEC31484 Human IL-

24	297	69.7	776	9	AEC31478	AEC31478 Human IL-
25	297	69.7	776	9	AEC31486	AEC31486 Human IL-
26	297	69.7	776	9	AEC31480	AEC31480 Human IL-
27	244	57.3	286	4	AAB90678	AAB90678 Human DA1
28	230	54.0	427	4	AAB19808	AAB19808 Human int
29	177	41.5	177	2	AAW58987	AAW58987 Homo sapi
30	91	21.4	134	8	ADP84617	ADP84617 Human bre
31	91	21.4	172	8	ADP84616	ADP84616 Human bre
32	91	21.4	226	8	ADP65618	ADP65618 Novel hum
33	50	11.7	82	8	ADO26844	ADO26844 Human rec
34	43	10.1	424	9	ADX97888	ADX97888 Murine IL
35	35	10.1	426	2	AAW09821	AAW09821 Mouse int
36	37	8.7	405	4	AAU69132	AAU69132 Canine in
37	22	5.2	22	2	AAV39425	AAV39425 Human int
38	22	5.2	22	5	AAU78025	AAU78025 Human int
39	17	4.0	17	10	AEEB6623	AEEB6623 Human ser
40	11	2.6	1214	4	ABB61851	ABB61851 Drosophi1
41	11	2.6	1214	8	ADO08007	ADO08007 Fly polyP
42	10	2.3	25	10	AEEB39126	AEEB39126 Human ser
43	10	2.3	149	8	ABO58726	ABO58726 Human gen
44	10	2.3	170	2	AAR04129	AAR04129 Stem cell
45	10	2.3	190	7	ABM86938	ABM86938 Rice abio

ALIGNMENTS

RESULT 1	
AAW09822	AAW09822 standard; protein; 426 AA.
XX	
AC	AAW09822;
XX	
DT	15-JUL-1997 (first entry)
XX	
DE	Human interleukin-12 receptor alpha chain NR4.
XX	
KM	NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine;
KW	allergy; asthma; therapy.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Peptide
FT	Protein
FT	Domain
FT	Modified-site
FT	Modified-site
FT	Domain
FT	Modified-site
FT	Region
FT	Domain
FT	Domain
FT	Domain
XX	
XX	WO9715663-A1.
XX	
XX	01-MAY-1997.
XX	
PF	23-OCT-1996; 96WO-AU000668.
XX	
XX	23-OCT-1995; 95AU-00006135.
PR	22-DEC-1995; 95AU-00007276.

```
PR 09-SEP-1996; 96AU-00002208.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX
XX WPI, 1997-259018/23.
XX
XX N-PSDB; AAT6165.
XX
XX DNA encoding animal haemopoietin receptor which interacts with
XX interleukin-13 - useful to treat asthma, allergy or condition exacerbated
XX by IGE production.
XX
XX Claim 5; Page 52-54; 93pp; English.
XX
XX Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),
XX designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
XX The human NR4 amino acid sequence was deduced from a composite DNA
XX sequence (AAT6165) derived from bone marrow cDNA clones. Recombinant
XX NR4, or fusion proteins including NR4, can be produced in transgenic
XX host cells. The receptor molecules and their components are useful in the
XX development of a range of agonists, antagonists, therapeutics and
XX diagnostic reagents based on ligand interaction with its receptor. esp.
XX for the development of cpds. capable of modulating the activity of IL-13
XX and related cytokines such as interleukin-4 for the treatment of allergy,
XX asthma and other conditions relating to IGE
XX
XX Sequence 426 AA;
SQ
Query Match 100.0%; Score 426; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEMPARLCGIMALLLCAGGGGGGGGAPTERQPPVTLNLSVENLCTVIWTNPNPEGASSN 60
DB 1 MEMPARLCGIMALLLCAGGGGGGGGAPTERQPPVTLNLSVENLCTVIWTNPNPEGASSN 60
QY 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLQVSGQCSSTNESEKPSILVEKCI 120
DB 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLQVSGQCSSTNESEKPSILVEKCI 120
QY 121 EGDPSAVYTELCITMHNLSYMKCSWLPGRNTSPDNTYTLTYMHRSLKIHOCENIFREGQ 180
DB 121 EGDPSAVYTELCITMHNLSYMKCSWLPGRNTSPDNTYTLTYMHRSLKIHOCENIFREGQ 180
QY 121 EGPBSAVYTELCITMHNLSYMKCSWLPGRNTSPDNTYTLTYMHRSLKIHOCENIFREGQ 180
DB 121 EGPBSAVYTELCITMHNLSYMKCSWLPGRNTSPDNTYTLTYMHRSLKIHOCENIFREGQ 180
QY 181 YFGCSFDLTKVKQSSFEQHSVOIMVKDNACKIRPSFNIVPLTSRVKDPPIHKNLSFPHND 240
DB 181 YFGCSFDLTKVKQSSFEQHSVOIMVKDNACKIRPSFNIVPLTSRVKDPPIHKNLSFPHND 240
QY 241 DLVYQWENPQNFISRCLFYEVENVNSQTEETHNFYVOEAKCENPEPERNVENTSCFVPG 300
DB 241 DLVYQWENPQNFISRCLFYEVENVNSQTEETHNFYVOEAKCENPEPERNVENTSCFVPG 300
QY 301 VLPDITANTYAIRKYTKMLCYEDDKLWMSQEMSIGKKRNTTYITMLLIVPIYVAGAIT 360
DB 301 VLPDITANTYAIRKYTKMLCYEDDKLWMSQEMSIGKKRNTTYITMLLIVPIYVAGAIT 360
QY 361 VLLLYLKRLKILIFPPIPDGKTFKEMFGPQNDLTHMKYDYLYEKQTEKETSVYLLEN 420
DB 361 VLLLYLKRLKILIFPPIPDGKTFKEMFGPQNDLTHMKYDYLYEKQTEKETSVYLLEN 420
QY 421 LKKASQ 426
DB 421 LKKASQ 426
RESULT 2
ADX97531
ID ADX97531 standard; protein; 414 AA.
XX
XX AC ADX97531;
XX
XX 21-APR-2005 (first entry)
```

```
XX
XX DE Pancreatic cancer associated human protein, SEQ ID 79.
XX
XX KW pancreas tumor; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN EPI471075-A2.
XX
XX PD 27-OCT-2004.
XX
XX PF 31-MAR-2004; 2004EP-00090124.
XX
XX PR 31-MAR-2003; 2003DE-01015834.
XX
XX (HINZ/) HINZMANN B.
XX (ROSE/) ROSENTHAL A.
XX (PIL/) PILARSKY C.
XX (DAHL/) DAHL E.
XX (SPEC/) SPECHT T.
XX (LICH/) LICHTNER R.
XX
XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T;
XX Lichtenner R, Straub E, Roepeke S, Li X;
XX
XX WPI; 2004-768082/76.
XX
XX N-PSDB; ADX97460.
XX
XX New nucleic acid differentially expressed in pancreatic tumor tissue, for
XX use as diagnostic agents and in screening for therapeutic agents.
XX
XX Claim 2; SEQ ID NO 79; 28pp; German.
XX
XX The invention relates to a novel human nucleic acid sequence of the
XX pancreas and its encoded protein. The invention further comprises:
XX proteins and peptides, preferably isolated, that contain a sequence
XX encoded by the novel nucleic acid; and methods for diagnosis and
XX treatment of pancreatic cancer, using a substance that inhibits or binds
XX to the protein or its DNA, including: an antisense oligonucleotide, short
XX interfering RNA or ribozyme directed against the pancreatic protein, an
XX organic molecule, particularly having a molecular weight below 5000,
XX especially 300, that binds to the pancreatic DNA, an aptamer or
XX (monoclonal) antibody, preferably human or humanized, that binds to the
XX pancreatic DNA, or an anti-idiotypic antibody raised against the
XX monoclonal antibody, any of which may be derivatized with a reporter
XX group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
XX human pancreatic proteins and their encoding DNA have cytostatic
XX activity. The novel sequences are useful for inhibiting transcription
XX and/or expression of genes and proteins associated with pancreatic
XX cancer. This sequence represents one of the novel human pancreatic
XX proteins of the invention. Note: This sequence is not shown in the
XX specification, it has been electronically downloaded from a DVD-ROM
XX provided with this specification by the European Patent Office.
XX
XX Sequence 414 AA;
SQ
Query Match 94.1%; Score 401; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETQPPVTLNLSVENLCTVIWTNPNPEGASSNCSLMYFSHFQDKODKKIAPETRRSI 85
DB 14 APTETQPPVTLNLSVENLCTVIWTNPNPEGASSNCSLMYFSHFQDKODKKIAPETRRSI 73
QY 86 EYPLNERICLQVSGQCSSTNESEKPSILVEKCISSPPGDPBSAVTELCITMHNLSYMKCSW 145
DB 74 EYPLNERICLQVSGQCSSTNESEKPSILVEKCISSPPGDPBSAVTELCITMHNLSYMKCSW 133
QY 146 LPERNTSPDNTYTLTYMHRSLKIHOCENIFREGQYFGGSPDLTKYKQSSFEQHSVOIMY 205
DB 134 LPERNTSPDNTYTLTYMHRSLKIHOCENIFREGQYFGGSPDLTKYKQSSFEQHSVOIMY 193
QY 206 KONAGIKIPSFNIVPLTSRVKDPPIHKNLSFPHNDLYQWENPQNFISRCLFYEVENVNN 265
```

```

Db      194 KDNAGKIKPSFNIYPLLSRVKPDPPHINKNSFHNDDLYVQWENPONSRLCFYEVEVNN 253
Qy      266 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 325
Db      254 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 313
Qy      326 WSNWSQEMSIGKRNSTLYITMLLIVPVIAGAIIVLLVLRKLIIFPPIDPGKIFK 385
Db      314 WSNWSQEMSIGKRNSTLYITMLLIVPVIAGAIIVLLVLRKLIIFPPIDPGKIFK 373
Qy      386 EMFGDQNDPDLHMKKYDIYEKQTEETDSVVLLENLKKASQ 426
Db      374 EMFGDQNDPDLHMKKYDIYEKQTEETDSVVLLENLKKASQ 414

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RESULT 3

AAW24973
ID AAW24973 standard; protein; 427 AA.

AC AAW24973;

DT 22-JUN-1998 (first entry)

DE Human interleukin-13 alpha receptor.

KM Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.

OS Homo sapiens.

PN MO9720926-A1.

PD 12-JUN-1997.

PF 07-NOV-1996; 96MO-FR001756.

PR 06-DEC-1995; 95FR-00014424.

PA (SNFI) SANOFI SA.

PI Caput D, Ferrara P, Laurent P, Vita N;

DR WPI; 1997-319773/29.

DR N-PSDB; AAT85827.

PT New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc.

PS Claim 8; Page 46-47; 83pp; French.

XX This sequence represents interleukin-13 (IL-13) alpha receptor. The
XX invention relates to new purified peptides comprising 380 or 427 amino
XX acid sequences, which are receptors for interleukin-13 (IL-13); the 380
XX and 427 aa proteins are designated IL-13R beta and alpha respectively.
XX The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
XX affinity, but acquires high affinity when associated with the IL-4
XX receptor. Nucleic acids encoding IL-13R beta and alpha are used as
XX diagnostic probes to identify aberrant synthesis or genetic anomalies
XX such as loss of heterozygosity and rearrangements, or chromosomal
XX anomalies. They are also used for production of recombinant IL-13R beta
XX and alpha which can be used as IL-13 antagonists, specifically to
XX regulate IL-13-induced responses for treatment of inflammation and
XX allergy. IL-13 receptors are also useful as antisense molecules for gene
XX therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
XX immunassays) to diagnose diseases associated with abnormal expression of
XX IL-13 receptors, when coupled to a toxin also for treatment of
XX overproduction of IL-13R. Cells that express IL-13R at the surface are
XX used to identify ligands and modulators of IL-13R

XX Sequence 427 AA;

Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      26 APTETOPVNNLSVSVENLCVIMTNPPRGASNCGLWFSHSGDQDKKIAETRSI 85
Db      27 APTETOPVNNLSVSVENLCVIMTNPPRGASNCGLWFSHSGDQDKKIAETRSI 86
Qy      86 EVPLNERICQVGSQCSTNSEKPSILVEKISPEEDPESAVTELQCIWHNLGYMKCSW 145
Db      87 EVPLNERICQVGSQCSTNSEKPSILVEKISPEEDPESAVTELQCIWHNLGYMKCSW 146
Qy      146 LPEGNTSPDNTNYLYVHRSLEKIHQCENIFREGQYFGCSFDLTRKVSFEGHSVQIMV 205
Db      147 LPEGNTSPDNTNYLYVHRSLEKIHQCENIFREGQYFGCSFDLTRKVSFEGHSVQIMV 206
Qy      206 KDNAGKIKPSFNIYPLLSRVKPDPPHINKNSFHNDDLYVQWENPONSRLCFYEVEVNN 265
Db      207 KDNAGKIKPSFNIYPLLSRVKPDPPHINKNSFHNDDLYVQWENPONSRLCFYEVEVNN 266
Qy      266 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 325
Db      267 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 326
Qy      326 WSNWSQEMSIGKRNSTLYITMLLIVPVIAGAIIVLLVLRKLIIFPPIDPGKIFK 385
Db      327 WSNWSQEMSIGKRNSTLYITMLLIVPVIAGAIIVLLVLRKLIIFPPIDPGKIFK 386
Qy      386 EMFGDQNDPDLHMKKYDIYEKQTEETDSVVLLENLKKASQ 426
Db      387 EMFGDQNDPDLHMKKYDIYEKQTEETDSVVLLENLKKASQ 427

```

RESULT 4

AAB19807
ID AAB19807 standard; protein; 427 AA.

AC AAB19807;

DT 05-MAR-2001 (first entry)

DE Human interleukin-13 receptor alpha-1.

KM Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;

KM atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;

KM dermatological; antiaesthetic; antiallergic; therapy; diagnosis.

OS Homo sapiens.

PN Location/Qualifiers

FT Key 1..26

FT Peptide /label= Sig_Peptide

FT Domain 27..347

FT Protein /label= Extracellular_domain

FT Peptide /label= Mature_protein

FT /note="MSXMS motif conserved in the type-1 cytokine

FT Domain 348..367

FT Domain /label= Transmembrane_domain

PN US6143871-A.

PD 07-NOV-2000.

PF 12-NOV-1997; 97US-00969125.

PR 13-DEC-1996; 96GB-00025899.

PA (GAUC/) GAUCHAR J.

QY 266 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNKLCEYDDKL 325
| | | | |
DB 267 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNKLCEYDDKL 326
| | | | |
QY 326 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 385
| | | | |
DB 327 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 386
| | | | |
QY 386 EMFGDQNDPDLHWKXYIYEKQTEETDSVLLIENLKASQ 426
| | | | |
DB 387 EMFGDQNDPDLHWKXYIYEKQTEETDSVLLIENLKASQ 427
| | | | |
RESULT 6
ADL82843
ID ADL82843 standard; protein: 427 AA.
XX
AC ADL82843;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human PRO2537, SEQ ID 45.
XX
KM Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KM Immune-mediated inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WT;
PI Wu TD;
XX
DR MPI; 2004-329389/30.
XX
DR N-PSDB; ADL82842.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 10; Fig 45; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyclonal
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic
CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SO Sequence 427 AA;
Query Match 94.1%; Score 401; DB 8; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETOPVNLISVSENLCTVITWNPBPASSNCSIMYPSHHGDDKDIAPETRRI 85
| | | | |
DB 27 APTETOPVNLISVSENLCTVITWNPBPASSNCSIMYPSHHGDDKDIAPETRRI 86
| | | | |
QY 86 EVPLNERICLVQSGQSTNSEKPSILVEKISPPEDPESAVTELOCIMHNLGYMKCSW 145
| | | | |
DB 87 EVPLNERICLVQSGQSTNSEKPSILVEKISPPEDPESAVTELOCIMHNLGYMKCSW 146
| | | | |
QY 146 LPGRNTPDNTNYTLVYHRSLEKIHQCCENIFREGQYFGCSFDLTRKVDSPREGHSVOIMV 205
| | | | |
DB 147 LPGRNTPDNTNYTLVYHRSLEKIHQCCENIFREGQYFGCSFDLTRKVDSPREGHSVOIMV 206
| | | | |
QY 206 KDNAGKIKPSFNIVPLLSRKPDPDPHILKNSFHHDDLVOQENPQNTSRCLFYEVEVNN 265
| | | | |
DB 207 KDNAGKIKPSFNIVPLLSRKPDPDPHILKNSFHHDDLVOQENPQNTSRCLFYEVEVNN 266
| | | | |
QY 266 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNKLCEYDDKL 325
| | | | |
DB 267 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNKLCEYDDKL 326
| | | | |
QY 326 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 385
| | | | |
DB 327 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 386
| | | | |
QY 386 EMFGDQNDPDLHWKXYIYEKQTEETDSVLLIENLKASQ 426
| | | | |
DB 387 EMFGDQNDPDLHWKXYIYEKQTEETDSVLLIENLKASQ 427
| | | | |

RESULT 7
ADN04504
ID ADN04504 standard; protein: 427 AA.
XX
AC ADN04504;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #445.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;
PI Wu TD;
XX
DR MPI; 2004-305105/28.
XX
DR N-PSDB; ADN04503.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 9; SEQ ID NO 898; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

XX	Sequence	427 AA;
XX	Query Match	94.1%; Score 401; DB 8; Length 427;
XX	Best Local Similarity	100.0%; Pred. No. 0;
XX	Matches 401; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	26	APTEQPPVTVNLSTSVENLCITYIMWNPPEGASNSCISLMTFSHPGDKDCKIAPETRRSI 85
DB	27	APTEQPPVTVNLSTSVENLCITYIMWNPPEGASNSCISLMTFSHPGDKDCKIAPETRRSI 86
QY	86	EVLPIERICLOVGSQCSSTNSESKEPSILVEKICISPEEGDPESAATBELQCIWHNLSTYKCSW 145
DB	87	EVLPIERICLOVGSQCSSTNSESKEPSILVEKICISPEEGDPESAATBELQCIWHNLSTYKCSW 146
QY	146	LPGRNTSPDNTVTLTYMHRSLSEKIHQCENIPFEGQIFGSGPDLTVKQSPFQSHVQIMV 205
DB	147	LPGRNTSPDNTVTLTYMHRSLSEKIHQCENIPFEGQIFGSGPDLTVKQSPFQSHVQIMV 206
QY	206	KDNAGKIPSPFNIVPLTSRVKEDPPEHINKLSFPHNDLLYQWENPQNIFSRCLFYEVEVNN 265
DB	207	KDNAGKIPSPFNIVPLTSRVKEDPPEHINKLSFPHNDLLYQWENPQNIFSRCLFYEVEVNN 266
QY	266	SQTEHNFNFYQOACENPEEFRRNVENTSCEFNVPGLPDLTNTVIRVKTNKLCTYEDDKL 325
DB	267	SQTEHNFNFYQOACENPEEFRRNVENTSCEFNVPGLPDLTNTVIRVKTNKLCTYEDDKL 326
QY	326	MSNMQSEMSIGKKRSTLYTMTLLVPVTVAGATVLLTYLRKLTIIPPIPDGKIFK 385
DB	327	MSNMQSEMSIGKKRSTLYTMTLLVPVTVAGATVLLTYLRKLTIIPPIPDGKIFK 386
QY	386	EMFGDQNDTLHMKYDIYEKQTEKETS SVLIENIKKASQ 426
DB	387	EMFGDQNDTLHMKYDIYEKQTEKETS SVLIENIKKASQ 427
RESULT 8		
ADN62575		
ID	ADN62575	standard; protein; 427 AA.
XX	ADN62575;	
AC		
XX	12-AUG-2004	(first entry)
DT		
DE	Human interleukin 13 (IL-13) receptor alpha 1 chain.	
XX		
KW	Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;	
KW	IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;	
KW	cancer; inflammatory disease; rheumatoid arthritis;	
KW	inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;	
KW	Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;	
KW	urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;	
KW	Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;	
KW	Lyme disease; tuberculosis; malaria; leishmaniasis.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..26
FT	Protein	/note= "Signal peptide"
FT		27..427
FT		/note= "Mature protein claimed in claim 1"
XX	US643604-B1.	
PN		
PD	01-JUN-2004.	
XX		
PF	06-APR-2000; 2000US-00545002.	
XX		
PR	13-DEC-1996; 96GB-00025899.	
PR	12-NOV-1997; 97US-00969125.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM CORP.	

PI	xx	Bonnefoy J, Gauchat J;
xx	xx	
DR	xx	WPI: 2004-409324/38.
xx	xx	
DR	xx	N-PSDB; ADN62574.
xx	xx	
PT	xx	New isolated nucleic acid molecule encoding a polypeptide capable of
xx	xx	binding human IL-13 and/or binding human IL-4, useful in medicine, in
xx	xx	diagnostics or for producing antibodies.
xx	xx	
PS	xx	Claim 1; SEQ ID NO 9; 24pp: English.
xx	xx	
CC	xx	The invention relates to an isolated nucleic acid molecule (ADN62574),
CC	xx	which encodes the mature form of a polypeptide capable of binding human
CC	xx	IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
CC	xx	IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
CC	xx	a vector comprising the nucleic acid molecule and a host cell comprising
CC	xx	the vector. The nucleic acids are useful as probes or primers or in the
CC	xx	analysis of allelic variation. The polypeptides are useful for binding
CC	xx	human IL-13 and/or binding human IL-4 and act as inhibitors by
CC	xx	interfering with the interaction between human IL-13 or IL-4 and their
CC	xx	natural receptors. They can also be used in medicine, e.g. for treatment
CC	xx	of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC	xx	asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC	xx	inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC	xx	lupus erythematosus, thyroiditis, diabetes, warts, psoriasis,
CC	xx	urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC	xx	Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC	xx	lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC	xx	used for producing antibodies, which can be used for diagnosing diseases.
CC	xx	The present sequence represents IL-13 receptor alpha 1 subunit.
xx	xx	
SQ	xx	Sequence 427 AA;
xx	xx	
Query Match	94.1%;	Score 401; DB 8; Length 427;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches	401;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	26	APETQPPTNLVSVENLCTVITWMPPEGASSNLSLWFSHFQKODKKAIPETRRSI 85
DB	27	APTETQPPVTNLVSVENLCTVITWMPPEGASSNLSLWFSHFQKODKKAIPETRRSI 86
QY	86	EVPLNERICLOVSGQCSSTNBEKRSILVEKCISSPBDPESAVELQCIWNNLSYMKCSW 145
DB	87	EVPLNERICLOVSGQCSSTNBEKRSILVEKCISSPBDPESAVELQCIWNNLSYMKCSW 146
QY	146	LPGRNTSPDNTYTLTYMHRSLEKIHQCENIFREQYFGCSFDLTKVXDSSEFQHSVOIMV 205
DB	147	LPGRNTSPDNTYTLTYMHRSLEKIHQCENIFREGQYFGCSFDLTKVXDSSEFQHSVOIMV 206
QY	206	KDNAGKIKPSNIVPLTSRVKPDPPHAIKNLSFHHDDLIVQWENQNFISRLCFEVEVNN 265
DB	207	KDNAGKIKPSNIVPLTSRVKPDPPHAIKNLSFHHDDLIVQWENQNFISRLCFEVEVNN 266
QY	266	SOTETHNVFVYQAKCENPEPERVWNTSCPMVGV.PDTLNTYRIIRKTKLCEYEDKL 325
DB	267	SOTETHNVFVYQAKCENPEPERVWNTSCPMVGV.PDTLNTYRIIRKTKLCEYEDKL 326
QY	326	WSNNSQEMSIKKRNSLTITMLLIPVYAGAILVLLLYKRLKIIIFPDPGKIFK 385
DB	327	WSNNSQEMSIKKRNSLTITMLLIPVYAGAILVLLLYKRLKIIIFPDPGKIFK 386
QY	386	EMFGDQNDTLHWKKYDIEYKQTEEDDSVLLENLKASQ 426
DB	387	EMFGDQNDTLHWKKYDIEYKQTEEDDSVLLENLKASQ 427
RESULT 9		
ABM82441		
ID	ABM82441	standard; protein; 427 AA.
xx	xx	
xx	xx	ABM82441;
xx	xx	

DT 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
DE
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW
XX tumour; diagnosis; cell proliferative disorder; breast cancer;
KW
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW
XX central nervous system cancer; bladder cancer; pancreatic cancer;
KW
XX cervical cancer; melanoma; leukaemia; hybridisation probe;
KW
XX chromosome identification; chromosome mapping; gene mapping;
KW
XX gene therapy; cytostatic.
OS
XX Homo sapiens.
XX
XX MO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX
XX 02-OCT-2002; 2002US-0414971P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
XX
XX WPI; 2004-347921/32.
XX
XX N-PSDB; ACN41073.
XX
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX
XX Claim 12; SEQ ID NO 6271; 7273pp; English.
PS
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acid and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment of
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
XX
XX Sequence 427 AA;
SQ
Query Match 94.1%; Score 401; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APFETOPVNLISVENVLCVITWNPBPAGASNCISWYFSGDKDKKIAPETRRASI 85
DB 27 APFETOPVNLISVENVLCVITWNPBPAGASNCISWYFSGDKDKKIAPETRRASI 86
QY 86 EVPLNERICQVSGSCSTNESEKPSILVEKCIISPPEGPPESAVELQCIWHNLSYMRCSW 145
DB 87 EVPLNERICQVSGSCSTNESEKPSILVEKCIISPPEGPPESAVELQCIWHNLSYMRCSW 146
QY 146 LFGKNTSPDNTNYTLYYWHRSLSEKTIHQCEINIFREGQYFGCSFDLTQKVDSSFEQHSVOIMV 205
|||||

DB 147 LFGKNTSPDNTNYTLYYWHRSLSEKTIHQCEINIFREGQYFGCSFDLTQKVDSSFEQHSVOIMV 206
QY KDNAGKIPSEFNIVPLTSRVKPPDPPIHINLSFHNDDLVYQWENPQNFIISRCLEFVEVNN 265
DB 207 KDNAGKIPSEFNIVPLTSRVKPPDPPIHINLSFHNDDLVYQWENPQNFIISRCLEFVEVNN 266
QY 266 SQTETHNVFVYQAEKACENPEERNVENTSCFVPGVLPDITNTVIRVKTNLCYEDDKL 325
DB 267 SQTETHNVFVYQAEKACENPEERNVENTSCFVPGVLPDITNTVIRVKTNLCYEDDKL 326
QY 326 WSNWSQEMSIGKKNSTLYITMLLIPVIVAGATVLLVLRKLIIFPPIPDGKIFK 385
DB 327 WSNWSQEMSIGKKNSTLYITMLLIPVIVAGATVLLVLRKLIIFPPIPDGKIFK 386
QY 386 EMFGQNDPDLHWKKYDIYEKOTKEETNSVLIENLTKRASQ 426
DB 387 EMFGQNDPDLHWKKYDIYEKOTKEETNSVLIENLTKRASQ 427
RESULT 10
AEC31473
ID AEC31473 standard; protein, 427 AA.
XX
XX AEC31473;
AC
XX
XX 03-NOV-2005 (first entry)
DT
XX
XX Human IL-13 receptor alpha-1 SEQ ID NO:3.
DE
XX
XX interleukin-13 receptor; fusion protein; therapeutic; antiasthmatic;
KW
XX antiallergic; dermatological; anti-inflammatory; immunosuppressive;
KW
XX cytostatic; hepatotropic; anti-HIV; virucide; gastrointestinal-gen;
KW
XX antibacterial; fungicide; antiparasitic; antitumor; antithyroid;
KW
XX nephrotropic.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 27.343
FT Domain /label = extracellular domain
FT
XX
XX US2005191730-A1.
XX
XX
XX 01-SEP-2005.
XX
XX 25-FEB-2005; 2005US-00067251.
XX
XX 27-FEB-2004; 2004US-0548541P.
PR 17-AUG-2004; 2004US-0602139P.
PR 16-NOV-2004; 2004US-0628343P.
XX
XX (REGG-) REGENERON PHARM INC.
PA
XX
XX Karow M, Fairhurst J;
PI
XX
XX WPI; 2005-590777/60.
XX
XX
XX New nucleic acid molecules encoding polypeptides capable of binding
PT interleukin-4 and interleukin-13, useful for diagnosing and/or treating
PT asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer
PT and infections.
XX
XX
XX Claim 1; SEQ ID NO 3; 35pp; English.
PS
XX
XX The invention relates to a novel nucleic acid molecule encoding a fusion
CC polypeptide. The fusion polypeptide consists of 231 amino acids
CC -231 and 24-231 of a fully defined sequence of 231 amino acids
CC (AEC31473), which sequences may comprise 1-10 modifications. R2 is a
CC fully defined sequence of 427 or 380 bp (AEC31473+AEC31474), which
CC sequences may comprise one to three modifications. F is a fusion
CC component, and x and y are each independently a positive integer 1. The F
CC is a multimerizing component, a serum protein, or a molecule capable of
CC binding a serum protein, where the multimerizing component is an

CC the methods above in the manufacture of a medicament for the prophylaxis
 CC or treatment of a condition associated with IL-13 activity. The antibody
 CC crystal and methods are useful for designing an agent that interacts with
 CC an IL-13 polypeptide. The agent is useful for treating an IL-13 condition
 CC chosen from allergic asthma or nonallergic asthma, cancer, airway
 CC inflammation, eosinophilia, fibrosis, excess mucus production,
 CC inflammatory condition of the skin, gastrointestinal organs, blood
 CC vessels or connective tissue, and an autoimmune condition of the skin,
 CC gastrointestinal organs, blood vessels, or connective tissue, chronic
 CC obstructive pulmonary disorder, cystic fibrosis, pulmonary fibrosis,
 CC allergic rhinitis, atopic dermatitis, inflammatory bowel disease, Crohn's
 CC disease, cirrhosis, scleroderma, or Hodgkin's lymphoma. The present
 CC sequence is the human IL-13 alpha receptor protein.

XX Sequence 427 AA:

Query Match 94.1%; Score 401; DB 10; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVNTLSVSVENLCTVIWTNPPGASNSCLMYFSHPGDKKIAPETRRSI 85
 DB 27 APTETQPPVNTLSVSVENLCTVIWTNPPGASNSCLMYFSHPGDKKIAPETRRSI 86
 QY 86 EVDLNERICLVQVSGQSTNESEKPSILVEKCISSPBGDPBSAVTELCIWHNLSYMKCSW 145
 DB 87 EVDLNERICLVQVSGQSTNESEKPSILVEKCISSPBGDPBSAVTELCIWHNLSYMKCSW 146
 QY 146 LPRGNTSPDNTNYTLVYHRSLEKIHOCENIFREGQYFGCSFDLTXYKDSFEQHSVOIMV 205
 DB 147 LPRGNTSPDNTNYTLVYHRSLEKIHOCENIFREGQYFGCSFDLTXYKDSFEQHSVOIMV 206
 QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVOMENPQNFISCLFYEVEVNN 265
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVOMENPQNFISCLFYEVEVNN 266
 QY 266 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
 DB 267 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
 QY 326 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIIVLLLYLKRKLTIIIPPIPDGKIFK 385
 DB 327 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIIVLLLYLKRKLTIIIPPIPDGKIFK 386
 QY 386 EMFGQNDPTLHWKXYDIYEKOTKEETDSVLLIENLKASQ 426
 DB 387 EMFGQNDPTLHWKXYDIYEKOTKEETDSVLLIENLKASQ 427

RESULT 12

ID AEF57817 standard; protein; 427 AA.

XX AEF57817;

XX 23-MAR-2006 (first entry)

DE Anti-IL-13-antibody associated polypeptide SEQ ID NO 37.

XX antiasthmatic; dermatological; respiratory-gen.; immunosuppressive;
 XX antiinflammatory; cytostatic; virucide; antiallergic;
 XX gastrointestinal-gen.; vaccine; antibody; diagnosis; therapeutic; asthma;
 XX antiasthmatic; chronic obstructive pulmonary disease; respiratory-gen.;
 XX infection; viral infection; virucide; autoimmune disorder;
 XX immunosuppressive; immune disorder; inflammatory bowel disease;
 XX antiinflammatory; gastrointestinal-gen.; gastrointestinal disease;
 XX inflammation; allergic rhinitis; antiallergic; ear, nose, throat disease;
 XX immune disorder; respiratory disease.

OS Homo sapiens.

XX WO2005123126-A2.

PD 29-DEC-2005.

PF 09-JUN-2005; 2005WO-US020160.

XX 09-JUN-2004; 2004US-0578473P.

FR 09-JUN-2004; 2004US-0578736P.

PR 22-JUN-2004; 2004US-0581375P.

XX (AMHP) WYETH.

PI Kasaian MT, Tchistiakova L, Veldman GM, Marquette KA, Tan X;
 PI Donaldson DD, Lin LL, Shane T, Tam AS, Feyfant E, Wood NL, Fitz LJ;
 PI Widom AM, Pariss KD, Goldman SJ;

XX WPI; 2006-172770/18.

PT New antibody against human interleukin-13, useful for diagnosing,
 PT preventing, and/or treating a disorder, e.g. asthma, tumors, allergic
 PT rhinitis, or inflammatory bowel disease.

PS Disclosure; SEQ ID NO 37; 169pp; English.

CC The invention describes an antibody, or its antigen-binding, that binds
 CC to interleukin (IL)-13. Also described are: a pharmaceutical composition
 CC comprising the antibody, or its antigen-binding fragment above and a
 CC pharmaceutical carrier; a nucleic acid that comprises a sequence that
 CC encodes a polypeptide that comprises a heavy chain immunoglobulin
 CC variable region or a light chain immunoglobulin variable region described
 CC above; a host cell comprising a nucleic acid sequence that encodes the
 CC antibody, or its antigen-binding fragment, above; providing a recombinant
 CC antibody; treating an IL-13-associated disorder; and detecting the
 CC presence of IL-13 in a sample. The antibody, composition, and method are
 CC useful for diagnosing, preventing, and/or treating IL-13 associated
 CC disorder, e.g. asthmatic disorders, atopic disorders, chronic obstructive
 CC pulmonary disease (COPD), conditions involving airway inflammation,
 CC eosinophilia, fibrosis and excess mucus production, inflammatory
 CC conditions, autoimmune conditions, tumors or cancers, viral infection,
 CC suppression of expression of protective type 1 immune responses, allergic
 CC rhinitis, or inflammatory bowel disease. This is the amino acid sequence
 CC of a polypeptide associated with anti-IL-13-antibodies of the invention.

XX Sequence 427 AA:

Query Match 94.1%; Score 401; DB 10; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVNTLSVSVENLCTVIWTNPPGASNSCLMYFSHPGDKKIAPETRRSI 85
 DB 27 APTETQPPVNTLSVSVENLCTVIWTNPPGASNSCLMYFSHPGDKKIAPETRRSI 86
 QY 86 EVDLNERICLVQVSGQSTNESEKPSILVEKCISSPBGDPBSAVTELCIWHNLSYMKCSW 145
 DB 87 EVDLNERICLVQVSGQSTNESEKPSILVEKCISSPBGDPBSAVTELCIWHNLSYMKCSW 146
 QY 146 LPRGNTSPDNTNYTLVYHRSLEKIHOCENIFREGQYFGCSFDLTXYKDSFEQHSVOIMV 205
 DB 147 LPRGNTSPDNTNYTLVYHRSLEKIHOCENIFREGQYFGCSFDLTXYKDSFEQHSVOIMV 206
 QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVOMENPQNFISCLFYEVEVNN 265
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVOMENPQNFISCLFYEVEVNN 266
 QY 266 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
 DB 267 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
 QY 326 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIIVLLLYLKRKLTIIIPPIPDGKIFK 385
 DB 327 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIIVLLLYLKRKLTIIIPPIPDGKIFK 386
 QY 386 EMFGQNDPTLHWKXYDIYEKOTKEETDSVLLIENLKASQ 426

Db 387 EMEFGDNDTLMWKYDIYEKQTKETDSVLIENLKASQ 427

RESULT 13

ADFL7835

ID ADFL7835 standard; protein; 427 AA.

XX ADFL7835;

XX 12-FEB-2004 (first entry)

XX Human IL-13 alpha 1 receptor (IL-13R) protein.

XX IL-13R; human; receptor; anaphylaxis; hay fever; asthma;

KW antiinflammatory; cytostatic; antitumor; dermatological; antiasthmatic;

KW antiasthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;

KW scleroderma; allergic rhinitis; oncological;

KW chronic obstructive pulmonary disease.

XX Homo sapiens.

OS WO2003080675-A2.

XX PN

XX 02-OCT-2003.

XX 21-MAR-2003; 2003WO-AU000352.

XX PF

XX 22-MAR-2002; 2002AU-00001301.

XX PR 03-FEB-2003; 2003AU-00900437.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Dunlop FM, Baca M, Nash AD, Fabri LJ;

XX DR MPI; 2003-876912/81.

XX N-PSDB; ADFL7834.

XX PT New monoclonal antibodies against interleukin-13 receptor alpha, useful

PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,

PT scleroderma, allergic rhinitis, oncological conditions, asthma or an

PT inflammatory disorder.

XX PS Disclosure; SEQ ID NO 4; 99pp; English.

XX This invention relates to a novel antibodies that function as interleukin

CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used

CC for treating certain conditions induced by IL-13. Specifically, it refers

CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13

CC and IL-4 induced signaling. IL-13 is a mediator in the immunostimulatory

CC system, such that it is involved in the induction of IgE, IgG4 and T-

CC helper cells and accordingly is implicated in conditions from anaphylaxis

CC to hay fever and asthma. As such, the present invention describes these

CC novel antibodies as antiinflammatory, cytostatic, antitumor,

CC dermatological, antiasthmatic and antiasthmatic. The methods and

CC compositions are useful for treating various disorders including

CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic

CC rhinitis, oncological conditions and chronic obstructive pulmonary

CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor

CC protein of the invention.

XX SQ

XX Sequence 427 AA;

Query Match 77.7%; Score 331; DB 7; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APEETOPPYTNLSVSVENLCTVIWMPPEGASSNCSLWYFSGKODKKIAPETRRSI 85

DB 27 APEETOPPYTNLSVSVENLCTVIWMPPEGASSNCSLWYFSGKODKKIAPETRRSI 86

QY 86 EYPLNRICTLOVSGOSTNESEKPSILVEKCSPPGSDPSATTELOCTWHNLSYMKCSW 145

DB 87 EYPLNRICTLOVSGOSTNESEKPSILVEKCSPPGSDPSATTELOCTWHNLSYMKCSW 146

QY 146 LPERNTSPDTNVTLYYHRSLEKIHOCENIFREGQYFGCSFDLTKYKSSFEQHSVOIMV 205

DB 147 LPERNTSPDTNVTLYYHRSLEKIHOCENIFREGQYFGCSFDLTKYKSSFEQHSVOIMV 206

QY 206 KDNAGKIKSPNIVPLTSRVKDPDPPIIKNLSFINDLTYQWENPQNFISRCLEFYEVYNN 265

DB 207 KDNAGKIKSPNIVPLTSRVKDPDPPIIKNLSFINDLTYQWENPQNFISRCLEFYEVYNN 266

QY 266 SOTETHNVFYVOEAKENEFERNVENTSCFMVPGVLPTLTATVRIRVKTNKLCTYEDDKL 325

DB 267 SOTETHNVFYVOEAKENEFERNVENTSCFMVPGVLPTLTATVRIRVKTNKLCTYEDDKL 326

QY 326 WSNWSQEMSIGKKRNSTLYITMLIVPIVA 356

DB 327 WSNWSQEMSIGKKRNSTLYITMLIVPIVA 357

RESULT 14

ADFL7814

ID ADFL7814 standard; protein; 427 AA.

XX ADFL7814;

XX 20-MAY-2004 (first entry)

XX Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.

XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;

KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;

KW mutant.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 358

XX US2004043921-A1.

XX 04-MAR-2004.

XX 29-SEP-2003; 2003US-00671697.

XX 13-DEC-1996; 96GB-00025899.

XX 12-NOV-1997; 97US-00969125.

XX 06-APR-2000; 2000US-00545002.

XX (BONN/) BONNEFOY J.

XX (GAUC/) GAUCHAT J.

XX Bonnefoy J, Gauchat J;

XX MPI; 2004-225726/21.

XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse

PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma

PT or AIDS, comprises administering a polypeptide or soluble polypeptide.

XX Claim 14; Page; 27pp; English.

XX The invention relates to polypeptides capable of binding human

CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The

CC invention also relates to a method of treatment of a disease in which

CC IL13 and IL4 cause adverse effects. The method is useful for treating a

CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic

CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides

CC of the invention are useful in raising antibodies. It is also useful in

CC gene therapy. The present sequence is human interleukin-13 receptor alpha

CC (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the

CC specification, however it is constructed based on human IL-13 Ralpha

CC protein shown as SEQ ID NO:9 in the specification.

XX Sequence 427 AA;
SQ
Query Match 77.7%; Score 331; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETQPPVTNLVSVENLCTVITWNPPEGASSNCSIMYFSHFQDKKXIADETRRI 85
DB 27 APTETQPPVTNLVSVENLCTVITWNPPEGASSNCSIMYFSHFQDKKXIADETRRI 86
QY 86 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLNLSYMKCSW 145
DB 87 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLNLSYMKCSW 146
QY 146 LPGNTSPDNTNYTLTYWHRSLKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 205
DB 147 LPGNTSPDNTNYTLTYWHRSLKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVOMENPQNFISRCLFYEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVOMENPQNFISRCLFYEVEVNN 266
QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 325
DB 267 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 326
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPIVA 356
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPIVA 357
RESULT 15
AAE13745
ID AAE13745 standard; protein: 322 AA.
AC AAE13745;
XX 26-FEB-2002 (first entry)
DT Human soluble cytokine IL-13 receptor alpha1 (IL-13RA1) protein.
XX DE
XX Human; Zalphal1; cytokine receptor; immunosuppressive; cytostatic;
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
KW viral infection; IL-13 receptor alpha1; IL-13RA1.
XX
XX Homo sapiens.
OS
XX
XX MO200177171-A2.
PN 18-OCT-2001.
PD
XX
XX 03-APR-2001; 2001WO-US010872.
PF
XX 05-APR-2000; 2000US-0194731P.
PR 28-JUL-2000; 2000US-0222121P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ,
XX
XX MPI: 2002-025988/03.
DR N-PSDB; AAD22979.
XX
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
PT antagonist for stimulating ligand activity-induced proliferation of
PT hematopoietic cells and for suppressing immune response in a mammal.
PS Claim 29; Page 236-237; 243pp; English.
XX

CC The invention relates to an isolated soluble zalphal1 cytokine receptor
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC haematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is human soluble cytokine IL-13 receptor alpha1 (IL-13RA1)
CC protein related to the invention
XX
SQ Sequence 322 AA;
Query Match 74.4%; Score 317; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 3,4e-306;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETQPPVTNLVSVENLCTVITWNPPEGASSNCSIMYFSHFQDKKXIADETRRI 85
DB 6 APTETQPPVTNLVSVENLCTVITWNPPEGASSNCSIMYFSHFQDKKXIADETRRI 65
QY 86 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLNLSYMKCSW 145
DB 66 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLNLSYMKCSW 125
QY 146 LPGNTSPDNTNYTLTYWHRSLKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 205
DB 126 LPGNTSPDNTNYTLTYWHRSLKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 185
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVOMENPQNFISRCLFYEVEVNN 265
DB 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLYVOMENPQNFISRCLFYEVEVNN 245
QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 325
DB 246 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 305
QY 326 WSNWSQEMSIGKKRNST 342
DB 306 WSNWSQEMSIGKKRNST 322

Search completed: July 8, 2006, 01:24:54
Job time : 199 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:25:13 ; Search time 41 Seconds

(without alignments)
999,716 Million cell updates/sec

Title: US-09-051-843D-4

Sequence: 1 MEMPARLCGMALLLCAGGG.....QTKETDSVVLIENTKRAQ 426

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR 80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	10.1	426	2 JC7773	IL-13Ralpha 1 prot
2	10	2.3	201	2 C40040	alternative splici
3	10	2.3	201	2 S26404	alternative splici
4	10	2.3	248	2 A40040	alternative splici
5	10	2.3	272	2 T02745	nucleic acid bindi
6	10	2.3	285	2 S69312	probable membrane
7	10	2.3	292	2 B40040	alternative splici
8	10	2.3	331	2 A36358	T-cell acute lymph
9	10	2.3	405	2 T29167	hypothetical prote
10	10	2.3	465	2 G02738	transcription fact
11	10	2.3	479	1 A41753	transcription fact
12	10	2.3	864	2 A48266	transcription fact
13	10	2.3	888	2 I58378	tyrosine kinase -
14	10	2.3	1433	2 A46053	bullous pemphigoid
15	10	2.3	1621	2 T30200	protein-tyrosine k
16	9	2.1	102	2 D71415	hypothetical prote
17	9	2.1	115	2 B84676	60S acidic ribosom
18	9	2.1	151	2 S43296	bone morphogenetic
19	9	2.1	199	2 T49450	hypothetical prote
20	9	2.1	201	2 J01094	hypothetical 20.2k
21	9	2.1	206	2 I53066	gene M-twist prote
22	9	2.1	211	2 T04098	CBP20 preproteol
23	9	2.1	212	2 T49559	related to prolina
24	9	2.1	212	2 A83680	spore germination
25	9	2.1	221	2 T04592	glycine-rich cell
26	9	2.1	238	2 T05344	hypothetical prote
27	9	2.1	253	2 A31444	homeotic protein U
28	9	2.1	255	2 B84777	hypothetical prote
29	9	2.1	256	2 T03571	glycine-rich prote

30	9	2.1	257	2 B84346	hypothetical prote
31	9	2.1	258	2 T13591	tail fiber adhesin
32	9	2.1	260	2 S00276	tail fiber protein
33	9	2.1	262	1 TLBPM1	tail fiber protein
34	9	2.1	263	2 A34466	calpain (EC 3.4.22
35	9	2.1	266	1 CTPGL	calpain (EC 3.4.22
36	9	2.1	267	1 CIRBL	calpain (EC 3.4.22
37	9	2.1	267	1 CTPGP	calpain (EC 3.4.22
38	9	2.1	268	1 CIHUL	calpain (EC 3.4.22
39	9	2.1	268	1 S09860	hypothetical prote
40	9	2.1	273	1 TVZMMB	anthocyanin biosyn
41	9	2.1	291	1 S31415	glycine-rich prote
42	9	2.1	301	2 B31219	collagen 2 - Caeno
43	9	2.1	307	2 T27609	hypothetical prote
44	9	2.1	311	2 T02783	probable homeotic
45	9	2.1	315	2 T41868	hypothetical prote

ALIGNMENTS

RESULT 1

JC7773
IL-13Ralpha 1 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: JC7773
R/Proct: C; Beniguel, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A/Title: Expression of a functional IL-13Ralpha1 by rat B cells.
A/Reference number: JC7773; PMID:11573960
A/Accession: JC7773
A/Molecule type: mRNA
A/Residues: 1-426 <PIR>
A/Cross-references: UNIPROT:Q8VHC2; UNIPARC:UP1000017CC49; GB:AY044251
C/Comment: This protein is an functionally binding protein involved in B cell prolifera
C/Genetics:
A/Gene: IL-13Ralpha1

Query Match

Best Local Similarity 100.0%; Score 43; DB 2; Length 426;
Matches 43; Conservative 0; Pred. No. 2e-35; Indels 0; Gaps 0;

QY 365 YLRKLIIPPIPDGKIFKEMFGQNDTLFMKKYDIYEKQ 407
DB 365 YLRKLIIPPIPDGKIFKEMFGQNDTLFMKKYDIYEKQ 407

RESULT 2

C40040
alternative splicing factor ASF-3 - human
C/Species: Homo sapiens (man)
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 05-Oct-2004
C/Accession: C40040
R/Ge: H.; Zuo, P.; Manley, J. L.
Cell 66, 373-382, 1991
A/Title: Primary structure of the human splicing factor ASF reveals similarities with D
A/Reference number: A40040; M01D:91309149; PMID:1855257
A/Accession: C40040
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-201 <GEA>
A/Cross-references: UNIPROT:Q07955; UNIPARC:UP1000017A383; GB:M72709
F;17-81/Domain: ribonucleoprotein repeat homology <RNM1>
F;122-182/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match

Best Local Similarity 2.3%; Score 10; DB 2; Length 201;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
DB 99 GGGGGGGGAP 108

RESULT 3
S26404
alternative splicing factor ASF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C:Accession: S26404
R:Tracke, R.; Boned, A.; Goridis, C.
Nucleic Acids Res. 20, 5482, 1992
A>Title: ASF alternative transcripts are highly conserved between mouse and man.
A:Reference number: S26404; PMID:93065226; PMID:1437571
A:Accession: S26404
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-201 <TAC>
A:Cross-references: UNIPARC:UP100000EB65E; EMBL:X66091
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1992
F:12-81/Domain: ribonucleoprotein repeat homology <RRM1>
F:12-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 2.3%; Score 10; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
|||||
DB 99 GGGGGGGGAP 108

RESULT 4
A40040
alternative splicing factor ASF-1 - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
C:Accession: A40040; B40041
R:Ge, H.; Zuo, P.; Manley, J.L.
Cell 66, 373-382, 1991
A>Title: Primary structure of the human splicing factor ASF reveals similarities with D
A:Reference number: A40040; PMID:91309149; PMID:1855257
A:Accession: A40040
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-248 <EBA>
A:Cross-references: UNIPROT:Q07955; UNIPARC:UP10000001220; GB:M72709; NID:g179073; PIDN:
R:Krainer, A.R.; Mayeda, A.; Kozak, D.; Bins, G.
Cell 66, 383-394, 1991
A>Title: Functional expression of cloned human splicing factor SF2: homology to RNA-bind
A:Reference number: A40041; PMID:91309150; PMID:1830244
A:Accession: B40041
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-248 <KRA>
A:Cross-references: UNIPARC:UP10000001220; GB:M69040; NID:g338046; PIDN:AAA03476.1; PID:
F:17-81/Domain: ribonucleoprotein repeat homology <RRM1>
F:12-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 2.3%; Score 10; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
|||||
DB 99 GGGGGGGGAP 108

RESULT 5
T02745
nucleic acid binding protein - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C:Accession: T02745; T02718
R:Yoon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.

submitted to the EMBL Data Library, February 1998
A:Description: The rice genome contains at least two different genes encoding nucleic a
A:Reference number: Z14712
A:Accession: T02745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <YOO>
A:Cross-references: UNIPROT:Q49228; UNIPARC:UP100000ABD51; EMBL:AF047428; NID:g4091116;
A:Experimental source: strain Ilpoombyeo
R:Yoon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.
submitted to the EMBL Data Library, January 1998
A:Description: Cloning and molecular characterization of nucleic acid binding protein g
A:Reference number: Z14705
A:Accession: T02718
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-181,183-272 <Y02>
A:Cross-references: UNIPARC:UP100000ABE67; EMBL:AF045571; NID:g2854124; PID:g2854125
A:Experimental source: strain Ilpoombyeo
C:Superfamily: Putative PHD-type Nucleic acid binding protein

Query Match 2.3%; Score 10; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
|||||
DB 15 GGGGGGGGAP 24

RESULT 6
S69312
probable membrane protein YLR38w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L8300.13-a
C:Species: Saccharomyces cerevisiae
C:Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: S69312
R:Du, Z.
submitted to the EMBL Data Library, January 1994
A:Description: The sequence of S. cerevisiae cosmid 8300.
A:Reference number: S69312
A:Accession: S69312
A:Molecule type: DNA
A:Residues: 1-288 <U02>
A:Cross-references: UNIPROT:Q94084; UNIPARC:UP1000006ABEE; EMBL:U19028; NID:g609380; PII
C:Keywords: transmembrane protein
F:142-158/Domain: transmembrane #status predicted <TM1>
F:201-217/Domain: transmembrane #status predicted <TM2>

Query Match 2.3%; Score 10; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGA 26
|||||
DB 240 AGGGGGGGA 249

RESULT 7
B40040
alternative splicing factor ASF-2 - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
C:Accession: B40040
R:Ge, H.; Zuo, P.; Manley, J.L.
Cell 66, 373-382, 1991
A>Title: Primary structure of the human splicing factor ASF reveals similarities with D
A:Reference number: A40040; PMID:91309149; PMID:1855257
A:Accession: B40040

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:21:52 ; Search time 299 Seconds
(without alignments)
1317.915 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426

Sequence: 1 MEWPARLCGLWALLCAGG.....QTKETDSVVLNKKASQ 426

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	94.1	427	1 I13R1_HUMAN	P78552 homo sapien
2	401	94.1	427	2 Q96BB4_HUMAN	Q96BB4 homo sapien
3	401	94.1	427	2 Q5JSL4_HUMAN	Q5JSL4 homo sapien
4	300	70.4	426	2 Q59EG2_HUMAN	Q59EG2 homo sapien
5	251	58.9	279	2 Q9UDY5_HUMAN	Q9UDY5 homo sapien
6	144	33.8	409	2 Q7YRV5_MACFA	Q7YRV5 macaca fasc
7	91	21.4	226	2 Q6ZW70_HUMAN	Q6ZW70 homo sapien
8	65	15.3	401	2 Q6U6T1_SHEEP	Q6U6T1 ovis aries
9	62	14.6	423	2 Q863Z6_PIG	Q863Z6 sus scrofa
10	43	10.1	252	2 Q8VDP7_MOUSE	Q8VDP7 mus musculus
11	43	10.1	424	1 I13R1_MOUSE	Q09030 mus musculus
12	43	10.1	424	2 Q8C1Z3_MOUSE	Q8C1Z3 mus musculus
13	43	10.1	426	2 Q561K3_RAT	Q561K3 rattus norv
14	43	10.1	426	2 Q8VHC2_RAT	Q8VHC2 rattus norv
15	40	9.4	424	2 Q8ENM4_MOUSE	Q8ENM4 mus musculus
16	37	8.7	349	2 Q97597_BOVIN	Q97597 bos taurus
17	37	8.7	405	2 Q951F1_CANFA	Q951F1 canis famil
18	26	6.1	399	2 Q3UPQ9_MOUSE	Q3UPQ9 mus musculus
19	11	2.6	307	2 Q3V913_9SPHN	Q3V913 sphingopyxi
20	11	2.6	444	2 Q76472_MUSDO	Q76472 musca domes
21	11	2.6	457	2 Q7G604_ORYSA	Q7G604 oryza sativ
22	11	2.6	1000	2 Q5JKR1_ORYSA	Q5JKR1 oryza sativ
23	11	2.6	1226	1 M1B_DROME	Q5JXR1 drosophila
24	10	2.3	51	2 Q5N8N0_ORYSA	Q5N8N0 oryza sativ
25	10	2.3	157	2 Q7XNH1_ORYSA	Q7XNH1 oryza sativ
26	10	2.3	170	2 Q6H5T9_ORYSA	Q6H5T9 oryza sativ
27	10	2.3	175	2 Q6AVT7_ORYSA	Q6AVT7 oryza sativ
28	10	2.3	191	2 Q5TQU2_ANOGA	Q5TQU2 anopheles g
29	10	2.3	224	2 Q6Z541_ORYSA	Q6Z541 oryza sativ
30	10	2.3	233	2 Q59FA2_HUMAN	Q59FA2 homo sapien
31	10	2.3	244	2 Q7XUT6_ORYSA	Q7XUT6 oryza sativ

RESULT 1

I13R1_HUMAN
ID I13R1_HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q95646; Q99656;
DT 01-NOV-1997, integrated into UniprotKB/Swiss-Prot.
DT 01-MAY-1997, sequence version 1.
DT 07-MAR-2006, entry version 50.
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).
GN Name=IL13RA1; Synonyms=IL13R, IL13RA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7; RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., Ferrara P.;
RA "Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";
FEBS Lett. 401:163-166(1997).
RL NUCLEOTIDE SEQUENCE [MRNA].
RA Gauchat J.F.M., Schlagenhaut E., Feng N.P., Moser R., Yamage M., Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL [3]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265; RA Anan M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;
RT "CDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";
J. Biol. Chem. 271:29265-29270(1996).
RL [4]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

ALIGNMENTS

32 10 2.3 245 1 SF1L1_BRARE
33 10 2.3 247 1 SFRS1_HUMAN
34 10 2.3 247 1 SFRS1_MOUSE
35 10 2.3 247 1 SFRS1_PONPY
36 10 2.3 248 2 Q3YLA6_PIG
37 10 2.3 248 2 Q3UCH2_MOUSE
38 10 2.3 253 2 Q7KR12_DROME
39 10 2.3 256 1 SFRS1_CHICK
40 10 2.3 267 1 SFRS1_XENTR
41 10 2.3 271 2 O49216_ORYSA
42 10 2.3 272 2 O49228_ORYSA
43 10 2.3 272 2 Q7F2Z1_ORYSA
44 10 2.3 274 2 O6H7A7_ORYSA
45 10 2.3 283 2 Q7SFQ1_NEUCR

Q7exp4 brachydanio
Q07955 homo sapien
Q6pdm2 mus musculus
Q5r7h2 pongo pygma
Q3yla6 sus scrofa
Q3uch2 mus musculus
Q7kr12 drosophila
Q3zml3 gallus gall
Q6dl12 xenopus tro
Q49216 oryza sativ
Q49228 oryza sativ
Q7f2z1 oryza sativ
O6h7a7 oryza sativ
Q7sfq1 neurospora

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
 CC can form a functional receptor for IL13. Also serves as an
 CC alternate accessory protein to the common cytokine receptor gamma
 CC chain for IL4 signaling, but cannot replace the function of gamma
 CC C in allowing enhanced IL2 binding activity.
 CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
 CC and possibly other components.
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -!- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
 CC skeletal muscle and ovary; lowest levels in brain, lung and
 CC kidney. Also found in B-cells, T-cells and endothelial cells.
 CC -!- DOMAIN: The WSXS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
 CC subfamily.

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 CC EMBL; Y10659; CAA71669.1; -; mRNA.
 DR EMBL; Y09328; CAA70508.1; -; mRNA.
 DR EMBL; U62858; AAB37127.1; -; mRNA.
 DR EMBL; U81379; AAD00510.3; -; mRNA.
 DR EMBL; BC009960; AAH09960.1; -; mRNA.
 DR Ensembl; ENSG00000131724; Homo sapiens.
 DR H-InvDB; HIX0017008; -;
 DR HGNC; HGNC:5974; IL13RA1.
 DR MIM; 300119; gene.
 DR GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR002996; Cytok rcpt B/G.
 DR InterPro; IPR003532; Hempt_rcpt_S_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 427
 FT Interleukin-13 receptor alpha-1 chain.
 FT /FTID=PRO_000010939.
 FT TOPO_DOM 22 343
 FT Extracellular (Potential).
 FT TRANSMEM 344 367
 FT Potential.
 FT TOPO_DOM 368 427
 FT Cytoplasmic (Potential).
 FT MOTIF 327 331
 FT WSXS motif.
 FT MOTIF 374 382
 FT Box 1 motif.
 FT CARBOHYD 37 37
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 61 61
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 105 105
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 138 138
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 157 157
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 235 235
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 265 265
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 293 293
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 329 329
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 341 341
 FT N-linked (GlcNAc. .) (Potential).
 FT DISULFID 46 95
 FT Potential.
 FT DISULFID 134 144
 FT By similarity.
 FT DISULFID 173 185
 FT By similarity.

FT CONFLICT 130 130 T -> I (in Ref. 3).
 FT CONFLICT 358 358 G -> D (in Ref. 3).
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3E8F554107B CRC64;
 Query Match 94.1%; Score 401; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 APTETOPVTNLSVSVENLCTVIWTNPPEGSSNCSLWYFHFHFGDKQDKKIAPETRSI 85
 DB 27 APTETQPPVTNLSVSVENLCTVIWTNPPEGSSNCSLWYFHFHFGDKQDKKIAPETRSI 86
 QY 86 EVPLNERICLVGSOCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 145
 DB 87 EVPLNERICLVGSOCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146
 QY 146 LPGRNTSPDTNLTLYYHRSLEKIHQCENIPREGQYFGCSFDLTKVKDSSPQHSVQIMV 205
 DB 147 LPGRNTSPDTNLTLYYHRSLEKIHQCENIPREGQYFGCSFDLTKVKDSSPQHSVQIMV 206
 QY 206 KDNAGKIKPSPNIVELTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 265
 DB 207 KDNAGKIKPSPNIVELTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 266
 QY 266 SQTETHNVFYVQEAACENPEPERNVENTSCFMPVGVLPDPLTNTVIRVKTNKLCEYEDDKL 325
 DB 267 SQTETHNVFYVQEAACENPEPERNVENTSCFMPVGVLPDPLTNTVIRVKTNKLCEYEDDKL 326
 QY 326 WSNNSQEMSGIKKRNTSLIYTMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIDPGKIKP 385
 DB 327 WSNNSQEMSGIKKRNTSLIYTMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIDPGKIKP 386
 QY 386 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLNIENLKKASQ 426
 DB 387 EMFGQNDTTLHWKDYDIYEKQTEEDTSVVLNIENLKKASQ 427

RESULT 2

Q96BB4 HUMAN
 ID Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.
 AC Q96BB4; Q8WX08;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 21-FEB-2006, entry version 23.
 DE Interleukin 13 receptor, alpha 1, .
 GN Name=IL13RA1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

```
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -1- DOMAIN: The WSXS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC -----
CC EMBL; BC015768; AA15768.1; -; mRNA.
CC Ensembl; ENSG00000131724; Homo sapiens.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC InterPro; IPR002996; Cytokn_rcpt_B/G.
CC InterPro; IPR003532; Hempt_rcpt_S_F2.
CC PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
CC Receptor; Transmembrane.
CC KW SEQUENCE 427 AA; 48677 MW; E6A42F7466A3A09 CRC64;
CC -----
Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFQKQDKKIAPETRRSI 85
DB 27 APETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFQKQDKKIAPETRRSI 86
QY 86 EYPLNERICLVQVGSQCSSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 145
DB 87 EYPLNERICLVQVGSQCSSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMV 205
DB 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMV 206
QY 206 KDNAGKIKPSFNIPLTSRVKDPDPPIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 265
DB 207 KDNAGKIKPSFNIPLTSRVKDPDPPIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
QY 266 SQTETHNVFYVQEAKECFERFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 325
DB 267 SQTETHNVFYVQEAKECFERFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 326
QY 326 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLIYKELKIIIPPPDPGKIFK 385
DB 327 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLIYKELKIIIPPPDPGKIFK 386
QY 386 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 426
DB 387 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 427
RESULT 3
QSUSL4 HUMAN
ID Q5JSI4_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5JSI4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1; ORFNames=RP13-12804.2-001;
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -1- DOMAIN: The WSXS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC -----
CC EMBL; AL391280; CA141410.1; -; Genomic DNA.
CC Ensembl; ENSG00000131724; Homo sapiens.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC InterPro; IPR002996; Cytokn_rcpt_B/G.
CC InterPro; IPR003532; Hempt_rcpt_S_F2.
CC PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
CC Receptor; Transmembrane.
CC KW SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
CC -----
Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFQKQDKKIAPETRRSI 85
DB 27 APETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFQKQDKKIAPETRRSI 86
QY 86 EYPLNERICLVQVGSQCSSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 145
DB 87 EYPLNERICLVQVGSQCSSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMV 205
DB 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTVKVDSSEFQHSVQIMV 206
QY 206 KDNAGKIKPSFNIPLTSRVKDPDPPIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 265
DB 207 KDNAGKIKPSFNIPLTSRVKDPDPPIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
QY 266 SQTETHNVFYVQEAKECFERFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 325
DB 267 SQTETHNVFYVQEAKECFERFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 326
QY 326 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLIYKELKIIIPPPDPGKIFK 385
DB 327 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLIYKELKIIIPPPDPGKIFK 386
QY 386 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 426
DB 387 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 427
RESULT 4
QS9EG2 HUMAN
ID Q59EG2_HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue-Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC
CC EMBL; AB209849; BAD93086.1; -; mRNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn_rcpt_B/G.
DR InterPro; IPR003532; Hempt_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;

Query Match 70.4%; Score 300; DB 2; Length 426;
Best Local Similarity 99.8%; Pred. No. 2.3e-291;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 APTEQPPVTNLVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRRSI 85
DB 26 APTEQPPVTNLVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRRSI 85

QY 86 EYPLNERICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145
DB 86 EYPLNERICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145

QY 146 LPGRNTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLTVKVQSSPFQHSVQIMV 205
DB 146 LPGRNTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLTVKVQSSPFQHSVQIMV 205

QY 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCCLFYEVVNN 265
DB 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCCLFYEVVNN 265

QY 266 SQTETHNVFYVQEAECENPEFERNVENTSCFVMPVGLPDTLNTVIRVTKNLCYEDDKL 325
DB 266 SQTETHNVFYVQEAECENPEFERNVENTSCFVMPVGLPDTLNTVIRVTKNLCYEDDKL 325

QY 326 WSNWQEMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKIIIPPPIDPGKIPK 385
DB 326 WSNWQEMSIGKRNSTLYITMLLIVPVIVAGAILVLLYLKRLKIIIPPPIDPGKIPK 385

QY 386 EMFGQNDTTLHWKYDYIEKOTKETSDSVLIENLKQASQ 426
DB 386 EMFGQNDTTLHWKYDYIEKOTKETSDSVLIENLKQASQ 426

RESULT 5
Q9UDY5 HUMAN
ID Q9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 21-FEB-2006, entry version 26.
DE Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha 1).
GN Name=IL13RA1; ORFNames=RP13-12804.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein (By similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; U81380; AAD00511.2; -; mRNA.
DR EMBL; AL391280; CA141409.1; -; Genomic DNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn_rcpt_B/G.
DR InterPro; IPR003532; Hempt_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;

Query Match 58.9%; Score 251; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-242;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTEQPPVTNLVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRRSI 85
DB 26 APTEQPPVTNLVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRRSI 85

QY 86 EYPLNERICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145
DB 86 EYPLNERICLVGSGCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145

QY 146 LPGRNTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLTVKVQSSPFQHSVQIMV 205
DB 146 LPGRNTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLTVKVQSSPFQHSVQIMV 205

QY 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCCLFYEVVNN 265
DB 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCCLFYEVVNN 265

QY 266 SQTETHNVFYV 276
DB 266 SQTETHNVFYV 277

RESULT 6
Q7YRV5 MACFA
ID Q7YRV5_MACFA PRELIMINARY; PRT; 409 AA.
AC Q7YRV5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13RA1;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;

```

RN NUCLEOTIDE SEQUENCE.
RP Maccarone P., Drinkwater C.C., Nash A.D.;
RA "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY312267; AAP78901.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytln rcpt B/G.
DR InterPro; IPR003532; Hemot_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON TER 1 1
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 33.8%; Score 144; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 5.4e-135;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 NPFFERNVENTSCFVPGVLPDILNTVIRVTKNKLCYEDDKLWSNWSQEMSIGKKNST 342
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 266 NPFFERNVENTSCFVPGVLPDILNTVIRVTKNKLCYEDDKLWSNWSQEMSIGKKNST 325

QY 343 LYITMLLIVPVIVAGAILVLLYLKRLIIFFPPDPGKIFKEMFGDQNDTLLHWKKYD 402
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 326 LYITMLLIVPVIVAGAILVLLYLKRLIIFFPPDPGKIFKEMFGDQNDTLLHWKKYD 385

QY 403 IYEQTKTEETSDSVLIENLKASQ 426
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 386 IYEQTKTEETSDSVLIENLKASQ 409

RESULT 7
Q62W70 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q62W70;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE CDNA FLJ41521 fis, clone BRHA2012980, moderately similar to
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (IL-13RA-1) (IL-13RA-1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Tissue=Thalamus;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AK123515; BAC85635.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 226 AA; 24825 MW; 0CBB9208934F18DF CRC64;

```

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Query Match 21.4%; Score 91; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.2e-82;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GKRNSTLYITMLLIVPVIVAGAILVLLYLKRLIIFFPPDPGKIFKEMFGDQNDT 395
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 136 GKRNSTLYITMLLIVPVIVAGAILVLLYLKRLIIFFPPDPGKIFKEMFGDQNDT 195

QY 396 LHWKKYDIYEQTKTEETSDSVLIENLKASQ 426
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 196 LHWKKYDIYEQTKTEETSDSVLIENLKASQ 226

RESULT 8
Q6U6T1 SHEEP PRELIMINARY; PRT; 401 AA.
AC Q6U6T1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Interleukin 13 receptor alpha 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN NUCLEOTIDE SEQUENCE.
RP Maccarone P., Drinkwater C.C., Nash A.D.;
RA "Cloning of the sheep interleukin 13 receptor alpha 1 cDNA.";
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC -----
DR EMBL; AY377582; AA083584.1; -; mRNA.
DR DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytln rcpt B/G.
DR InterPro; IPR003532; Hemot_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN <1 401 interleukin 13 receptor alpha 1.
FT NON TER 1 1
SQ SEQUENCE 401 AA; 45834 MW; 4E7AD6162BD42B25 CRC64;

Query Match 15.3%; Score 65; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.3e-56;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 IVLLLYLKRLLIIFFPPDPGKIFKEMFGDQNDTLLHWKKYDIYEQTKTEETSDSVLIE 419
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 335 IVLLLYLKRLLIIFFPPDPGKIFKEMFGDQNDTLLHWKKYDIYEQTKTEETSDSVLIE 394

QY 420 NLKKA 424
DB |||||
DB 395 NLKKA 399

RESULT 9
Q863Z6 PIG PRELIMINARY; PRT; 423 AA.
AC Q863Z6;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 14.
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.

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OX NCBI_TaxID=9823;
RN [1]_NUCLEOTIDE SEQUENCE.
RP PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RX Zarlenga D.S., Dawson H., Kringel H., Solano-Aguilar G.,
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
RT 1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and
RT Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234 (2004).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -!- DOMAIN: The WXXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -----
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CC -----
CC EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn rcpt B/G.
DR InterPro; IPR003532; Hempt rcpt S_F2.
DR PROSITE; PS01356; HEMATOPOIETIN_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 47985 MW; EA636PB6BCA533D9 CRC64;

Query Match 14.6%; Score 62; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 8.8e-53;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 358 AIIIVLLYLKRLIIFFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQTSVVL 417
Db |||||
355 AIIIVLLYLKRLIIFFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQTSVVL 414

OY 418 IE 419
Db ||
415 IE 416

RESULT 10
Q8VDP7 MOUSE
ID Q8VDP7; MOUSE PRELIMINARY; PRT; 252 AA.
AC Q8VDP7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE IL13ral protein (Fragment).
GN Name=Il13ral;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; BC021472; AAH21472.1; -; mRNA.
DR Ensembl; ENSMUSG0000017057; Mus musculus.
DR MGI; MGI:105052; Il13ral.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0016021; C:integral to membrane; RCA.
FT NON_TER 1
SQ SEQUENCE 252 AA; 29044 MW; E303CF276C7A5E81 CRC64;

Query Match 10.1%; Score 43; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 YLKRLKIIFFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQ 407
Db |||||
191 YLKRLKIIFFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQ 233

RESULT 11
I13R1 MOUSE
ID I13R1; MOUSE STANDARD; PRT; 424 AA.
AC O09030; Q7TT27;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1997, sequence version 1.
DT 07-MAR-2006, entry version 52.
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
DE 13RA-1) (Interleukin-13-binding protein) (NR4) (CD213a1 antigen).
GN Name=Il13ral; Synonyms=Il13r, Il13ra,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
RT 13 receptor that is also a component of the interleukin 4 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
 CC can form a functional receptor for IL13. Also serves as an
 CC alternate accessory protein to the common cytokine receptor gamma
 CC chain for IL4 signaling, but cannot replace the function of gamma
 CC in allowing enhanced IL2 binding activity (By similarity).
 CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
 CC and possibly other components (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -!- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
 CC testis, stomach, brain, skin, and colon; but not skeletal muscle.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
 CC subfamily.
 CC
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 CC
 CC EMBL: S80963; AAB50695.1; -; mRNA.
 CC EMBL: BC052425; AAH52425.2; -; mRNA.
 CC EMBL: BC058939; AAH58939.1; -; mRNA.
 CC Ensembl: ENSMUSG0000017057; Mus musculus.
 CC MGI: MGI:105052; Il13ral.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC InterPro: IPR002986; Cytok_rcpt_B/G.
 CC InterPro: IPR003532; Hempt_rcpt_S_F2.
 CC PROSITE: PS01356; HEMATOPOI_REC_SF2; 1.
 KW Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.
 FT /FTID:PRO_0000010940.
 FT TOPO_DOM 26 340 Extracellular (Potential).
 FT TRANSMEM 341 364 Potential.
 FT TOPO_DOM 365 424 Cytoplasmic (Potential).
 FT MOTIF 324 328 WSXWS motif.
 FT MOTIF 371 379 Box 1 motif.
 FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 338 338 N-linked (GlcNAc...) (Potential).
 FT DISULFID 44 93 Potential.
 FT DISULFID 132 142 By similarity.
 FT DISULFID 171 183 By similarity.
 SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;
 Query Match 10.1%; Score 43; DB 1; Length 424;
 Best Local Similarity 100.0%; Pred. No. 9.8e-34;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 365 YLRLKLIIFPIPPDGKIFKEMFGDQNDTLHWKXYDIYEKQ 407
 Db 363 YLRLKLIIFPIPPDGKIFKEMFGDQNDTLHWKXYDIYEKQ 405
 RESULT 12
 Q8C123 MOUSE PRELIMINARY; PRT; 424 AA.
 ID Q8C123_MOUSE
 AC Q8C123;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 21-FEB-2006, entry version 22.
 DE Colon RCB-0549 C1e-H3 cDNA, RIKEN full-length enriched library.
 DE clone:G430044I06 product:interleukin 13 receptor, alpha 1, full insert
 DE sequence.
 GN Name=Il13ral; (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidin V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guncicich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Takt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammaja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tonaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Inamuro K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: July 8, 2006, 01:31:52 ; Search time 21 seconds
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Title: US-09-051-843D-4

Perfect score: 426

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Gapop 60.0 , Gapext 60.0

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Word size : 1

Total number of hits satisfying chosen parameters: 112925

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA New.*

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- 4: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	4.0	17	7	US-11-134-871-727
2	10	2.3	25	7	US-11-134-871-3230
3	10	2.3	175	6	US-10-449-902-33914
4	10	2.3	176	6	US-10-449-902-32626
5	10	2.3	274	6	US-10-449-902-43265
6	10	2.3	285	6	US-10-449-902-51966
7	10	2.3	538	6	US-10-449-902-51820
8	10	2.3	623	6	US-10-449-902-56221
9	10	2.3	1493	6	US-10-511-814-18
10	9	2.1	29	7	US-11-134-871-2683
11	9	2.1	35	6	US-10-449-902-34876
12	9	2.1	96	6	US-10-953-349-14842
13	9	2.1	98	6	US-10-953-349-9576
14	9	2.1	99	6	US-10-953-349-9575
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17	9	2.1	125	6	US-10-449-902-47247
18	9	2.1	139	6	US-10-953-349-27506
19	9	2.1	139	6	US-10-449-902-34201
20	9	2.1	146	6	US-10-449-902-35115
21	9	2.1	159	6	US-10-449-902-56503
22	9	2.1	170	6	US-10-449-902-30189
23	9	2.1	173	6	US-10-449-902-50881
24	9	2.1	183	6	US-10-449-902-42575
25	9	2.1	185	6	US-10-449-902-34633

26	9	2.1	186	6	US-10-449-902-42360	Sequence 42360, A
27	9	2.1	189	6	US-10-449-902-42125	Sequence 42125, A
28	9	2.1	191	6	US-10-449-902-43679	Sequence 43679, A
29	9	2.1	196	6	US-10-449-902-34401	Sequence 34401, A
30	9	2.1	204	6	US-10-449-902-49137	Sequence 49137, A
31	9	2.1	208	6	US-10-449-902-40257	Sequence 40257, A
32	9	2.1	222	6	US-10-449-902-32123	Sequence 32123, A
33	9	2.1	227	6	US-10-449-902-28912	Sequence 28912, A
34	9	2.1	230	6	US-10-449-902-56230	Sequence 56230, A
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36	9	2.1	244	6	US-10-449-902-42341	Sequence 42341, A
37	9	2.1	246	6	US-10-449-902-54590	Sequence 54590, A
38	9	2.1	248	6	US-10-449-902-49085	Sequence 49085, A
39	9	2.1	257	6	US-10-953-349-38261	Sequence 38261, A
40	9	2.1	265	6	US-10-449-902-37490	Sequence 37490, A
41	9	2.1	269	7	US-11-234-731-617	Sequence 617, App
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ALIGNMENTS

RESULT 1
US-11-134-871-727
; Sequence 727, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aehersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 727
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-727

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Best Local Similarity 100.0%; Pred. No. 7.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 RNTSPDNTYLYWHRS 165
DB 1 RNTSPDNTYLYWHRS 17

RESULT 2
US-11-134-871-3230
; Sequence 3230, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aehersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3230

; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3230

Query Match 2.3%; Score 10; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26
Db 10 AGGGGGGGGA 19
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RESULT 3
US-10-449-902-33914
; Sequence 33914, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33914
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33914

Query Match 2.3%; Score 10; DB 6; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26
Db 19 AGGGGGGGGA 28
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RESULT 4
US-10-449-902-32626
; Sequence 32626, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32626
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32626

Query Match 2.3%; Score 10; DB 6; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
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RESULT 5
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; Sequence 43265, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
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; LENGTH: 274
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43265

Query Match 2.3%; Score 10; DB 6; Length 274;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26
Db 46 AGGGGGGGGA 55
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US-10-449-902-51966
; Sequence 51966, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51966
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51966

Query Match 2.3%; Score 10; DB 6; Length 285;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-09-051-843D-4

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Word size : 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	22	5.2	22	2	US-09-028-937-25
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21	10	2.3	1593	2	US-08-628-829-4
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28	9	2.1	29	2	US-09-270-767-53673	Sequence 53673, A
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31	9	2.1	36	2	US-09-428-082B-349	Sequence 349, App
32	9	2.1	36	2	US-09-428-082B-354	Sequence 354, App
33	9	2.1	36	2	US-09-428-082B-355	Sequence 355, App
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36	9	2.1	36	2	US-09-422-838C-12	Sequence 12, App1
37	9	2.1	36	2	US-09-422-838C-13	Sequence 13, App1
38	9	2.1	36	2	US-09-422-838C-21	Sequence 21, App1
39	9	2.1	36	2	US-09-422-838C-24	Sequence 24, App1
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41	9	2.1	36	2	US-09-422-838C-27	Sequence 27, App1
42	9	2.1	36	2	US-09-422-838C-28	Sequence 28, App1
43	9	2.1	36	2	US-09-422-838C-29	Sequence 29, App1
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45	9	2.1	38	2	US-09-428-082B-351	Sequence 351, App

ALIGNMENTS

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RESULT 1
US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicols, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jitan
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PM6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PM7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PM2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MEMPARICGIMALLCAGGCGGGGAGTETQPPYTNLSVSEVULCTYIWMNPEEGASSN 60
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DB      61 CSLMYSHFEDKODKXIAPETRSIEVPLNERICLOVSGCSTNESKPSILVEKCTSP 120
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QY      241 DLVYQENPNQNFISRCIFVEVEVNSQTEHTHVFYQEAECNPEFERNVENTSCFVAVPG 300
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Db 301 VLPDNTNVRIRKTKMLCYEDDKLWNSWQEMSIGKRNSTLYITMLLIVPIVAGAIL 360
QY 361 VLLLYLKRKLIIFFPIPDGKIFKEMFGDQNDTLHWKXYDIYEKQTEETDSVVLLEN 420
Db 361 VLLLYLKRKLIIFFPIPDGKIFKEMFGDQNDTLHWKXYDIYEKQTEETDSVVLLEN 420
QY 421 LKXASQ 426
Db 421 LKXASQ 426

RESULT 2

US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTEPOPVTNLSVSEVNLCTVIWTNPPREGASSNSCLWYFSGDKODKRIAPETRRSI 85
Db 27 APTEPOPVTNLSVSEVNLCTVIWTNPPREGASSNSCLWYFSGDKODKRIAPETRRSI 86
QY 86 EYPLNRIQLQVSGQSTNESEKPSILVEKCIAPPREGDPEASATVLEQCIWHNLSYMKCSW 145
Db 87 EYPLNRIQLQVSGQSTNESEKPSILVEKCIAPPREGDPEASATVLEQCIWHNLSYMKCSW 146
QY 146 LFGRLTSPDTNVTLYYWHNSLEKIHQECENIFREGQYFGCSFDLTKYKXSSFEQHSVQIMV 205

|||||
Db 147 LFGRLTSPDTNVTLYYWHNSLEKIHQECENIFREGQYFGCSFDLTKYKXSSFEQHSVQIMV 206
QY 206 KDNAGIKDPSFNVLPTLSRVKPPPHIKNLSPFNDDLQVQWENPQNFISRLCFYEEVWNS 265
Db 207 KDNAGIKDPSFNVLPTLSRVKPPPHIKNLSPFNDDLQVQWENPQNFISRLCFYEEVWNS 266
QY 266 SQTEHNVFYVOEAKCENPEFERVENTSCFVWPVGVLPTLNTNVRIRKTKMLCYEDDKL 325
Db 267 SQTEHNVFYVOEAKCENPEFERVENTSCFVWPVGVLPTLNTNVRIRKTKMLCYEDDKL 326
QY 326 WSNWQEMSIGKRNSTLYITMLLIVPIVAGAILVLLYLKRKLIIFFPIPDGKIFK 385
Db 327 WSNWQEMSIGKRNSTLYITMLLIVPIVAGAILVLLYLKRKLIIFFPIPDGKIFK 386
QY 386 EMFGDQNDTLHWKXYDIYEKQTEETDSVVLLENLKKASQ 426
Db 387 EMFGDQNDTLHWKXYDIYEKQTEETDSVVLLENLKKASQ 427

RESULT 3

US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTEPOPVTNLSVSEVNLCTVIWTNPPREGASSNSCLWYFSGDKODKRIAPETRRSI 85
Db 27 APTEPOPVTNLSVSEVNLCTVIWTNPPREGASSNSCLWYFSGDKODKRIAPETRRSI 86

QY 86 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 145
DB 87 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 146
QY 146 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 205
DB 147 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 266
QY 266 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 325
DB 267 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 326
QY 326 WSNWSQEMSIGKKNSTLYITMLIVPVIYAGAIIVLLYKRLKIIIFPPIPDGKIFK 385
DB 327 WSNWSQEMSIGKKNSTLYITMLIVPVIYAGAIIVLLYKRLKIIIFPPIPDGKIFK 386
QY 386 EMFGDQNDDTLHMKKYDIYEKQTEETDSVVLINLKKASQ 426
DB 387 EMFGDQNDDTLHMKKYDIYEKQTEETDSVVLINLKKASQ 427

RESULT 4
US-09-949-016-6094
Sequence 6094, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6094
LENGTH: 427
TYPE: PRT
ORGANISM: Human
US-09-949-016-6094

Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPTNLSVSVENLCTVITWNPPEGASNSCLWYFSHRGDKKXIAETRSI 85
DB 27 APTETOPPTNLSVSVENLCTVITWNPPEGASNSCLWYFSHRGDKKXIAETRSI 86
QY 86 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 145
DB 87 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 146
QY 146 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 205
DB 147 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 266
QY 266 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 325

DB 267 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 326
QY 326 WSNWSQEMSIGKKNSTLYITMLIVPVIYAGAIIVLLYKRLKIIIFPPIPDGKIFK 385
DB 327 WSNWSQEMSIGKKNSTLYITMLIVPVIYAGAIIVLLYKRLKIIIFPPIPDGKIFK 386
QY 386 EMFGDQNDDTLHMKKYDIYEKQTEETDSVVLINLKKASQ 426
DB 387 EMFGDQNDDTLHMKKYDIYEKQTEETDSVVLINLKKASQ 427

RESULT 5
US-09-825-561A-82
Sequence 82, Application US/09825561A
Patent No. 6775319
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6775319ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825, 561A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 82
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match 74.4%; Score 317; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 5,4e-310;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPTNLSVSVENLCTVITWNPPEGASNSCLWYFSHRGDKKXIAETRSI 85
DB 6 APTETOPPTNLSVSVENLCTVITWNPPEGASNSCLWYFSHRGDKKXIAETRSI 65
QY 86 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 145
DB 66 EVPLNERICLVGSGCSTNESEKPSILVEKCIISPBGDPESAVTELQCIWHNLSYMKCSW 125
QY 146 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 205
DB 126 LRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYFGCSFDLTKVXDSFEQHSVOIMV 185
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 265
DB 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLTVQWENPONTISRLCFYEVEVNN 245
QY 266 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 325
DB 246 SÖTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDITNTVIRIKVTKNKLCEYEDKL 305
QY 326 WSNWSQEMSIGKKNST 342
DB 306 WSNWSQEMSIGKKNST 322

RESULT 6
US-09-313-942-30
Sequence 30, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.

```

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30
```

```

Query Match      74.4%; Score 317; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 26 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||||||
DB 239 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 298
    |||||||
QY 86 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 145
    |||||||
DB 299 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 358
    |||||||
QY 146 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 205
    |||||||
DB 359 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 418
    |||||||
QY 206 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 265
    |||||||
DB 419 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 478
    |||||||
QY 266 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 325
    |||||||
DB 479 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 538
    |||||||
QY 326 WSNWSQEMSIGKKRNST 342
    |||||||
DB 539 WSNWSQEMSIGKKRNST 555
    |||||||
```

```

RESULT 7
US-10-282-162-30
; Sequence 30, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30
```

```

Query Match      74.4%; Score 317; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 26 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||||||
DB 239 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 298
    |||||||
QY 86 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 145
    |||||||
DB 299 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 358
    |||||||
QY 146 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 205
    |||||||
DB 359 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 418
    |||||||
QY 206 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 265
    |||||||
DB 419 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 478
    |||||||
QY 266 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 325
    |||||||
DB 479 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 538
    |||||||
QY 326 WSNWSQEMSIGKKRNST 342
    |||||||
DB 539 WSNWSQEMSIGKKRNST 555
    |||||||
```

```

RESULT 8
US-09-313-942-32
; Sequence 32, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32
```

```

Query Match      74.4%; Score 317; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 26 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||||||
DB 27 APTETQPPVTNLVSVEENLCTVITWNNPPEGASSNCSLMYFSGHGDKODKXIAPETRRSI 86
    |||||||
QY 86 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 145
    |||||||
DB 87 EVPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDESAVTELOCIWHNLSYMKCSW 146
    |||||||
QY 146 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 205
    |||||||
DB 147 LPERNTSPDTNVTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTKYKDSFEQHSVOIMV 206
    |||||||
QY 206 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 265
    |||||||
DB 207 KDNAGKIKPSFNIIVPLTSRKVPDPPIKXLSFHNDDLTYQWENPQNFISCLFEYEVANN 266
    |||||||
QY 266 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 325
    |||||||
DB 267 SOTETHNVFYVOAKCENPEFERNVENTSCFMVPGVLPDLTAVTRIRVKTNKLCEYEDDKL 326
    |||||||
QY 326 WSNWSQEMSIGKKRNST 342
    |||||||
```

Db 327 WSNWSQEMSIGKKNST 343

RESULT 9
US-10-282-162-32

; Sequence 32, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

Query Match 74.4%; Score 317; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPTNLISVSVENLCVITWNPPEGASNSCLMTFHSFGDKQDKKIAPETRSI 85
Db 27 APETOPPTNLISVSVENLCVITWNPPEGASNSCLMTFHSFGDKQDKKIAPETRSI 86
QY 86 EPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW 145
Db 87 EPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW 146
QY 146 LPRNTSPDNTNLYLWYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVQIMV 205
Db 147 LPRNTSPDNTNLYLWYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVQIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNTISCLFEYEVVNN 265
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNTISCLFEYEVVNN 266
QY 266 SQTETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTLNTVRIKTKNKLCEYEDDKL 325
Db 267 SQTETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTLNTVRIKTKNKLCEYEDDKL 326
QY 326 WSNWSQEMSIGKKNST 342
Db 327 WSNWSQEMSIGKKNST 343

RESULT 10
US-09-949-016-8550

; Sequence 8550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8550

Query Match 54.2%; Score 231; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e-223;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 KIAPETRSIEVPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELQCIW 135
Db 1 KIAPETRSIEVPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELQCIW 60
QY 136 HNLSTYMKCSWLPGRNTSPDNTNLYLWYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDS 195
Db 61 HNLSTYMKCSWLPGRNTSPDNTNLYLWYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDS 120
QY 196 FEQHSVQIMWKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNTISR 255
Db 121 FEQHSVQIMWKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNTISR 180
QY 256 CLFEYEVVNNSTQETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTL 306
Db 181 CLFEYEVVNNSTQETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTL 231

RESULT 11
US-09-688-286D-2

; Sequence 2, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willison, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, J'ian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding sam
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-286D-2

Query Match 10.1%; Score 43; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 YLRLKILIFPPIPDDGKIFKEMFGQNDTTLWKKYDIYEKO 407
Db 363 YLRLKILIFPPIPDDGKIFKEMFGQNDTTLWKKYDIYEKO 405

RESULT 12

US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.

APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 405
TYPE: PRT
ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 LLLYLRKLIIPPIPPDKIFKEMFGDONDDTLHM 398
Db 341 LLLYLRKLIIPPIPPDKIFKEMFGDONDDTLHM 377

RESULT 13
US-09-028-937-25
Sequence 25, Application US/09028937
Patent No. 6333031
GENERAL INFORMATION:
APPLICANT: Oleson, Lemart
TITLE OF INVENTION: Receptor Derived Peptides As Modulators
TITLE OF INVENTION: Of Receptor Activity
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleht, Hobdach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,937
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/788,820
FILING DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,999
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-028-937-25

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 KODKIAPEPTRRSIEVPLNERI 93
Db 1 KODKIAPEPTRRSIEVPLNERI 22

RESULT 14
US-09-949-016-8825
Sequence 8825, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8825
LENGTH: 289
TYPE: PRT
ORGANISM: Human
US-09-949-016-8825

Query Match
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27
Db 140 GGGGGGGGAP 149

RESULT 15
US-09-949-016-6323
Sequence 6323, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6323
LENGTH: 331
TYPE: PRT
ORGANISM: Human
US-09-949-016-6323

Query Match
2.3%; Score 10; DB 2; Length 331;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:30:58 ; Search time 188 Seconds
(Without alignments)
1049.625 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 426
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Published Applications_AA_Main:*

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- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	401	94.1	427	4	US-10-671-697-9	Sequence 9, Appl1
2	401	94.1	427	6	US-11-067-251-3	Sequence 3, Appl1
3	401	94.1	427	6	US-11-185-330-4	Sequence 4, Appl1
4	401	94.1	427	6	US-11-182-384A-4	Sequence 4, Appl1
5	401	94.1	427	6	US-11-183-599A-4	Sequence 4, Appl1
6	401	94.1	427	6	US-11-149-309-37	Sequence 3, Appl1
7	331	77.7	427	5	US-10-850-270-4	Sequence 4, Appl1
8	317	74.4	322	3	US-09-825-561A-82	Sequence 82, Appl1
9	317	74.4	322	5	US-10-872-087-82	Sequence 82, Appl1
10	317	74.4	664	5	US-10-850-270-10	Sequence 10, Appl1
11	317	74.4	776	3	US-09-935-868-36	Sequence 36, Appl1
12	317	74.4	780	3	US-09-935-868-34	Sequence 36, Appl1
13	317	74.4	784	3	US-09-313-942-30	Sequence 30, Appl1
14	317	74.4	784	3	US-09-935-868-30	Sequence 30, Appl1
15	317	74.4	784	4	US-10-287-035-30	Sequence 30, Appl1
16	317	74.4	784	4	US-10-282-162-30	Sequence 30, Appl1
17	317	74.4	784	6	US-11-134-114-30	Sequence 30, Appl1
18	317	74.4	783	3	US-09-313-942-32	Sequence 32, Appl1
19	317	74.4	783	3	US-09-935-868-32	Sequence 32, Appl1
20	317	74.4	783	4	US-10-287-035-32	Sequence 32, Appl1
21	317	74.4	783	4	US-10-282-162-32	Sequence 32, Appl1
22	317	74.4	783	6	US-11-134-114-32	Sequence 32, Appl1
23	313	73.5	776	4	US-10-287-035-40	Sequence 40, Appl1
24	311	73.0	776	4	US-10-287-035-34	Sequence 34, Appl1
25	297	69.7	776	3	US-09-935-868-40	Sequence 40, Appl1
26	297	69.7	776	3	US-09-935-868-44	Sequence 44, Appl1
27	297	69.7	776	6	US-11-067-251-8	Sequence 8, Appl1

28	297	69.7	776	6	US-11-067-251-10	Sequence 10, Appl1
29	297	69.7	776	6	US-11-067-251-12	Sequence 12, Appl1
30	297	69.7	776	6	US-11-067-251-14	Sequence 14, Appl1
31	297	69.7	776	6	US-11-067-251-16	Sequence 16, Appl1
32	297	69.7	778	3	US-09-935-868-46	Sequence 46, Appl1
33	297	69.7	778	3	US-09-935-868-50	Sequence 50, Appl1
34	297	69.7	778	4	US-10-287-035-46	Sequence 46, Appl1
35	297	69.7	778	4	US-10-287-035-50	Sequence 50, Appl1
36	297	69.7	778	4	US-10-287-035-56	Sequence 56, Appl1
37	297	69.7	778	4	US-10-287-035-60	Sequence 60, Appl1
38	297	69.7	780	3	US-09-935-868-38	Sequence 38, Appl1
39	297	69.7	780	3	US-09-935-868-42	Sequence 42, Appl1
40	297	69.7	782	3	US-09-935-868-48	Sequence 48, Appl1
41	297	69.7	782	3	US-10-287-035-52	Sequence 52, Appl1
42	293	68.8	776	4	US-10-287-035-36	Sequence 36, Appl1
43	293	68.8	776	4	US-10-287-035-44	Sequence 44, Appl1
44	291	68.3	780	4	US-10-287-035-38	Sequence 38, Appl1
45	291	68.3	780	4	US-10-287-035-42	Sequence 42, Appl1

ALIGNMENTS

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RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/671,697
FILING DATE: 29-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/545,002
FILING DATE: 06-APR-2000
APPLICATION NUMBER: US 08/969,125
FILING DATE: 12-NOV-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9
Query Match 94.1%; Score 401; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETOPVNLIVSVENLCTVITWNPFGASNGSLWYFSHRGDDKDKIAETPRSI 85
Db 27 APTETOPVNLIVSVENLCTVITWNPFGASNGSLWYFSHRGDDKDKIAETPRSI 86
QY 86 EVPLNERICLQVSGQSTNESEKPSILVERKISPPGDPESAVTELOCIWHNLNYSKCSW 145
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Db      87 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 146
      146 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 205
      147 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 206
Qy      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 265
      207 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 266
Qy      266 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
      267 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 326
Db      326 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 385
      327 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 386
Qy      386 EMFGQNDDTLHWKXYDIYEKQTKETSDSVLIENLKKASQ 426
      387 EMFGQNDDTLHWKXYDIYEKQTKETSDSVLIENLKKASQ 427
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RESULT 2
US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastaSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3
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Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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      27 APTEQPPVTNLSVSVENLCITVITWNNPPEGASSNCSLWFSHFQKODKKIAPETRRSI 86
Db      86 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 145
      87 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 146
Qy      146 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 205
      147 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 206
Db      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 265
      207 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 266
Qy      266 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
      267 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 326
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Qy      326 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 385
      327 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 386
Db      386 EMFGQNDDTLHWKXYDIYEKQTKETSDSVLIENLKKASQ 426
      387 EMFGQNDDTLHWKXYDIYEKQTKETSDSVLIENLKKASQ 427
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RESULT 3
US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vito, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4
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Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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      27 APTEQPPVTNLSVSVENLCITVITWNNPPEGASSNCSLWFSHFQKODKKIAPETRRSI 86
Db      86 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 145
      87 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 146
Qy      146 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 205
      147 LRGRTNSPDTNYTLTYWHSLSLEKIHOCENIFREGQYFGCSFDLTJKVDSFEQHSVQIYW 206
Db      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 265
      207 KUNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLTYQWENPQNFISRCLEFYEEVANN 266
Qy      266 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
      267 SOTETHNVFYVOAKACENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 326
Db      326 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 385
      327 WSNWSQEMSIGKKRNSTLYITMLLIYPVIVAGAIIVLLLYLKRKLIIPPIPDGKIFK 386
Qy      386 EMFGQNDDTLHWKXYDIYEKQTKETSDSVLIENLKKASQ 426
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RESULT 4
US-11-182-384A-4
; Sequence 4, Application US/11182384A
; Publication No. US20060035855A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
```

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; APPLICANT: Laurent, Patrick
; APPLICANT: Vltá, Natallio
; TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
; FILE REFERENCE: IVD924 US Div 2
; CURRENT APPLICATION NUMBER: US/11/182,384A
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 09/077,817
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-384A-4

Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPVNLSVSVENLCTVITWNPPEGASNCSLMTFSHGDKQDKKIAPETRSI 85
DB 27 APTETOPPVNLSVSVENLCTVITWNPPEGASNCSLMTFSHGDKQDKKIAPETRSI 86
QY 86 EVPLNERICLVQSGQSTNESEKPSILVEKCIISPEDGPSAVTELQCIWHNLSYMKCSW 145
DB 87 EVPLNERICLVQSGQSTNESEKPSILVEKCIISPEDGPSAVTELQCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTNLTLYYHRSLEKIHQECNIFREGQYGCSPDLTKVDSSEQHSVQIMV 205
DB 147 LPRGNTSPDNTNLTLYYHRSLEKIHQECNIFREGQYGCSPDLTKVDSSEQHSVQIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRKPDPPHKNLSFHNDLIYVQWENPQNFISRCLEFEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRKPDPPHKNLSFHNDLIYVQWENPQNFISRCLEFEVEVNN 266
QY 266 SÖTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 325
DB 267 SÖTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 326
QY 326 WSNWSQEMSGIKRNSLTLYTMLLIYVIVAGAIIVLLLYKRLKIIIFPIPDGKIFK 365
DB 327 WSNWSQEMSGIKRNSLTLYTMLLIYVIVAGAIIVLLLYKRLKIIIFPIPDGKIFK 366
QY 366 EMFGDQNDDTLHMKKYDIYEKÖTKEETDSVLLIENLKKAQ 426
DB 387 EMFGDQNDDTLHMKKYDIYEKÖTKEETDSVLLIENLKKAQ 427

RESULT 5
US-11-183-599A-4
; Sequence 4, Application US/11183599A
; Publication No. US20060035856A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vltá, Natallio
; TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
; FILE REFERENCE: IVD924 US Div 1
; CURRENT APPLICATION NUMBER: US/11/183,599A
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 09/077,817
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-183-599A-4

Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPVNLSVSVENLCTVITWNPPEGASNCSLMTFSHGDKQDKKIAPETRSI 85
DB 27 APTETOPPVNLSVSVENLCTVITWNPPEGASNCSLMTFSHGDKQDKKIAPETRSI 86
QY 86 EVPLNERICLVQSGQSTNESEKPSILVEKCIISPEDGPSAVTELQCIWHNLSYMKCSW 145
DB 87 EVPLNERICLVQSGQSTNESEKPSILVEKCIISPEDGPSAVTELQCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTNLTLYYHRSLEKIHQECNIFREGQYGCSPDLTKVDSSEQHSVQIMV 205
DB 147 LPRGNTSPDNTNLTLYYHRSLEKIHQECNIFREGQYGCSPDLTKVDSSEQHSVQIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRKPDPPHKNLSFHNDLIYVQWENPQNFISRCLEFEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRKPDPPHKNLSFHNDLIYVQWENPQNFISRCLEFEVEVNN 266
QY 266 SÖTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 325
DB 267 SÖTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 326
QY 326 WSNWSQEMSGIKRNSLTLYTMLLIYVIVAGAIIVLLLYKRLKIIIFPIPDGKIFK 365
DB 327 WSNWSQEMSGIKRNSLTLYTMLLIYVIVAGAIIVLLLYKRLKIIIFPIPDGKIFK 366
QY 366 EMFGDQNDDTLHMKKYDIYEKÖTKEETDSVLLIENLKKAQ 426
DB 387 EMFGDQNDDTLHMKKYDIYEKÖTKEETDSVLLIENLKKAQ 427

RESULT 6
US-11-149-309-37
; Sequence 37, Application US/11149309
; Publication No. US20060063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasaiian, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertnida M.
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Donaldson, Debora D.
; APPLICANT: Lin, Laura Long
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepui
; APPLICANT: Feyfiant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
; APPLICANT: Widom, Angela M.
; APPLICANT: Parris, Kevin D.
; APPLICANT: Goldman, Samuel J.
; TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
; FILE REFERENCE: 16156-048001 / AM101493
; CURRENT APPLICATION NUMBER: US/11/149,309
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/578,473
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/581,375
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/578,736
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-149-309-37
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Query Match 94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 85
DB 27 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 86
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 145
DB 87 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 146
QY 146 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205
DB 147 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 206
QY 206 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 265
DB 207 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 266
QY 266 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 325
DB 267 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPVIAGAIIYLLLYLKRKLIIPPIPDGKIFK 385
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPVIAGAIIYLLLYLKRKLIIPPIPDGKIFK 386
QY 386 EMFGDNDTLMWKKYDIYKQKRETDSTVLIENLKKASQ 426
DB 387 EMFGDNDTLMWKKYDIYKQKRETDSTVLIENLKKASQ 427

RESULT 7
US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/ECJ
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
US-10-850-270-4

Query Match 77.7%; Score 331; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 36-302;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 85
DB 27 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 86
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 145
DB 87 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 146
QY 146 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205

DB 147 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 206
QY 206 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 265
DB 207 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 266
QY 266 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 325
DB 267 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 326
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPVIYA 356
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPVIYA 357

RESULT 8
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match 74.4%; Score 317; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 3-5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 85
DB 6 APTETQPPVTNLSVSVENICTVIWNNPPGASSNCSLMYFSHFGDKODKKIAPETRRS1 65
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 145
DB 66 EYPLNERICLQVGSQOSTNESEKPSILVEKCIAPPEGDPSAATELOCIWHNLSYMKCSW 125
QY 146 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205
DB 126 LFGRTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 185
QY 206 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 265
DB 207 KDNAGKIKPSFNIIVPLTSRKPDPPHINKLSFHNDLLYQWENPQNFISRCLEFEVEVNN 266
QY 266 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 325
DB 246 SOTETHNVFYVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCEYEDDKL 305
QY 326 WSNWSQEMSIGKKRNST 342
DB 306 WSNWSQEMSIGKKRNST 322

RESULT 9

```
US-10-872-087-82
; Sequence 82, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1
; CURRENT APPLICATION NUMBER: US/10/872,087
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/825,561
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-82

Query Match          74.4%; Score 317; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 3,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 85
DB 6 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 65
QY 86 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 145
DB 66 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 125
QY 146 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 126 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 185
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNTISRCLFYEVAVNN 265
DB 186 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNTISRCLFYEVAVNN 245
QY 266 SQETHNHVFYVQAKCENPEFERNVENTSCEFVPGVLPDITLVIRIVKTNKLCYEDDKL 325
DB 246 SQETHNHVFYVQAKCENPEFERNVENTSCEFVPGVLPDITLVIRIVKTNKLCYEDDKL 305
QY 326 WSNWSQEMSIGKKRNST 342
DB 306 WSNWSQEMSIGKKRNST 322

RESULT 10
US-10-850-270-10
; Sequence 10, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 1215890/BJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
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; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 664
; TYPE: PRT
; ORGANISM: human
US-10-850-270-10

Query Match          74.4%; Score 317; DB 5; Length 664;
Best Local Similarity 100.0%; Pred. No. 6,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 85
DB 45 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 104
QY 86 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 145
DB 105 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 164
QY 146 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 165 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 224
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNTISRCLFYEVAVNN 265
DB 225 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNTISRCLFYEVAVNN 284
QY 266 SQETHNHVFYVQAKCENPEFERNVENTSCEFVPGVLPDITLVIRIVKTNKLCYEDDKL 325
DB 285 SQETHNHVFYVQAKCENPEFERNVENTSCEFVPGVLPDITLVIRIVKTNKLCYEDDKL 344
QY 326 WSNWSQEMSIGKKRNST 342
DB 345 WSNWSQEMSIGKKRNST 361

RESULT 11
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneration Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36

Query Match          74.4%; Score 317; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 7,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 85
DB 232 APETOPPVNTLSVSVENLCTVIWTPNPPGASSNCSLMYFSHFGDKODKKIAPETRRSI 291
QY 86 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 145
DB 292 EVPLNERICLOVGSQOSTNSEKPSILVEKCISSPEEDPSAVTELOCIWHNLSYMKCSW 351
QY 146 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 352 LPRNTSPDNTNLTLYWHRSLKTIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 411
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QY 146 LPERNTSPDTNYTLVYWHRSLEKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 205
 Db 359 LPERNTSPDTNYTLVYWHRSLEKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 418
 QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLIVQWENPQNFTSRCLFYEVEVNN 265
 Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLIVQWENPQNFTSRCLFYEVEVNN 478
 QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 325
 Db 479 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 538
 QY 326 WSNWSQEMSIGKKRNST 342
 Db 539 WSNWSQEMSIGKKRNST 555

Db 539 WSNWSQEMSIGKKRNST 555
 Search completed: July 8, 2006, 01:34:51
 Job time : 189 secs

RESULT 15
 US-10-287-035-30
 ; Sequence 30, Application US/10287035
 ; Publication No. US20030104567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neil Stahl and George D. Yancopoulos
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203DA
 ; CURRENT APPLICATION NUMBER: US//10/287,035
 ; PRIOR FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: USSN 09/935,868
 ; PRIOR FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: USSN 09/787,835
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: USSN 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 784
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-287-035-30

Query Match 74.4%; Score 317; DB 4; Length 784;
 Best Local Similarity 100.0%; Pred. No. 7.5e-289;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLVSVENICTVITWTNMPREGASSNCSLWFSHFQDKODKKIAPETRSI 85
 Db 239 APTETQPPVTNLVSVENICTVITWTNMPREGASSNCSLWFSHFQDKODKKIAPETRSI 298
 QY 86 EYPLNERICLOVSSQCSSTNESSEKPSILVEKISPPREGDPESAVTELOCIMHNLSTYMKCSW 145
 Db 299 EYPLNERICLOVSSQCSSTNESSEKPSILVEKISPPREGDPESAVTELOCIMHNLSTYMKCSW 358
 QY 146 LPERNTSPDTNYTLVYWHRSLEKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 205
 Db 359 LPERNTSPDTNYTLVYWHRSLEKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 418
 QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLIVQWENPQNFTSRCLFYEVEVNN 265
 Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLIVQWENPQNFTSRCLFYEVEVNN 478
 QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 325
 Db 479 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 538
 QY 326 WSNWSQEMSIGKKRNST 342

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